ÇUKUROVA UNIVERSITY
INSTITUTE OF NATURAL AND APPLIED SCIENCES

Ph.D. THESIS

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DEPARTMENT OF SOIL SCIENCE AND PLANT NUTRITION

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ABSTRACT

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Sweet sorghum (*Sorghum bicolor* var. s*accharatum* (L.) Mohlenbr) can be used as bioenergy crop for either biomass or sugar and bio-ethanol yield. A total of 16 sweet sorghum genotypes were screened under filed and greenhouse conditions. Field work was set up in Adana and Şanlıurfa locations during year 2016 and 2017. Greenhous study was concluded with same 16 the sweet sorghum genotypes on Adana (Menzilat) and Şanlıurfa (Harran) soils. For both experiment plant shoot and root growth parameters such as C and N concentration in soil and plant tissue and also root mycorrhizal colonization were determined.

The field experiment results shown that under different climate and geographical regions diverse sorghum genotypes increased plant growth parameters and sequestrated carbon to soil. After harvest plant growth parameters such as plant height, dry weight, root parameters, root colonization and plant tissue C and N concentration were found to be divers with both locations. In greenhouse experiment results shown that indigenous mycorrhizal fungi have the capability to improve yields and plant nutrient supply compare to non-inoculated genotypes. Indigenous mycorrhizae may help to increase C and N concentrations in plant tissue of sweet sorghum genotypes.

Our findings confirm that indigenous mycorrhizae can improve sweet sorghum productivity through C and N balance. Thus, indigenous mycorrhizae have the potential to increase C input in sweet sorghum genotypes.

Key words: Genotype, Sorghum**,** Soil type, Carbon budget, AMF symbiosis association, CO_2.

ÖZ

DOKTORA TEZİ

TARLA VE SERA KOŞULLARINDA TATLI SORGUM (*SORGHUM BİCOLOR VAR. SACCHARATUM (L.)* MOHLENBR.) GENOTİPLERİNİN KARBON TUTMA KAPASİTESİ ÜZERİNE MİKORİZA VE KÖK GELİŞİMİNİN ETKİLERİ

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Tatlı sorgum (*Sorgum bicolor* var. s*accharatum* (L.) Mohlenbr) hem biokütle hem şeker içeriği ile biyoenerji bitkisi olarak kullanılmaktadır. Araştırma, tarla ve sera koşullarında olmak üzere iki farklı aşamalı olarak yürütülmüştür. Araştırmada 16 farklı tatlı sorgum genotipi materyali kullanılmıştır. Tarla denemeleri, Türkiye'nin güneyinde yer alan Adana ve Şanlıurfa gibi iki farklı lokasyonunda 2016 ve 2017 yıllarında yürütülmüştür. Sera çalışmasında aynı genotipler Çukurova ve Harran serisi topraklarına doğal mikoriza mantarları sporları aşılaması ile gerçekleştirmiştir. Araştırmada mikoriza uygulanan ve uygulanmayan topraklarda yetiştirilen sorgum gentoiplerinin mikorizal kök enfeksiyonu ve bitki dokularında C-N dinamiği üzerine etkileri incelenmiştir.

Araştırma bulguları Türkiye'nin farklı iklim ve toprak koşullarında farklı sorgum genotiplerinin biokütle verimine ve toprağa C bağlamak için iyi birer kaynak olduğu anlaşılmıştır. Tarla denemesi bitkileri hasat sonrası sürgün ve kök kuru ağırlıkları, bitki boyu, bitki çapı, kök enfeksiyonu, mikorizal bağımlılık, bitki dokularında karbon (C) ve azot (N) analizleri gerçekleştirilmiştir. Her iki bölgede, farklı sorgum genotiplerinin Türkiye'deki mevcut (doğal) sorgum genotiplerinden daha verimli olduğunu göstermektedir. Sere koşullarında doğal mikoriza uygulamasının bitki kuru madde verimi ve besin elementi alımını artırdığı belirlenmiştir. Doğal mikoriza uygulaması her iki toprakta yetiştirilen sorgum genotiplerinin bitki dokusundaki C ve N konsantrasyonlarını artırdığı belirlenmiştir. Bulgularımız, doğal mikoriza uygulamasının bitki ve toprakta C ve N dengesi yoluyla tatlı sorgum verimliliğini artırabildiğini doğrulamaktadır. Bu nedenle, doğal mikorizalar tatlı sorgum genotiplerinde C alımını artırma potansiyeline sahiptirler.

Anahtar kelimeler: Genotip, sorgum, Toprak tipi, Karbon bütçesi, Mikorizal simbiyosis, CO_2.

EXTENDED ABSTRACT

Field Experiments: The response of sweet sorghum (*Sorghum bicolor* var. *saccharatum* (L.) Mohlenbr.) genotypes to root traits and relation with soil carbon (C) pool under two different soil and climate conditions were not well understood. Biomass yield exhibited non-significant differences among genotypes. A total of 16 sweet sorghum genotypes were screened in two separates locations like Adana and Şanlıurfa of Turkey in the year 2016 and 2017. The aims of this studies were to characterize and compare root biomass and root traits of the sweet sorghum genotypes at field condition and to estimate their C input to into soil. In contrast, significant differences were observed in between Adana and Şanlıurfa locations in term of biomass yield. The shoot dry weight of the genotypes varies from 29.1 Mg ha^{-1} to 49.2 Mg ha^{-1} and 31.3 Mg ha^{-1} to 65.0 Mg ha^{-1} in the year 2016 and 2017 respectively in Adana location. The shoot dry weight varies 30.0 Mg ha^{-1} to 42.8 Mg ha^{-1} and 31.7 Mg ha^{-1} to 54.5 Mg ha^{-1} in the year 2016 and 2017 respectively in Şanliurfa location. Roots and shoots were analyzed for C concentration and CO_2 was calculated. Root samples were collected through monolith root sampling techniques. Root morphological characteristics like root surface area and root volume were differed between locations as well as locations × genotypes interactions. Root surface area varies from 423.800 to 887.800 m^2 ha^{-1} in Mediterranean soil and 339.100 to 579.600 m^2 ha^{-1} for Harran soil. All sweet sorghum genotypes inputs root and shoot C as well as CO_2 higher in Çukurova than Harran soil. Root C input varies from 140 to 386 Mg ha^{-1} in Çukurova soil and 112 to 224 Mg ha^{-1} for Harran soil. A greater diversity of root traits was found on the sweet sorghum genotypes in term of plant biomass C inputs into the soil. However, compared to the sweet sorghum genotypes, their lower C input to soil needs to be recognized to ensure a balanced C budget. This study concluded that the sweet sorghum genotypes can be a good source of soil C sequestration under different climatic conditions of Turkey.

Greenhouse Experiment: Arbuscular mycorrhizal fungi (AMF) have the capability to improve crop yields by increasing plant nutrient supply. It is less known whether indigenous mycorrhizae enhance carbon (C) and nitrogen (N) up take by sweet sorghum or not. Therefore, a study was conducted in a greenhouse at the University of Çukurova, Department of Soil Science and Plant Nutrition, Adana, Turkey, to investigate the effects of indigenous mycorrhizae inoculums which were collected at rhizosphere soil sweet sorghum genotypes growth response, root colonization, C and N uptake and carbon dioxide fixation in plant tissue under sterile soil conditions. Upon harvest, the data collected included shoot and root dry weights, plant height, plant diameters, root colonization, mycorrhizal dependency, tissue C and N concentration of the sweet sorghum genotypes. Indigenous mycorrhizal inoculated sweet sorghum genotypes had more plant biomass than non-mycorrhizal plants. Indigenous mycorrhizae assisted to increase soil C sequestration. Bulk soil organic C was significantly ($p<0.05$) higher in mycorrhizae amended pot than non-mycorrhizae amended pot.

The shoot dry weight (SDW) was found 56.0 to 62.3 g pot^{-1} at mycorrhiza added treatment and 46.8 to 56.0 g pot^{-1} non-mycorrhizae added treatment in Adana soils. Similarly, the shoot biomass was found 56.0 to 90.0 g pot^{-1} for mycorrhiza added treatment and 37.7 to 58.7 g pot^{-1} for non-mycorrhiza added treatment in Şanlıurfa soils.

The shoot N% was higher in mycorrhizae amended soil than non-mycorrhizae amended soil in both of Adana and Şanlıurfa soils. Shoot N% varies from 2.08 to 3.89% in Adana soils and 1.80 to 2.42% in Şanlıurfa soils at mycorrhizae amended soil. Likewise, shoot N% varies from 1.80 to 2.37% in Adana soils and 1.73 to 2.43 in Şanlıurfa soils at non-mycorrhizae amended soil.

In general, shoot C% concentration was higher in mycorrhizae amended soil than non-mycorrhizae amended soil. Shoot C% were highly significant ($p<0.001$) between mycorrhizae and non-mycorrhizae amendment among genotypes and genotypes × treatments interaction. In the mycorrhizae amended soil, the shoot

C% concentration of sweet sorghum genotypes varies from 38.82 to 50.40% in Adana soils and 38.4 to 50.0% in Şanlıurfa soils. In the non-mycorrhizae amended soil C concentration varies from 36.1 to 43.0 % in Adana soils and 36.1 to 40.4% in Şanlıurfa soils. Total C uptake and CO_2 by sixteen sweet sorghum genotypes was highly significant on mycorrhizae as well as mycorrhizae × genotypes interactions.

Root colonization of the sweet sorghum genotypes varies from 30 to 65% in Adana soils and 30 to 70% in Şanlıurfa soil among the sweet sorghum genotypes. In Adana soil, the lowest root colonization was 30% for No91 sweet sorghum genotype and in Şanlıurfa soil, the lowest root colonization was30% for Williams sweet sorghum genotype. Likewise, the highest root colonization was 65% for Roma sweet sorghum and 70% for No5 sweet sorghum genotype in Adana and Şanlıurfa soils, respectively. Our findings confirmed that indigenous mycorrhizae can improve sweet sorghum productivity through C and N balance. Thus, indigenous mycorrhizae have the potential to increase C and N uptake among sweet sorghum genotypes. Also, indigenous mycorrhizal inoculation significantly fixed C and mitigated atmospheric CO_2 among the sorghum genotypes.

GENİŞLETİLMİŞ ÖZET

Tüm dünyada olduğu gibi ülkemizde de sanayiye hammadde sağlayan ormanlarımızın yer yer her geçen gün yok olması veya verimliliklerinin korunamaması nedeniyle, sanayide kullanılacak selülozik hammadde sıkıntısı yaşanmaktadır. Ayrıca, karbon yutak alanları olarak da bilinen ormanların, selülozik hammadde amaçlı olarak kullanılması nedeniyle orman vejetasyonun çıplak kalması sonucu, yer yüzeyinden atmosfere CO_2 salınımının artması doğrudan ve dolaylı yollardan küresel ısınmaya da neden olmaktadır. Diğer taraftan sanayide selülozik hammadde olarak kullanılacak alternatif hammadde bulma arayışları da özellikle daha fazla karbon fiksasyonu yapan bitki tür ve çeşitlerinin belirlenmesi ve üretilmesi konusundaki bilimsel çalışmalar devam etmektedir.

Özellikle son yıllarda artan sera gazları nedeniyle meydana gelen iklim değişikleri sonucu abiyotik koşullara (kuraklık, yüksek sıcaklık ve tuzlulaşma) toleranslı yeni bitki tür ve çeşitlerinin geliştirilmesi ayrıca önemli olmaktadır. Tatlı sorgumun kuraklığa ve sıcağa daha toleranslı olması ve çok amaçlı kullanılması (etanol, yem, gıda) nedeniyle, ileriki yıllarda üzerinde daha fazla durulması gereken en önemli bitki türlerinin başında gelmektedir.

Bunun yanı sıra, iklim değişiklikleri ile topyekûn mücadele etmek için çevreye zararlı olan fosil yakıtların enerji amaçlı kullanımındaki oranının azaltılması, bitki üzerinden toprakta karbon tutunma miktarının da fotosentez yolu ile tutulmasının artırılması da önemli olmaktadır. Yapılan hesaplamalara göre yanlış tarım-toprak yönetimi sonucu atmosfere salınan sera gazlarının atmosfere salınan sera gazlarının %14-25'ini oluşturduğu tahmin edilmektedir (NOAA 2015). Diğer taraftan atmosferde artan CO_2 miktarının seviyesinin düşürülmesinde teknolojik ve kültürel önlemler kadar tarımsal modellerin amaca uygun olarak yönetilmesi de önemsenmelidir.

Türkiye topraklarının genel olarak organik madde (OM) konsantrasyonu düşük olup, % 2'den daha düşük içerikte olan topraklarımızın oranı % 69 gibi

yüksek bir düzeydedir (Ülgen and Yurtsever 1988); Bunun en önemli nedenlerinden bir tanesi, Türkiye'nin coğrafi konumu ve iklim durumudur. Yarı kurak iklim koşullarının yüksek sıcaklık, kireç ve kili toprak yapısı altında ayrışmasının yüksek olması nedeniyle, OM konsantrasyonu genelde düşük kalmaktadır. Buna ek olarak geçmişten günümüze kadar bilinçsizce yapılan geleneksel tarım uygulamaları başta toprak işleme ve mono kültür bitkisel üretim ile toprakların devamlı sömürülmesi sonucu toprakların organik madde miktarının azalmasıdır. Yoğun toprak işleme sonucu toprakların yapısı bozulmakta ve organik madde miktarı yetersiz olan topraklar OM'nin oksitlenmesi sonucu hızlı bir şekilde verimsizleşmektedir. Bir diğer önemli neden ise ticari gübrelerin tarım toprakları üzerinde meydana getirdiği fiziksel ve çevresel sorunlar gösterilebilir. Kimyasal gübrelerin topraklardaki yaralı mikroorganizma popülasyonunu aktif durma getirdikleri ve bunun sonucu olarak toprak biyolojik verimliliğinin azaldığı ve bunun sonucunda bitkisel verimlilik ve kalitesi düşmektedir (Ortaş 2019).

Günümüzde gübre kullanımı özellikle de fosforlu gübre kullanımına karşın, cm kök uzunluğu başına 100'lerce m hif üreten mikorizanın (Ortas 1997) mantar miselleri yardımıyla bitkiye topraktan alımı yavaş ve zor olan besin elementlerin alımını kolaylaştırmaktadır. Doğada % 80-90'ın üzerindeki bitki türünün beslenme ve gelişimi için mikorizaya bağımlı oldukları bilinmektedir. Mikoriza ile bitki kökleri arasındaki karşılıklı simbiyotik ilişki, bitki gelişimini olumu yönde etkilemektedir.

Bitki kökleri ile mikoriza arasındaki karşılıklı simbiosis ilişki sonucu bitki köklerinde mikorizal enfeksiyon oluşmaktadır. İyi bir mikorizal enfeksiyonun gerçekleşmesi sonucu bitki sağlığı ve toprak kalitesinin geliştiği bildirilmektedir (Ortas ve ark. 2013). Mikorizanın bitki gelişimi ve kuru madde üzerindeki olumlu etkisinin karbon bağlama kapasiteni artıracağı beklenilmektedir.

Dünyada artan sera gazlarına bağlı olarak artan iklim değişimlerine karşın bilim dünyası fosil hidro-karbonlu yakıtlar yerine biyo-yakıt kullanımı gibi birçok alternatif enerji projelerini devreye sokmuştur. Tatlı sorgum gibi etanol potansiyeli yüksek türlerde etkin gentotiplerin seleksiyonu önemli bir strateji olarak önerilebilir. Bu bağlamda kullanılacak genotpilerin bitki gelişimi ve toprak karbon

tutulması üzerine de bitki kök gelişimi ve doğal mikorizanın etkinliğinin bilinmesi önemli bir tarımsal strateji ve yönetim modeli oluşturacağı düşünülmektedir. Bitki kök gelişiminin ve mikorizanın bitki gelişimi ve karbon bağlaması üzerindeki etkisinin bilinmesi ileriye yönelik sorgum genotiplerinin kullanımı ve ıslahı içinde ön bilgi oluşturabilir. Toprakta artan karbon bağlanmasının aynı zamanda doğrudan bitkilerin topraktaki su ve mineral elementlerden daha fazla yararlanma potansiyellerini de artıracağı beklenilmektedir. Bu bağlamda farklı sorgum genotiplerinin farklı ekolojik bölge koşullarında bitki kök gelişimi ve doğal mikorizal gelişimleri ile bitkide ve toprakta karbon tutma potansiyeli üzerine etkilerinin araştırılması günümüz iklim değişimi koşullarında büyük önem arz etmektedir.

Bu bağlamda iki farklı hipotezin test edilmesi hedeflenmiştir.

Hipotez 1: Farklı ekolojik bölge koşullarında farklı sorgum genotiplerinin karbon bağlama potansiyeli farklıdır.

Hipotez 2: Sorgum genotiplerinin gelişimlerinin farklılıkları mikorizal kök infeksiyonunun farklılığından kaynaklanıyor.

Hipotez 3: Sorgum genotiplerinin kök sistemleri farklılığı bitkinin karbon tutma potansiyelini etkilemektedir.

Proje kapsamında, tatlı sorgum genotiplerinin toprağa bırakmış oldukları organik karbon miktarının tespit edilmesinin yanı sıra, genotiplerin kök uzunluğu, yoğunluğu ve yüzey alanı gibi özellikleri de tespit edilerek, genotiplerin karbonu rizosferde ve bitki kökleri üzerinden toprağa aktarma potansiyelleri incelendi.

Projenin Amacı: Farklı ekolojik toprak koşulları altında tatlı sorgum genotiplerinin kök gelişimleri ve mikorizal infeksiyon oranlarının bitkilerin bio-kütle verimi ve toplam karbon bağlanma kapasitesi üzerine etkilerinin araştırılmasıdır. Bu amaca uygun olarak tarla ve sera koşullarında 16 farklı tatlı sorgum genotipinin ekimi yapıldı. Tarla koşullarında genotipler, 2 yıl süre ile taranarak sürdürüldü ve en etkin genotipler belirlenmeye çalışıldı. Ayrıca belirlenen genotipler sera koşullarında doğal mikorizaya bağımlılıkları ve mikorizanın karbon bağlama üzerine olan etkisi araştırılmıştır.

Tarla denemesi: Çalışmanın amacı, tarla koşullarında farklı tatlı sorgum genotiplerinin kök biokütlesi, kök özelliklerini karakterize etmek, kıyaslamak ve toprağa C girdisini tahmin etmektedir. Tatlı sorgumunun [*Sorghum bicolor* (L.) Moench] iki farklı iklim koşulunda kök özellikleri ve karbon bütçesine etkisi henüz tam olarak anlaşılmış değildir. Biokütle bakımından genotipler arasında dikkate değer bir fark görülmemektedir. 2016 ve 2017 yıllarında Türkiye'nin Adana ve Şanlıurfa gibi iki ayrı lokasyonunda toplam 16 tatlı sorgum genotipi tarandı. Araştırma bulguları beklenenin aksine biokütle verimi bakımından Adana ve Şanlıurfa arasında dikkate değer bir fark belirlenmiştir. Adana lokasyonunda 2016 yılında toprak üstü biyomas veriminin genotiplere göre değişmekle birlikte 29048 kg ha^{-1} ile 49.17 Mg ha^{-1} arasında , 2017 yılında ise 31.30 Mg ha^{-1} ila 65.01 Mg ha^{-1} arasında değiştiği saptanmıştır

Şanlıurfa lokasyonun da ise 2016 yılında toprak üstü biyomas veriminin genotiplere göre 29.96 Mg ha^{-1}ila 42.76 Mg ha^{-1} arasında değişim gösterirken, 2017 yılında 31.68 Mg ha^{-1} ila 54.50 Mg ha^{-1} arasında değişim göstermiştir. Bitki kök ve sürgünlerinin C içerikleri analiz edilerek tutulan CO_2 miktarı hesaplanmıştır. Bitki kökleri, monolit örnekleme tekniğine göre örneklenmiştir. Kök morfolojik özellikleri (kök yüzey alanı ve kök hacmi gibi) lokasyonlar ve lokasyon x genotip etkileşimlerine bağlı olarak farklılık göstermiştir. Kök yüzey alanı Akdeniz Bölgesi toprağında genotiplere bağlı olarak 423.800 ila 887.800 m^2 ha^{-1} arasında farklılık gösterirken Harran toprağında ise 339.100 ila 579.600 m^2 ha^{-1} arasında değişmiştir. Tüm tatlı sorgum genotiplerinde, Çukurova Bölgesinin Harran Bölgesinden daha yüksek CO_2 bağlamanın yanı sıra kök ve sürgün C tutumu da daha yüksek olduğu belirlenmiştir. Kök C konsantrasyonu Çukurova toprağında 140 ila 386 Mg ha^{-1} iken, Harran toprağı için 112 ila 224 Mg ha^{-1} arasında değişmiştir. Bununla birlikte, dengeli bir C bütçesi sağlamak için toprağa daha düşük C girdisinin uygulanması gerekmektedir. Bu çalışma, çeşitli tatlı sorgum genotiplerinin Türkiye'nin farklı iklim koşulları altında toprağa iyi bir C bağlama kaynağı olabileceği sonucuna varılmıştır.

Sere denemesi: Arbuscular mikorizalar (AM), bitki besin alımını artırarak bitki verimini arattırabilmektedir. Yerli (Doğal) mikorizaların tatlı sorgum

tarafından karbon (C) ve Azot (N) alımını artırıp artırmadığı henüz tam olarak anlaşılmış değildir. Bu nedenle, Adana, Çukurova Üniversitesi Toprak Bilimi ve Bitki Besleme Bölümü serasında, rizosfer toprağından toplanan doğal mikoriza aşılarının tatlı sorgum genotiplerinin gelişimi, steril toprak koşulları altında bitki dokusunda C ve N alımı, karbondioksit fiksasyonu ve kök kolonizasyonuna etkilerini araştırılması amacıyla bir çalışma yapılmıştır. Hasattan sonra, sürgün ve kök kuru ağırlıkları, bitki boyu, bitki çapları, kök kolonizasyonu, mikorizal bağımlılık, çeşitli tatlı sorgum genotiplerinin doku C ve N konsantrasyonları incelenmiştir. Doğal mikorizal aşılanmış tatlı sorgum genotipleri, mikorizasız bitkilerden daha fazla bitki biokütlesi oluşturmuştur. Doğal mikorizalar, toprak C tutulumunu artırmaya yardımcı olup mikoriza uygulanan saksılarda mikoriza uygulanmayan saksılara kıyasla toprak organik C değeri dikkate değer bir fark ($p < 0.05$) oluşturmuştur.

Sürgün kuru ağırlığı (SKA), Çukurova topraklarında mikoriza aşılanan saksılarda 56 ila 62.3 g saksı$^{-1}$ değişmekte iken mikorizasız saksılarda 46.8 ila 56 g saksı$^{-1}$ arasında değişmiştir. Benzer şekilde, Şanlıurfa topraklarında mikoriza aşılanan saksılarda SKA 56-90 g saksı$^{-1}$ iken mikoriza aşılanmayan saksılar için 37.7-58.7 g pot^{-1} arasında değişmiştir. Mikoriza aşılanan saksılarda sürgün % N'u, hem Çukurova (Adana) hem de Harran (Şanlıurfa) topraklarında aşılanmayan saksılara kıyasla daha yüksek bulunmuştur. Mikoriza aşılanan saksılarda sürgün N% konsantrasyonu Adana topraklarında %2.08 ile %3.89 arasında iken Şanlıurfa topraklarında%1.80 ile 2.42 arasında değişmiştir. Benzer şekilde, mikoriza uygulanmayan topraklarda sürgün N% Adana topraklarında % 1.80 ile 2.37 arasında değişmekte iken, Şanlıurfa topraklarında 1.73 ile 2.43 arasında değiştiği saptanmıştır.

Genel olarak mikoriza aşılanan bitkilerde %C konsantrasyonu mikoriza aşılanmayanlara göre daha yüksek olmuştur. Sürgün %C konsantrasyonu bakımından mikorizalı ve mikorizasız uygulamalar ile farklı genotip x uygulama kombinasyonları arasında oldukça anlamlı ($p < 0.001$) bir fark göstermiştir. Mikoriza uygulanan saksılarda sorgum genotiplerinin sürgün %C konsantrasyonu Adana topraklarında % 38.82 ile % 50.4 ve Şanlıurfa topraklarında ise % 38.4 ile

% 50 arasında değişmiştir. Mikoriza uygulanmamış saksılarda toprak C konsantrasyonu Adana topraklarında % 36.1 ile % 43 arasında, Şanlıurfa topraklarında ise % 36.1 ile % 40.4 arasında değişmiştir. İncelenen tatlı sorgum genotipleri tarafından tutulan toplam C ve CO_2 fiksasyonu, mikoriza uygulaması ve mikoriza x genotip etkileşimlerinden önemli derecede etkilenmiştir.

İncelenen i tatlı sorgum genotiplerinin mikorizal kök kolonizasyonuna etkisi incelendiğinde Adana topraklarında % 30 ila 65 arasında, Şanlıurfa toprağında ise % 30 ila 70 arasında tatlı sorgum genotiplerine bağlı olarak değişim göstermektedir.

Adana topraklarında en düşük mikorizal kök kolonizasyonu % 30 ile No91 tatlı sorgum genotipinde saptanırken, Şanlıurfa topraklarında en düşük kök kolonizasyonu % 30 ile Williams tatlı sorgum genotipinde saptanmıştır. Benzer şekilde, Adana topraklarında en yüksek kök kolonizasyonu % 65 ile Roma tatlı sorgum genotipinde bulunurken, Şanlıurfa topraklarında % 70 ile No5 tatlı sorgum genotipinde belirlenmiştir. Bulgularımız, doğal mikorizaların C ve N alımını arttırması yoluyla tatlı sorgum verimini artırabildiğini doğrulamıştır. Bu nedenle, topakların doğal mikorizaları, tatlı sorgum genotiplerinde C ve N alımını artırma potansiyeline sahiptir. Ayrıca, doğal mikoriza uygulaması sorgum genotiplerinde C ve atmosferik CO_2 fiksasyonunu önemli ölçüde arttırmıştır.

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LIST OF SYMBOLS AND ABBREVIATIONS

AM	: Arbuscular Mycorrhiza
ANOVA	: Analysis of Variance
AMF	: Arbuscular Mycorrhizae Fungus
C	: Carbon
^{o}C	: Degree of Celsius
CEC	: Cation Exchange Capacity
cm	: Centimeter (s)
CO_2	: Carbon Dioxide
DAS	: Days
FAO	: Food and Agriculture Organization of the United Nations
g	: Gram (s)
GPS	: Global Positioning System
GT	: Giga Tone
Ha	: Hectare (s)
ICRISAT	: International Crops Research Institute for the Semi-Arid Tropics
GCC	: Global Carbon Cycle
GHG	: Greenhouse Gases
LOC	: Labile Organic Carbon
LOI	: Loss-on-ignition
m	: Meter (s)
+M	: With Mycorrhizae
-M	: Non-Mycorrhizae
mm	: millimeter (s)
MD	: Mycorrhizal Dependency
Mg	: Mega Gram
NOAA	: National Oceanic and Atmospheric Administration Earth
NSSC	: non-structural soluble carbohydrate

NUE : Nitrogen Use Efficiency
OC : Organic Carbon
PCA : Principal Components Analysis
PH : Plant Height
Pg : Petagram
PIS : photo-insensitive
PS : photosensitive
RC : Root Carbon
RD : Root Diameter
RDW : Root Dry Weight
RN : Root Nitrogen
SAS : Statistical Analysis System
SAP : Southeastern Anatolia Project
SDW : Shoot Dry Weight
Sh.C : Shoot Carbon
Sh. N : Shoot Nitrogen
SOC : Soil Organic Carbon
SOM : Soil Organic Matter
TOC : Total Organic Carbon
TC up : Total Carbon uptake
TN up : Total Nitrogen uptake
TSP : Triple Super Phosphate
US : United States
USDA : U.S. Department of Agriculture

1. INTRODUCTION

In general, Turkish soil organic matter (SOM) content is low. Nearly 69% of arable land has less than 2% of SOM content (Ülgen and Yurtsever, 1998). One of the most important reasons for this is the geographical position and the Mediterranean climate in part of Turkey. Due to the high decomposition of semi-arid climatic conditions under high temperature, lime and clay soil structure soil OM content is generally low. In addition to this, traditional agricultural practices and the permanent exploitation of land use results a decrease in the amount of organic matter in soil is exist. Also because of intensive soil tillage/cultivation, soil structure deteriorates and soils with insufficient amount of organic matter quickly develop. Another important point is the physical and environmental problems of commercial fertilizers use on agricultural lands.

Sweet sorghum [*Sorghum bicolor var saccharatum* (L.) Mohlenbr] is the fourth most important cereal and is known as a multipurpose crop since it is used for grain, forage, syrup, fodder and bio-ethanol production (Mareque et al. 2015). Sweet sorghum cultivation is rapidly expanding throughout the world (Balat and Balat 2009). Cultivated varieties of sweet sorghum exhibit diverse phenotypic and morphological traits (Codesido et al. 2013). Sweet sorghum is characterized by high photosynthetic efficiency and energy production capacity (Wortmann et al. 2010). Sweet sorghum is also a C4 crop with low agricultural input requirements for cultivation (Mathur et al. 2017). Sweet sorghum belongs to Poaceae family (Monteiro et al. 2012). Sweet sorghum is a major crop which produces high yielding green biomass and ethanol against per unit consumption of nutrients, water and time (Vermerris et al. 2007). Cultivation of sweet sorghum on marginal lands with minimal agricultural inputs and high energy gain (Regassa and Wortmann 2014) is currently the most auspicious solution to prevent energy crises and reduce CO_2 emissions (Tian et al. 2009). Sweet sorghum is also a C4 photosynthesis pathway produce sucrose for energy storage, which is easily

convertible to ethanol (Ali et al. 2008). Sweet sorghum can grow under a diverse climate and soil conditions (Teetor et al. 2011). Sweet sorghum genotypes also differ greatly in their qualities and adaptation to various soil and climatic conditions (Ratnavathi et al. 2010). Therefore, it is essential to screen the sweet sorghum genotypes for dry weight and nutrient uptake under diverse climatic conditions such as semi-arid Mediterranean climate. Sweet sorghum has a versatile genetic base with near 4000 sweet sorghum cultivars distributed across the world (Grassi et al. 2004). Due to the fact of the extensive commercial interest in sweet sorghum production, plant residue potentially becomes a significant supplier of biomass for animal forage.

There are a few of cellulosic raw materials to be used in the industry that disappearing every day in Turkey as well as over the world. In addition, as forest vegetation is naked due to the use of forests, which are also known as carbon sink areas, for the purpose of cellulosic raw material, the increase of CO_2 emission causes direct and indirect global warming. On the other hand, the search for alternative raw materials to be used as cellulosic raw materials for the industry continues.

It is also important to find new crop species that are tolerant to biotic conditions (drought, high temperature and salinity) as a result of climate changes caused by increasing greenhouse gases in recent years. Because of the great tolerance of the sweet sorghum to drought and heat, it will be one of the most important plant species to be focused on in the coming years.

In addition, it is important to reduce the rate of fossil fuel uses which are release of harmful greenhouse gases that are harmful to the environment, while increasing the amount of carbon adsorption through the plant by photosynthesis in to the soil. According to calculations, it is estimated that the greenhouse gases released into the atmosphere as a result of poor agriculture-land management constitute 14-25% of the greenhouse gases released into the atmosphere (NOAA, 2015).

Increasing fossil fuels base energy supply causes climate changes that release CO_2 to the atmosphere. In order to mitigate atmospheric greenhouse gases the researchers have introduced many alternative energy supply projects such as the use of biofuels instead of fossil hydro-carbon fuels. Selection of genotypes in high-ethanol species such as sweet sorghum can be proposed as an important alternative strategy. In this context, it is thought that genotypes to be used in this study will also constitute an important agricultural strategy and management model on plant growth and soil carbon retention. Knowing the effect of plant root growth and mycorrhizae on plant growth and carbon binding can also provide preliminary information for the use and breeding of forward-looking sorghum genotypes.

It is known that over 90% of the plant species in the nature are dependent on mycorrhizae for their nutrition and water uptake and development (Bonfante and Genre 2010). Mycorrhizal infection occurs in plant roots as a result of mutual symbiosis between plant roots and mycorrhizal fungi. This mutually symbiotic relationship between mycorrhiza and plant roots directly affects plant growth in the direction of good growth (Ortas et al. 2017). I has been reported that plant health and soil quality is improved as a result of a good mycorrhizal colonization (Ortas et al. 2017).

Besides their role in nutrient uptake, roots constitute a major source of carbon (C) for soil (Rasse et al. 2005) and root biomass might be a good indicator of crop C input to soil (Monti and Zatta 2009a). The positive effect of mycorrhiza on plant growth and dry matter is expected to increase carbon sequestration to the soil as well. Soils contain the largest amount of C in the terrestrial ecosystem with roughly twice the amount of C stored in the soil as found in the atmosphere (Batjes 1996; Lal and Follett 2009; Powlson et al. 2011). Sweet sorghum produces a net C fixation from the atmosphere to the soil (Le Quéré et al. 2012). It is essential to estimate the ability of the soil to sequester C back from the atmosphere (Schulp et al. 2008) and to mitigate the emissions of CO_2 into the atmosphere. Increasing soil carbon may play a critical role in mitigating atmospheric CO_2 emissions.

Consequently, relatively small changes to the soil C pool can influence the global C balance (McNally et al. 2015). Since studying root morphology is time-consuming and labor-intensive (Costa et al. 2002; Dowdy et al. 1998; Monti and Zatta 2009a; Nickel et al. 1995) there is less work in the carbon capture between roots parameters and carbon fixation or carbon sequestration. Little information is available on root morphological characteristics of sweet sorghum [*Sorghum bicolor var saccharatum* (L.) Mohlenbr.] crops under field conditions, which can be a major determinant of C input to soil (Thivierge et al. 2016). However, the influence of sweet sorghum genotypes on root traits and carbon fixation and C pool was poorly understood.

Arbuscular mycorrhizae fungi (AMF) are symbiotic associations between plants and soil fungi (Smith and Read 2008a). It is an essential component of the soil microflora that promotes nutrient uptake in plants (Hameeda et al. 2007). The AMF is also playing a vital role in plant nutrient supply (Beringer et al. 1987; Marschner 1995; 1996). The beneficial effect of indigenous AMF is most important for sustainable crop production (Allen and Allen 1986; Ortaş 2019). Therefore, indigenous mycorrhizae have a great potential to use as a bio-fertilizer for sustainable sweet sorghum production. The AMF is the common biotic factor of ecosystem which establishes symbiotic relationship with terrestrial plants, which help increase plant growth, plant protection, quality of the soil and mineral as well as water uptake (Maillet et al. 2011). The AMF is able to produce enzymes to mobilize N locked up in soil organic matter, a strategy that is advantageous in sites where greater re-translocation keeps soil fertility low, but also requires greater C expenditure to gain N (Read and Perez-Moreno 2003). It needs to be developed the sweet sorghum productivity under divers soil and climate conditions. Climatic conditions also important to quantify existing sweet sorghum yield in semi-arid south east part of Turkey.

The specific objective was to examine the collected several sweet sorghum genotypes effects on dry weight, nutrient uptake, soil carbon and nitrogen

sequestration under two divers' soil and climate conditions located in south east part of Turkey. In another presentation, the aims of this work were to characterize and compare root biomass and root traits of the sweet sorghum genotypes at field and greenhouse conditions and to estimate their C input and transferred into soil.

In another presentation, the aims of this work were to characterize and compare root biomass and root traits of the sweet sorghum genotypes at field and greenhouse conditions and to estimate their C input and transferred into soil.

Main project hypothesis was sweet sorghum genotypes accumulate/fixed atmospheric C and can leak carbon into soil through root growth.

In this context, three different sub-hypotheses were determined to be tested:

Hypothesis 1: Different sweet sorghum genotypes have different carbon binding potential under different ecological zone conditions.

Hypothesis 2: Different sweet sorghum genotypes have different mycorrhizal root infection level which develop plant growth and nutrient uptake.

Hypothesis 3: The differences in root systems of sweet sorghum genotypes affect the plant's carbon-holding potential.

The objectives of present study were to examine of the collected sweet sorghum genotypes in terms of dry weight and nutrient uptake under two divers soil locations. The aims of this study were to characterize and compare root biomass and root traits of the sweet sorghum genotypes at field and greenhouse conditions and to estimate their C input to into soil.

Therefore, this study was undertaken:

1. To evaluate the biomass yield potential and nutrient uptake (C and N) responses of some sweet sorghum genotypes under two locations that differ both soil and climatic conditions.
2. To determine the most suitable sweet sorghum cultivars and lines with biomass and nutrient uptake under semi-arid climate conditions in Turkey.

3. To screen the most suitable sweet sorghum genotypes or lines with root biomass production and their C input into the soil.
4. The study is based on hypothesized that (i) growth performance of sweet sorghum genotypes will be better at indigenous mycorrhizae amended soils than non-mycorrhizae amended soils (ii) shoot and root C, as well as N uptake will be higher in mycorrhizae amended soils than non-mycorrhizae amended soils.

In the study, the effects of root growth and mycorrhizal infection rates on the biomass yield and total carbon binding capacity of sweet sorghum genotypes under different ecological soil conditions were investigated. For this purpose, sixteen different sweet sorghum genotypes were used under two locations for two successive years under field conditions. In addition, the search the sorghum genotypes mycorrhizal dependence and relationship with carbon fixation capacity. Under greenhouse conditions.

Within the scope of the project, besides the determination of the amount of organic carbon (OC) released by sweet sorghum genotypes, the effects of genotypes on root length, density and surface area were determined and the potential of genotypes to transfer carbon to soil via rhizosphere. Increased carbon binding in soil was also expected to directly increase the potential of plants to benefit more from water and mineral elements in the soil. In this context, the investigation of the effects of different sweet sorghum genotypes on plant root development and indigenous mycorrhizal development in different ecological zone conditions and on the potential of carbon sequestration in plants and soil is very important for today's climate change conditions.

2. LITERATURE REVIEW

2.1. Origin and Development of Sorghum Plant

The genus Sorghum is formed of C4 cane grasses located mainly in Africa and Asia. Cultivated sorghum [*Sorghum bicolor* (L.) Moench] belongs to the genus. The species S. *halepense* (Johnson grass) was introduced as a forage crop to the United States (US) but soon became wild. The *S. bicolour* varieties are grasses with a range of 0.5 to 6 m of height (Smith and Frederiksen 2000). Each of the stems is able to produce a panicle which comes in a variety of architectures. The stems of sorghum can be juicy or dry, and the sweet sorghums accumulate soluble sugars in the stem juice, like sugarcane (Zhao et al. 2009).

The forage sorghum genotypes produce massive amounts of tillers in comparison to the grain and sweet sorghum genotypes. Forage sorghum stems are thin, about 0.5–3.5 meters tall, and the panicles frequently opened (Smith and Frederiksen 2000). The wild races of S. bicolour (*S. bicolorssp. verticilliflorum and S. bicolour ssp. drummondii*) are mainly located in Africa.

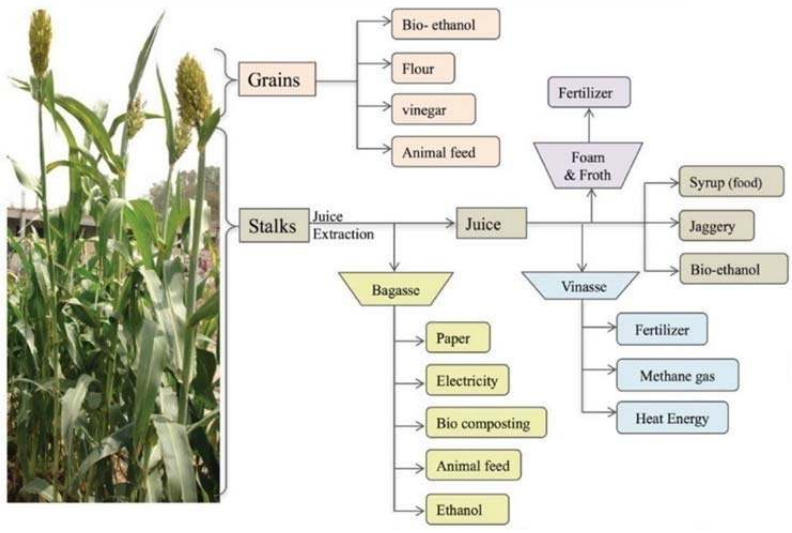

Figure 2.1. Sweet sorghum is a multipurpose crops (Mathur et al. 2017).

Sorghum is mainly cultivated for grain, forage and syrup, but lately for biofuel production (Figure 2.1). The selection in sorghum has resulted in elite lines optimized for a different type of uses. From the bioenergy point of view, sorghum can be used to feed three important processes: grain starch, which has similar value as corn starch ethanol production, high- soluble sugar concentration in stem juice that could be utilized for fermentation, and the felt over bagasse after juice extraction that could be used as biomass feedstock for fermentation or as boiler fuel.

Grain sorghum, also known as grate millet, has a grain to biomass ratio; they are short, with a small number of tillers and suitable to combine harvesting. Because of human selection pressure, most grain sorghum types produce a single compact or semi-compact panicle. The average grain yield of sorghum in the U.S.A. in 2013 was 3.7-ton ha^{-1} and is expected to increase to 4.0-ton ha^{-1} by the end of 2014 (USDA, 2014).

Since ethanol production from grain sorghum requires similar processes as the production from corn kernels, they can be used together in the same bio-refinery plants. Stover yield from grain sorghum (milo) after grain harvest is similar to corn (roughly 4 to 5-ton per hectar). This lingo cellulosic material can be harvested for animal forage or for lignocellulosic ethanol production. Therefore, in areas where grain sorghum production is important, the lignocellulosic material left after harvest could be utilized as a source of structural carbohydrates present on biomass. Forage sorghum types are known as sorghum, sometimes as Sudan grass or ultimately Sorghum-Sudan grass hybrids. They produce abundant tillers and some types are perennial in tropical and sub-tropical zones. Tillering types produce multiple panicles located in the basal nodes or branches that develop from stem nodes. Lignocellulosic material is the primary product, usually harvested before physiological maturity (Hamelinck et al. 2005). Lignocellulosic material digestibility and total yield are the main reasons for cultivar selection. Forage sorghum yield varies widely due to the genotype used and ranges from 14 to 16

tons of dry biomass per ha (Corredor et al. 2009; Rocateli et al. 2012).

Usually, sweet sorghum types produce low grain yield, but, recently, new varieties with more balanced non-structural (grain) and structural (soluble sugars) carbohydrates production have been developed in Asia (Li et al. 2004); (Reddy et al. 2007). There is growing interest to produce ethanol-fuel from sweet sorghum stems due to the simple extraction of promptly fermentable sugars combined with high lignocellulosic biomass yield. Sweet sorghum has been used as the preferred renewable source for ethanol production in developed countries since the first energy crisis in the 1970s (Nathan 1978). Fresh lignocellulosic biomass yields vary with variety and location from 25–130-ton per ha, with extractable juice ranging from 30 - 50%, and soluble sugar content, measured in degree Brix (°Brix), of 15-22% (Channappagoudar et al. 2007); (Tew et al. 2008). The major non-structural soluble carbohydrate (NSSC) in the stem juice is sucrose (~90%) followed by soluble glucose and fructose (~8%) and starch (~2%) (Sherwood 1923); (Vogel et al. 2010); (Han et al. 2013). Many approaches have been proposed to produce, harvest and process sweet sorghum at commercial scale. Usually, the key organic compound obtained and fed into the ethanol production is the saccharine juice. The stems are harvested, the panicles removed, and the stems are crushed, allowing the complete extraction of the juice. The same plants designed to process sugarcane stalks to produce ethanol could use sweet sorghum stalks as feedstock, with the soluble carbohydrates extracted from the stem juice, typically fermented by yeast to produce ethanol. Researchers and engineers have proposed new alternatives to enhance the sugarcane ethanol production model, to be adapted for sweet sorghum. They suggest directly juice extraction and fermentation during harvesting (Li et al. 2004); (Kundiyana et al. 2006).

2.2. Definition and Production of Sweet Sorghum

Sweet sorghum is a multi-purpose C4 crop in the grass family of plants. Scientifically, the plant is known as *Sorghum bicolour* var. *saccharatum* (L.)

Mohlenbr. Local names given to sweet sorghum are English Sweet Sorghum, German Zuckerhirse, African Durra, Jowar, and Ethiopian Bachanta. It is a highly photosynthetic efficient plant. This plant was originally cultivated in the North and East of Africa as it is preferable to drier and warmer climatic conditions to thrive. Thus it is a drought-tolerant crop with high water use efficiency (Köppen et al. 2009). Sweet sorghum is mostly grown for forage, silage and the production of syrup. While the crop produces food from the grains, it also yields fuel from its stem juice. Additionally, biomass and sugar are also produced from this plant.

2.2.1. Botanical Properties of Sweet Sorghum Plant

As aforementioned, sweet sorghum is a drought-resistant crop in the grass family, thus characteristically, the plant is widely, waterlog tolerant, has high sugar content, biomass and is saline-alkali tolerant all which ensures the plant has a rapid growth rate. The plant has a small grain that ranges from 2-4 mm in diameter, grows to 1-5 m in length and has a very large root and leaf surface area ratio. The plant's height is varied as that of other sorghum plant varieties as sweet sorghum is primarily for feed and energy purposes (Guiying et al. 2003).

2.2.2. Sweet Sorghum Root System

The root system is an important organ of plants. It absorbs water and nutrients from soil and supplies to plant tops for their metabolic activities. Roots also give plants a mechanical support and supply hormones that help plants in many physiological and biochemical processes associated with growth and development. Roots are also responsible for the mitigation of greenhouse gases by storing a large amount of C in the soils. A vigorous root system is responsible for the development of healthy plants and, consequently, greater yields. Roots that are left in the soil after crop harvest improve soil organic matter content, nitrogen cycling, and microbial activities. All these activities improve soil structure, soil

water holding capacity, and water infiltration rate in the soil and reduce soil bulk density and soil erosion, which ultimately leads to higher soil productivity.

Root growth is controlled genetically and also influenced by environmental factors. Environmental factors that influence plant root growth are soil temperature, soil moisture content, solar radiation, and the physical, chemical, and bioat the 0–20 cm soil depth. This may be associated with a large amount of organic matter, nutrient accumulation, and water availability in the topsoil layer compared to lower soil depths. The root system of cereals has a more vigorous compared with legumes. Overall, root contributes 10%–20% of total plant weight. Deeper and vigorous root system helps in the absorption of water from deeper soil layers during water shortage or drought period. When environmental conditions are favorable, a smaller root system or less vigorous root system can produce maximum economic yield. Root length, as well as root weight, has a positive association with grain yield in crops. Crop plants having C_4 photosynthetic pathway produce a more vigorous root system compared to crop plants with C_3 photosynthetic pathway. Sweet sorghum consists of a layer with a very strong root system and the epidermis of the root covered with dislocate. The root develops by maturing in the form of a complete silicon column, which provides sufficient mechanical density and also prevents the root system from collapsing over a dry period (Guiying et al. 2003).

2.3. Sweet Sorghum and Environmental Conditions

Being a drought-tolerant C4 plant, sweet sorghum grows under extreme weather conditions ranging from 12-37 ^{o}C. It is highly adaptable in that it also grows in toxic soils and high altitudes as well. Ideally, temperatures for best growth and photosynthesis are between 32 to 34 ^{o}C. More-so, the plant requires at least a 10 to 14-hour day's length. Furthermore, the ideal rainfall for the plant would be ranging from at least 550 mm to 800 mm considering the plant's tolerance to drought. In terms of atmospheric conditions, the plant thrives relatively

between 15 to 50% of humidity. Under such climatic and environmental conditions, sweet sorghum produces a favorable yield. However, the lower the diurnal and nocturnal temperature differential, the less stalk sugar accumulation is observed.

Sweet sorghum is a short-day photosensitive (PS) species. Its high photoperiod sensitivity allows for it to have high biomass production and makes it susceptible to high lignin content and a lower moisture stand out for cogeneration. The plant's flower induction is initiated when day length is less than 12 hours and 15–20 minutes (Rooney et al. 2007). Subsequently, in the adaptation of sorghum to temperate environments; a mutation of the dominant MA1 maturity gene to ma1 was selected to develop photo-insensitive sorghum that will normally flower 60–75 days after germination.

The sweet sorghum cultivars currently being developed in Brazil and the US are photo-insensitive (PIS) and they normally flower 60–80 days after germination. Consequently, they reach peak sugar concentration around physiological maturity of the grain at 120–130 days after germination or 40–70 days after flowering. The growing seasons of sweet sorghum in Brazil and in the US have longer day periods of at least 12 hours 20 minutes. This translates to sweet sorghum having longer growing seasons of up to 8-9 months for the energy sorghum. Thus, there are critical environmental factors surrounding the growth of sweet sorghum (Rooney et al. 2007).

2.4. Sweet Sorghum and Water

Sweet sorghum is a high water use efficient crop. It can survive with less than a 300 mm supply of water per 100 days in a season. The plant has the capability to preserve its water content in times of long dry spells. The plant can roll its leaves in order to preserve water that may otherwise be used in the transpiration process. Additionally, this feedstock is advantaged in that it can become dormant, especially in the vegetative phase, under adverse conditions and

can resume growth after a relatively severe drought instead of dying. The leaves are coated with a layer of a cuticle wax which makes water preservation within the plant possible. However, in as much as the plant is a drought-tolerant crop, sweet sorghum responds favorably with additional rainfall or irrigation water. Typically, sweet sorghum needs between 500 and 1,000 mm of water (rain and/or irrigation) to achieve good yields, i.e., 50–100 t ha^{-1} total aboveground biomass (fresh weight). Furthermore, although this crop is susceptible to sustained flooding particularly at early vegetative phase, it tolerates water logging better than maize and sugar beet (Srinivasa Rao et al. 2009).

2.5. Nutrients Removal by Sweet Sorghum

Many factors are involved in determining the mineral requirement of sweet sorghum (Maiti 1996). Such as;

1. Amount of available and residual mineral elements in the soil.
2. Physicochemical properties of soil.
3. Availability of soil moisture.
4. Yield and yield components desired.

Cultivars producing large amounts of biomass remove greater quantities of soil nutrients. Sorghum crop producing 5.5 t ha^{-1} grain removes a total of 335 kg nutrients (149 kg N + 61 kg P_2O_5 +125 kg K_2O) ha^{-1} from soil. High-yielding varieties of sorghum removed 22 kg N, 9 kg P_2O_5 and 30 kg K_2O ha^{-1} to produce 1.0 t of grain (Tandon and Kanwar 1984). In another work it has been reported that sorghum crop yielding approximately 8 t of grain ha^{-1} removes about 250 kg N, 40 kg P_2O_5, 160 kg K_2O, 45 kg Mg and 40 kg S ha^{-1} from soil (Maiti 1996).

2.6. Effect of Nitrogen Fertilizer on Sweet Sorghum Productivity

The application of nitrogen fertilizer on sweet sorghum enhances the

development of the overall plant. The application enhances the growth of the plant in height and also influences the development of the roots. The chlorophyll content, fresh weight, grain weight and dry matter are also significantly increased. In some instances, the application of nitrogen fertilizer affects the chemical composition of the plant in that the crude protein in the plant is increased while the crude fiber is decreased.

Studies have shown that in other instances, the effects of nitrogen fertilizers are on sweet production in sweet sorghum. The sweetness of sorghum is increased in the vegetation state of the plant and the maximum sweet content is observed the milk-waxy ripeness stage of the grain. Most of the sweet was contained in the middle internodes. While in some studies, it was noted that most crop plants utilize less than half of nitrogen added to the soil. According to Maiti (1996), only about 50% of the N applied to soil is taken up and used by plants. The remaining is left for microbial use, leaching, denitrification or incorporated into the organic fractions through immobilization and many other reactions and processes occurring in the soil.

Nitrogen is one of the most abundant mineral nutrients required for sweet sorghum's effective growth. The level of nitrogen fertility has more influence on the growth and yield of grain sorghum than any other single plant nutrient. The amount of fertilizer N required will vary depending on the yield potential of the cultivar and the amount of residual N available in the soil prior to planting. Pre-plant soil analysis can be very useful in estimating the nitrogen need of the crop. Most of the sweet sorghum growing soils contain a low amount of nitrogen and hence require supplemental nitrogen applied in the form of fertilizer for optimal productivity.

2.7. Nitrogen Uptake Theories by Sweet Sorghum

The N-uptake curve is generally similar to a sigmoidal growth curve in sweet sorghum. Nitrogen accumulation rate by the whole plant was usually slower

in the early growth stage, became faster in the log phase of crop growth and again slowed down at maturity (Srivastava and Singh 1971).

The recovery of N is influenced by the rates and method of N application, soil types, variety, soil moisture and management practices. The results from a study with 15N labelled urea at ICRISAT, (1982 and 1983), revealed that sorghum recovered 62.5 % of added N in the alfisol and 55.0 % in the vertisol. About 27.1 % of applied N was distributed in the alfisol profile and 38.6 % in the vertisol profile accounting to 89.6 % and 93.6 % N by the soil + crop system.

In alfisols, crop recovery of N varied from 46.3 to 51.1 % as N levels increased from 40 to 160 kg N ha-1. At the highest N level tested, soil + crop system could account for 78.9 % of added N, as compared to 93.2 % at 40 kg N ha-1. Although considerable fertilizer N was present in the soil profile after the harvest of rainy season sorghum, this residual N was of limited value either for safflower grown in the post-rainy season or for sorghum grown in the following rainy season (Moraghan et al. 1984). The N response (kg grain kg-1 nitrogen applied) of rainfed sorghum to optimum or near optimum levels of N during rainy season varied from 21.7 kg in alfisols, 18.32 kg in vertisols, 11.9 kg in mollisols and 20.15 kg in entisols (Tandon and Kanwar 1984).

A significant positive interaction between nitrogen and moisture has been well established in sorghum, and this interaction is stronger in an alfisol than in a vertisol (Kanwar 1978). Nitrogen uptake was also improved by P and Fe fertilization in calcareous soils (Patil 1979).

2.8. Sweet Sorghum and Nitrogen versus Genotype Interaction

Sweet Sorghum genotypes greatly influence the nutrient accumulation in plants due to variation in the rate of absorption, translocation and accumulation of nutrients in plant tissues. Genotypic difference in N uptake partitioning and NUE (unit dry matter per unit N in dry matter) has been reported for grain sorghum (Maranville et al. 2002). The varietal differences between N and P uptake might be

due to additive gene action for N and non-additive for P (Krishna et al. 1985). In general, hybrids deplete a greater amount of nutrients than line varieties. Sorghum genotypes vary significantly for various root characteristics which may affect the nutrient uptake (Seetharama et al. 1990). Long-term studies conducted in vertisols indicated that sorghum absorbs a mere 5 % of the total N during the first 5 weeks followed by rapid N uptake. The crop accumulated 88 kg N ha^{-1} in 40–70 days, at the rate of about 3 kg N/ha/day (ICRISAT 1986).

2.9. Sweet Sorghum Is Ideal for Double Cropping

Double cropping sweet sorghum for biomass production has always been ideal considering that the feedstock will also be doubled and the growing season is extended. Furthermore, double-cropping enables the reduction of soil erosion which is beneficial for proper root and plant stability. Also, the biomass per hectar is increased. Additionally, when double-cropping is conducted under adverse weather conditions, the chemical composition of the plants differs. This is also owing to the environmental differences the crops are exposed to as well as the differing maturing time.

Notwithstanding, sorghum grown for biomass can be harvested before it is fully mature; therefore, it is possible to grow it in a double-crop sequence with a winter annual. Winter annuals are planted in the fall, grow rapidly in the spring and reach harvest anytime during late spring to early summer. Sorghum, which is well adapted to germination under limited moisture, can be no-till planted into the stubble of a winter annual crop.

2.10. Sorghum Crop for Biomass and Biofuels

Biomass can be used to generate electricity or to produce liquid transportation fuels. Among the various types of renewable fuels (such as wind, solar, and geothermal), biomass is unique because it is the only current renewable resource of liquid transportation fuel. Sweet sorghum is a type of sorghum that has

a high concentration of soluble sugars in the juice, similarly, does sugarcane. Also, it has high characteristics of fermentable sugars, efficient nutrient use, high water use efficiency (1/3 of sugarcane and 1/2 of corn), short growing period with PIS and long growing season with PS sorghum cultivars, and the ability to adapt well to the diverse climate and soil conditions make sweet sorghum a potential feedstock for ethanol production (Wu et al. 2008). The present-day sweet sorghum hybrid varieties, on an average, yield about 3-5 t ha^{-1} of grain and 50-80 t ha^{-1} of biomass per hectare. The other biomass crops such as banana grass and miscanthus (also known as ornamental grass) also yield above 50 t ha^{-1}, while a highly invasive species like water hyacinth gives much higher yields (Srinivasa Rao et al. 2009).

2.11. Plant Root Characteristics

2.11.1. Root Length

Water and nutrient uptake of plants influence the root's length. In many cases, the root's length is the used parameter to describe plant root systems and for predicting the root's response to changing environments. The architecture of roots is manipulated by genotypic selection and irrigation management. In a study by Liang et al. (2016), it was established that plants under deficit irrigation of up to 25% of the full plant throughout the season increases the angle, number of crown roots as well as root length. Furthermore, the length of the root informs of the plant's nutrient and water uptake. Also, adequate root length and root diameter are the components determining the size of the root surface area, which determines water and nutrient uptake potential of the root system (Barber and Silberbush 1984); (Eissenstat 1997); (Eissenstat 1992); (Noulas et al. 2010).

2.11.2. Root Dry Weight

The development of root patterns and above-ground plant developments also influence the dry root weight. Root dry weight is generally controlled as well as influenced by environmental factors (Fageria 1992). Consequently, root weight

is normally the parameter used in studies of root growth in response to the environment and for characterizing total mass of root in soil. Aspects such as salt stress in the soil increases the root dry weight. In periods of drought, the dry root weight is likely to be less in comparison to when the plant grows under normal conditions.

To determine the dry weight, the roots are washed and dried in the oven at 105°C for about 10–20hours, depending on the quantity of roots (Bohm 1979). Alternatively, the roots can be dried at 60°C–75°C as this has the advantage of preventing roots from being pulverized or volatilizing nitrogenous compounds. The measurement of root dry weight is also commendable because it is also easy to measure in the experiments of controlled conditions.

2.11.3. Root Surface Area

Besides length and weight, the surface area is an important parameter of the root system in crop plants. The form of root systems and their development conditions greatly affect the surface area of roots. The surface area of roots has a high positive correlation with the amount of nutrient absorption (Takenaga 1995).

2.11.4. Root Depth and Density

Rooting depth and density or distribution pattern in soil determines the zone of water and nutrient availability to plants and also resistance to biotic and abiotic stresses (Castonguay et al. 2006). Root density is a result of the growth of varied roots. The depth and density are motivated by the trajectory of the seminal and nodal roots. Additionally, the further the roots go is determined by the direction in which the roots go. Furthermore, the depth and density are also influenced by environmental aspects. The increase in root size and depth influences the water uptake of the roots (Karcher et al. 2008). This is a mechanism used by sweet sorghum roots to withstand drought because the larger the root size and deeper the depth, the more the root takes up soil water resources. Factors that affect

root growth and rooting depth of crop plants can be restricted because of physical and chemical impediments (Gregory 2006). Almost all the roots growing through soil experience some degree of mechanical impedance. Also, if continuous pores of appropriate size do not already exist then the root tip region must exert sufficient force to deform the soil (Gregory 2006). Noteworthy is the fact that root density usually decreases with depth (Kalisz et al. 1987); (Klepper, 1990).

The greater amount of roots, especially fine roots, occurs near the soil surface where conditions are more favorable for root growth (Singh and Sainju 1998). These layers are usually rich in organic matter, nutrients, CEC, and porosity and are low in bulk density (Sainju and Good 1993). In that same vein, (Sainju and Good 1993) and (Sainju and Kalisz 1990) found an exponential decline in root density with soil depth, reflecting declining fertility, reduced organic matter concentration, and decreasing aeration.

2.11.5. Root Development Relative to Plant Growth Stage

There is a close correlation between the plant's root and plant growth. Roots are the facilitators of macro-nutrient and micro-nutrient acquisition required for plant growth. Thus, they are growth determinants. The architecture of the root systems in sweet sorghum plays a crucial role in the plant's adaptability to varied soil types and environmental conditions. First roots are fibrous. These roots then grow into adventurous roots and lateral roots which spread up to 1.5metres around the plant. Wet and cold soil conditions can alter the growth rate of the root system and consequently, the plant itself.

2.12. Sweet Sorghum and Soil Carbon

Soil organic carbon (SOC) is known to be a sensitive indicator of soil quality and necessary for the functioning of agricultural ecosystems as it affects many chemical, physical and biological parameters in soil. It is reported that agriculture is a major source of CO_2 emissions and that this ratio will be reduced by various agricultural management systems (such as tillage, fertilizing methods and crop rotation) (Bavin et al. 2009). However, carbon stock in soil has many strategic

aims such as restoration of deteriorated soil, improvement of soil fertility and variability, protecting the environment by reducing CO_2 emissions and consequently reducing climate change by balancing greenhouse gases (Wang et al. 2010).

Soils are the largest carbon reservoirs of the terrestrial carbon cycle (Figure 2.2). Soils contain about three times more C than vegetation and twice as much as that present in the atmosphere (Batjes 1996). Also, soils contain much more C (1500 Pg of C to 1 m depth and 2500 Pg of C to 2 m; 1 Pg = 1 X 10^{15} g) than is contained in vegetation (650 Pg of C) and twice as much C as the atmosphere (750 Pg of C) (USEPA, 1995). Carbon in the form of organic matter is a key element to healthy soil. It is estimated that each tone of plant dry matter releases 3.667 tons of CO_2, which is lost into the atmosphere. Similarly, the build-up of each tone of soil organic matter removes 3.667 tons of CO_2 from the atmosphere (Bowen and Rovira 1999).

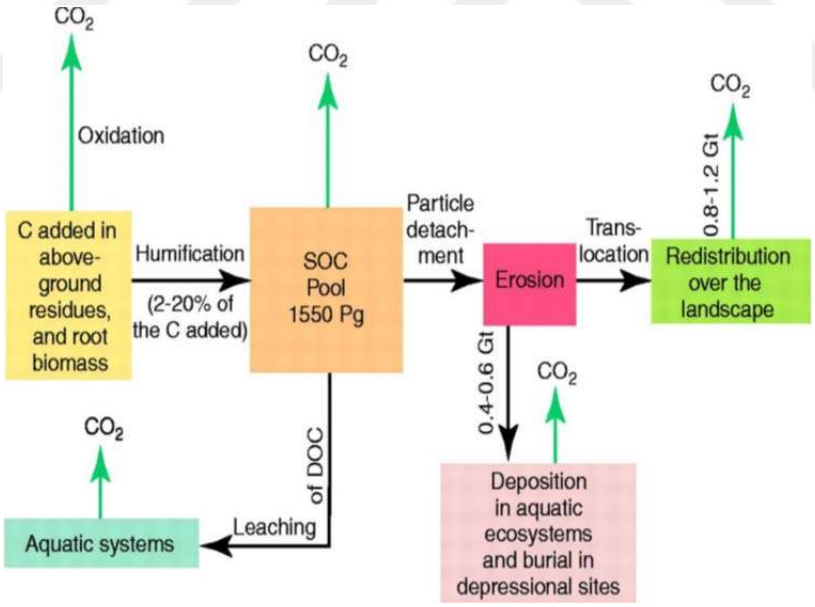

Figure 2.2. Short Term Carbon Cycle (Lal 2004)

2.13. Global Soil Carbon

The global soil carbon (C) pool of 2500 gigatons (Gt) includes about 1550 Gt of soil organic carbon (SOC) and 950 Gt of soil inorganic carbon (SIC). The soil C pool is 3.3 times the size of the atmospheric pool (760 Gt) and 4.5 times the size of the biotic pool (560 Gt). The SOC pool to 1-m depth ranges from 30 tons/ha in arid climates to 800 tons ha^{-1} in organic soils in cold regions and a predominant range of 50 to 150 tons ha^{-1} (Figure 2.2). The SOC pool represents a dynamic equilibrium of gains and losses. Conversion of natural to agricultural ecosystems causes depletion of the SOC pool by as much as 60% in soils of temperate regions and 75% or more in cultivated soils of the tropics. The depletion is exacerbated when the output of C exceeds the input and when soil degradation is severe. Some soils have lost as much as 20 to 80 tons C ha^{-1}, mostly emitted into the atmosphere. Severe depletion of the SOC pool degrades soil quality, reduces biomass productivity, and adversely impacts water quality, and the depletion may be exacerbated by projected global warming (Lal 2004).

The short-term carbon cycle includes daily carbon cycling that occurs in the soil with the cumulative effects evidenced over a time-scale of hundreds to thousands of years as soils are created (Berner 1998); (Lal 2004). By means of photosynthesis, plants utilize energy from the sun to convert CO_2 in the atmosphere into carbohydrates that form the above- and below-ground (root) plant biomass.

2.14. Organic Carbon in the Soil

It has been reported that degraded cultivated soils could give 1-ton ha of carbon to the soil carbon pool and yield of 20-40 kg ha^{-1} of wheat, 10-20 kg ha^{-1} of maize and 0.5-1 kg ha^{-1} of cowpea (Lal 2004). In this context, if different sorghum genotypes are tested, it is important to be aware of the effects of the genotypes on the soil organic carbon (Govaerts et al. 2009). According to different sorghum cultivation methods have shown that the soil organic carbon changed to 30 cm deep (Ortas and Lal 2014) in different years of the addition of different organic

matter increased the content of organic matter and determined that a direct correlation relationship with the increase in yield was detected. As a result, more C extraction is ensured and the greenhouse gases (such as CO_2, CH_4, N_2O), which have been heavily released into the atmosphere as a result of incorrect territorial administrations as well as increasing soil efficiency. On account of different development and photosynthesis of plant genotypes, the subsoil root development was also reported by Ortas and Akpınar (2011), which would be naturally different. It is clear that different root systems will have an impact on the dynamics of the rhizosphere and the content and amount of organic carbon in the soil.

Due to the secretions of plant roots, carbon binding in soil and the development of soil quality will be different. Naturally, the capacity of carbon binding will be different when the plant produces biomass differently. The binding of more carbon in the soil improves the sustainability of the soil and ensures a more efficient and quality soil formation (Ortas et al. 2013). During the vegetation period of sweet/sugar sorghum, the absorption of carbon dioxide (CO_2) is between 30-45 Mg ha^{-1} and is reported by (Roman et al. 1995), which have 3 times more capacity than the scrub vegetation. It restores 4% of its absorbed CO_2 (1.5 Mg ha^{-1} CO_2) to the atmosphere with the respiratory tract.

2.15. Nitrogen in Soil

The amount of N in the soil is very low compared to the nitrogen found in the atmosphere. The total N content of most mineral soil varies between 0.02% and 0.5%, with an average amount of 0.15%. A large part of the soil nitrogen is in organic form. Under Normal conditions, up to 2-3% of organic nitrogen is mineralized every year. Only 8% of the nitrogen found in the surface soil and 40% of the nitrogen in the lower soil depths are fixed by clay minerals in the form of NH_4, in this form (Bao et al. 2006). The compost applied to the soil, especially nitrogen content and, accordingly, the C/N ratio is important for the decomposition of organic material mixed in the soil. The C/N ratio and high lignin content reduce

mineralization (Mengel and Schmeer 1985). Organic nitrogen is biologically mineralized before ammonium nitrogen, which is nitrification and ultimately becomes nitrate nitrogen (Sağlam 2005).

2.16. Arbuscular Mycorrhizal Fungus

About 90% of all vascular plant species form arbuscular mycorrhiza (AM), which is an underground symbiotic association between plants and AM fungi (Smith and Read 2008a). This is a functionally important group of soil fungi involved in many terrestrial ecosystem processes (Fitter 2005); (Rosendahl 2008). Notably, symbiosis is older than 450 million years old and was important in ensuring the colonization of the soil by plants (Redecker 2002). The AM fungi were accompanied by plants from the water to the soil from the outset and evolved in various terrestrial and aquatic ecosystems. They are important actors in the basic soil functions such as the biogeochemical cycle of basic macro-nutrients and minerals and the preservation of soil structure.

There are many benefits of being mycorrhizal for plants; AM makes it easier to plant mineral nutrients, affecting plant water relations and pathogen and pollutant resistance and tolerance (Smith and Read 2008a). Indeed, as the most exposed function, mycorrhizal fungi provide a significant amount of N and P to host plants in natural ecosystems, particularly those in which the presence of nutrients in the soil has decreased (Fitter 2005); (Van Der Heijden et al. 2015). Therefore, AM is common in many stressful environments and have been shown to increase plant survival and viability in these ecosystems. They receive all their carbons from host plants and have central roles in many habitats (e.g. nutrient cycles). Some indicators suggest that the benefits of AM fungi to plants will gain more importance due to the increased abiotic stresses caused by climate change (Hanson and Weltzin 2000).

Understanding the AM fungal ecology and defining key determinants of community-level processes apply to a wide range of habitats. It has a profound

impact on the dynamics and diversity of the plant community by providing a number of benefits to the facility (Fitter 2005); (Van der Heijden et al. 1998). Recent molecular studies have shown that AM mushroom populations in nature are more diverse than the ones initially considered on the basis of spore morphology. AM fungal spores still serve as basic taxonomic characteristics because AM fungi cannot be identified morphologically in roots (Merryweather and Fitter 1998). However, it is known that soil spore counts do not reflect AM fungal diversity in plant roots and do not necessarily correlate with physiologically active AM fungal taxa that form mycorrhiza (Clapp et al. 1995); (Renker et al. 2005).

Molecular approaches are needed for a more detailed description of the communities as the morphological properties of the structures of AM fungi in plant roots allow only low levels of identification. Most ecological studies on AM mushrooms have been built on DNA-based techniques developed to measure AM fungi in field and plant roots collected from the 1990s (Helgason et al., 1998). Although there are more than 250 morph species ph. Glomeromycota has been described (Walker and Trappe 1993); (Schüßler et al. 2008), molecular data indicate that there are significantly more AM mushroom taxa, but is currently only known to environmental sequences (Helgason et al. 2002); (Öpik et al. 2013); (Öpik et al. 2014). However, the heterogeneous and dynamic nature of soil ecosystems makes it difficult to examine the impact of soil environment on in situ natural microbial communities.

2.17. Arbuscular Mycorrhizal Fungus in Soil

AM fungus, which is naturally found in nature, constitutes the most important part of the nutrient cycle of the plant (Fitter et al. 2011); (Marschner and Rengel 2012). As aforementioned, mycorrhizal symbiosis which is 450 million years old, is the most common and oldest mutualistic relationship in the world (Parniske 2008). Mycorrhizae are the most common associations between microorganisms and highly structured plants. Plants that are not mycorrhizae are

highly impaired in extreme wetlands, in very dry or salted environments, or in places where soil efficiency is extremely high or low. When an effective mycorrhizal root infection is performed, the host plant, which is infecting the AM fungus, enables the retrieval of many nutrients, mainly phosphorus (P) and zinc (Zn) (Cameron 2010); (Ortas and Akpinar 2011); (Ortas 2012). In the studies conducted in organic production systems, it was determined that the AM mushroom increased P intake in the soil by affecting the microbial activity and root secretions (Nelson and Janke 2007). In addition to increasing the CO_2 exchange rates of plants along with the atmosphere, Mycorrhizae also provides carbon transportation between plants through its hives (Raman and Mahadevan 1996).

Additionally, mycorrhizae do not only assist plants in the intake of nutrients and water but also increases the resistance of the plant to diseases and pathogenic organisms (Smith and Read 2008a). Furthermore, excessive fertilizer use in agricultural soil (P and N), chemical drug and soil management models adversely affect the potential of indigenous mycorrhizae (Gollner et al. 2011); (Ortas and Coskan 2016b). When there is excessive phosphorus in the soils, the HIF distribution of mycorrhizae fungus is stopped and phosphor carrier genes are put under pressure to stop the intake of P (Ortas et al. 1996a); (Nagy et al. 2009); (Ortas and Lal 2012).

In recent years, various cultivating techniques have been used for the production of mycorrhizae Mushroom (Ortas et al. 1999). These are tested all over the world as soil and substrate-related methods, ungrounded culture methods and in-vitro cultivation methods (IJdo et al. 2011).

2.18. Carbon Flow to Arbuscular Mycorrhizal Fungi

Mechanism of C transfer to AMF is still elusive (Casieri et al. 2013); (Field et al. 2017). Arbuscules are supposed to be the main (but not the only one) place of the C influx (Casieri et al., 2013; Manck-Götzenberger and Requena, 2016). It has been suggested that sucrose is exported from plant cells, cleaved in the interfacial

space and then the monosaccharides are transported into the fungal cells (Doidy et al. 2012). However, this paradigm is now challenged in more than one way – e.g. other organic compounds are suspected to be transferred from plants to AMF.

There are some plant monosaccharide transporters (MSTs) with the expression patterns influenced by the presence of AMF, but none of them showed activation exclusive to mycorrhiza (Casieri et al. 2013); (Garcia et al. 2016). Recently, researchers focus on the plant transporter family with beautiful apt name "sugars will eventually be exported transporters" (SWEETs), which can be responsible for both influx and efflux of saccharides to/from protoplast (Manck-Götzenberger and Requena 2016). None of them was discovered to have mycorrhiza-exclusive activation, but many of them were found to have expression influenced by the presence of AMF. It is suggested now that the sucrose is both exported to the apoplast (and cleaved there by cell wall-bound invertases) and cleaved in the cortical cells (and glucose is then exported to apoplast) to supply sugars to AMF (Manck-Götzenberger and Requena 2016). One MST responsible for the sugar uptake from the symbiotic interface was so far identified in AMF *Rhizophagus irregularis* (Garcia et al. 2016).

2.19. Mycorrhizae on Carbon Sequestration

The biological effects of rising atmospheric CO_2 concentrations and temperature as a part of climate change which has focused on plant growth and carbon fixation through photosynthesis. However, the crucial component of terrestrial ecosystems, especially in the soil, has received less attention. AM fungi form symbiotic association with more than 80-90% of terrestrial plant species and are known to improve nutritional status of host plants besides providing tolerance to abiotic and biotic stress conditions. The host plants have the ability to control the C flow into the soil where it may get accumulated or be oxidized to the atmosphere as well as nutrient flow to the host plants and thereby indirectly controlling the photosynthetic activities of host plants (Dixon et al. 1994). In many works it has

been revealed that mycorrhizal inoculation has significant contribution on plant growth and carbon fixation (Ortaş et al. 2017; Ortaş et al. 2016).

2.20. Concluding Remarks and Research Gaps

However, little is known about the mechanisms by which mycorrhizae enhance sweet sorghum genotypes growth and yield. Also, the relationship between genotypes diversity related with root growth parameters and mycorrhizal colonization is vital question to be searched. Furthermore, the majority of previous studies have been conducted on sorghum plant; this thesis used the sweet sorghum genotypes to study the indigenous mycorrhizae impact on soil, sweet sorghum genotypes growth and yield response. Therefore, the inoculation of indigenous or selected mycorrhizal inoculation is necessary for selecting the efficient sweet sorghum genotypes under divers soil and climate conditions.

3. MATERIAL AND METHODS

3.1. Sources of Sweet Sorghum Genotypes Used in Study

Total 16 sweet sorghum genotypes mentioned in the study were tested under two different field conditions and effective genotypes determined for both locations. The sweet sorghum genotypes used in trial were commercial varieties, which were grown in almost all parts of the world, and used as materials in various research studies. Selected 16 sweet sorghum genotypes were obtained from different sources such as from University of Nebraska, the gene bank in the İsmail Dweikat laboratory (Table 3.1).

Table 3.1. Sweet sorghum genotypes used in the study

No.	Genotype Name	Name of organization
1	Cowley	Nebraska University/USA
2	Grassi	Nebraska University/USA
3	M81-E	Nebraska University/USA
4	Nebraska sugarcane	Nebraska University/USA
5	P1575753	Nebraska University/USA
6	Ramada	Nebraska University/USA
7	Roma	Nebraska University/USA
8	Smith	Nebraska University/USA
9	Theis	Nebraska University/USA
10	Topper 76	Nebraska University/USA
11	Trcay	Nebraska University/USA
12	UNL.hybrid-3	Nebraska University/USA
13	Williams	Nebraska University/USA
14	No91 (Taiwan)	USDA/USA
15	No5 (S. Africa	Nebraska University/USA
16	Gülşeker	Uludağ University/Turkey

Most of the genotypes used in this study were collected from the Nebraska University, USDA (USA) and one genotype (Gülşeker) from Uludag University (Bursa), Turkey.

3.2. Experimental Locations

Experiments were located under filed conditions in Çukurova soil series (Adana) and Harran soil series (Şanlıurfa) as shown in (Figure 3.1). The two locations have different environmental conditions as described in the Table 3.2 and Table 3.3.

Figure 3.1. Selected sites across Adana and Şanlıurfa-Turkey
Key: A. Adana, Ş. Şanlıurfa

3.2.1. Adana Location

Field experiments were located at the Eastern Mediterranean Agricultural Research Institute (Adana, 36°51' 35" K and 35° 20' 43" D). Under the semi-arid climate conditions, the average temperature for June to October in 2016 and August – September in 2017 was higher than 41 °C. The average relative humidity for this period was 83.1% and total

rainfall was 63.8 kg m-^{2}. It was concluded that this amount of precipitation is not sufficient for growing sorghum and must be watered (Table 3.2).

The average temperature for June-October in Adana was 24.8 °C and this average was very similar to average temperature for many years. However, it was found that temperature was 42 - 43 °C in July-August. The average relative humidity for this period was79.0% and total rainfall was 46.2 kg m^{2} (Table 3.2). Then mean Monthly temperature for June-October 2017 in Adana was 25.1 °C and this average is very similar to average temperature for 2017 and long years. However, it was found that temperature was around 40 °C in June –August (Table 3.2).

The average relative humidity for this period was 79.6% and total rainfall was 48.2 kg m^{-2} (Table 3.2). In this context, working with sweet sorghum in context of this study is an accurate and strategically correct product choice. As it is known, sorghum is a C4 plant and it has the highest total temperature demand, total temperature of photosynthesis to turn into carbohydrate accumulation is also included in product group that has the highest.

Table 3.2. Mean monthly temperature (°C), precipitation (kg m-^{2}) and humidity (%) during the growing season of sweet sorghum for study years 2016-2017, Adana location.

2016						
Climate Factors	June	July	August	September	October	Mean
Mean Temperature	25.3	27.7	27.7	24	20.5	25.1
Max. Temperature	41.5	36.8	39.3	34.9	36.4	37.8
Mim. Temperature	16.2	18.6	19.6	9.5	7.3	14.2
Humidity %	79.4	81.6	83.7	77.3	72.8	79
Precipitation (kg/m2)	15.2	1.4	1	26.6	2	46.2
2017						
Climate Factors	June	July	August	September	October	Mean
Mean Temperature	24.4	28	27.3	25	19.4	24.8
Max. Temperature	36.1	43.7	42.4	37.4	33.1	38.5
Mim. Temperature	14.8	18.5	19.5	14.1	7.4	14.9
Humidity %	81.5	79.9	84	81.9	70.7	79.6
Precipitation (kg/m2)	7.8	4	0.8	1.8	33.8	48.2
Long years (1929-2017)						
Climate Factors	June	July	August	September	October	Mean
Mean Temperature	25.8	28.2	28.7	26.1	21.6	25.4
Max. Temperature	31.7	33.8	34.6	33.1	28.9	38.1
Mim. Temperature	19.6	22.8	23.2	20	15.5	19.5
Humidity %	85.1	85	81	82.9	84.6	83.1
Precipitation (kg/m2)	20.4	6.3	5.6	17.8	42.1	139.5

Source: Turkish state meteorological service

3.2.2. Şanlıurfa Location

Field experiments were located at the South-eastern Anatolia Project (GAP) area, Şanlıurfa-Turkey (360 42’ K, 380 58’ D) during the second crop season. When the study was conducted, higher temperature values were observed in July, August and September compared to other months. During these months, temperature increased to over 40 ºC. There was a clear difference between day and night temperatures in Şanlıurfa. Especially in early morning hours before the sunrise, temperature

decreased, but with rise of the sun, temperature increased rapidly. Therefore, temperature values were low. However, during the day, temperature values were similar to highest temperature values. In June, July, August and September (2017), average relative humidity was 28%, 25.4%, 30.6% and 32.1%, respectively (Table 3.3), the relative humidity in Şanlıurfa was below 50% in summer.

The climatic values in June-October 2016 and 20017 survey periods are given (Table 3.3). In 2016 and 2017, higher temperature values were observed in June, July and August than in other months. During these months, temperature increased to over 40 ºC. There was also a serious difference between day and night temperatures in Şanlıurfa. Especially in early morning hours before the sunrise, temperature decreased, but with rise of the sun, temperature increased rapidly. Therefore, average temperature values appeared low. However, during day, temperature values were similar to the highest temperature values. In June, July, August and September (2016), average relative humidity was 42.1%, 40.5%, 49.8% and 48.1%, respectively. In June, July, August and September, in year 2017, average relative humidity was 28.0%, 25.4%, 30.6% and 32.1% below 50%, respectively. In both trial years, relative humidity values increased partly in night and early morning, but at the lowest levels throughout the day with sunrise (Table 3.3).

Table 3.3. Mean monthly temperature (°C), precipitation (kg m-^{2}) and humidity (%) during the growing season of sweet sorghum for study years 2016-2017, Şanlıurfa location.

2016						
Climate Factors	June	July	August	September	October	Mean
Mean Temperature	27.1	30.6	29.2	26.9	20.8	26.9
Max. Temperature	40.5	41.8	42.2	36.2	31	38.3
Mim. Temperature	13.1	15.4	16.2	14	9.2	13.6
Humidity %	42.1	40.5	49.8	48.1	60	48.1
Precipitation (kg/m2)	0	0	0	1	15.8	3.4
2017						
Climate Factors	June	July	August	September	October	Mean
Mean Temperature	29.8	33	33.2	26.4	22.1	28.9
Max. Temperature	42	43	43	39.3	33.9	40.2
Mim. Temperature	18.9	20.9	21.2	14.7	12.3	17.6
Humidity %	28	25.4	30.6	32.1	35.9	30.4
Precipitation (kg/m2)	0.6	0.2	0	0	22	4.6
Long years (1929- 2017)						
Climate Factors	June	July	August	September	October	Mean
Mean Temperature	28.2	31.9	31.2	26.8	20.2	27.7
Max. Temperature	44	46.8	44.8	42	37	42.9
Mim. Temperature	10	16	16	11.2	2.5	11.1
Humidity %	32.8	30.1	33.1	35.8	46.4	35.6
Precipitation (kg/m2)	3.6	0.6	0.8	3.3	27.4	7.1

Source: Turkish state meteorological service

3.2.3. Soil Conditions of Experimental Sites

Initial soil physio-chemical properties are shown in (Table 3.4) Soil samples were taken from 0-30 cm depth from experimental sites in Adana and Şanlıurfa locations. Adana soil series are Arik. The Adana soil initial physio-chemical properties were as pH 7.72, average lime content 20%, organic matter 2%, sand 27.8%, clay 31.2% and silt was 41%. The experiment under field conditions of Şanlıurfa was conducted in the Harran soil Series, which is a wide spread area in the region and is located

entirely in research station. These soils series have alluvial parent material, flat and nearly flat inclined deep-profiled soils (Irmak and Surucu 2007). Typical red profiles are clayey textured and the entire profile was very calcareous (Table 3.4). A, B, C horizon soils, pH was 7.3 - 7.8, organic matter content was low, cation exchange capacity was high. The average temperature for June-October period was 29.5 ºC, the mean sunshine duration was11.48 hours, the highest temperature was 44.4 ºC and average relative humidity was around 36.5% (Anonymous 2017).

Table 3.4. Some Chemical and physical properties of soil at depths of 0–30 cm in Adana and Şanlıurfa Location

Location	Adana		Şanlıurfa	
pH (1:2.5 H2O)	7.4	±0.01	7.6	±0.02
EC (dS/m) (1:2.5 H2O)	0.18	±0.03	0.2	±0.04
OM (%)	1.16	±0.07	0.67	±0.01
Total N (%)	0.11	±0.02	0.059	±0.03
Available P (mg/kg)	0.63	±0.02	0.39	±0.04
CaCo3 (%)	30.3	±0.01	40.8	±0.03
Spore number (spore/10g soil)	35	±0.5	45	±0.04
Sand (%)	25.2	±0.5	28.3	±0.02
Silt (%)	42	±1.4	26.7	±0.01
Clay (%)	32.8	±0.2	45	±0.01
Textural class	clay loam		clay	

Values were means of three replicates ±S.D.

3.3. Method

Used as a four-step study in field and greenhouse experiments flow chart. The flow chart of the method and the work done is as given in Figure 3.2.

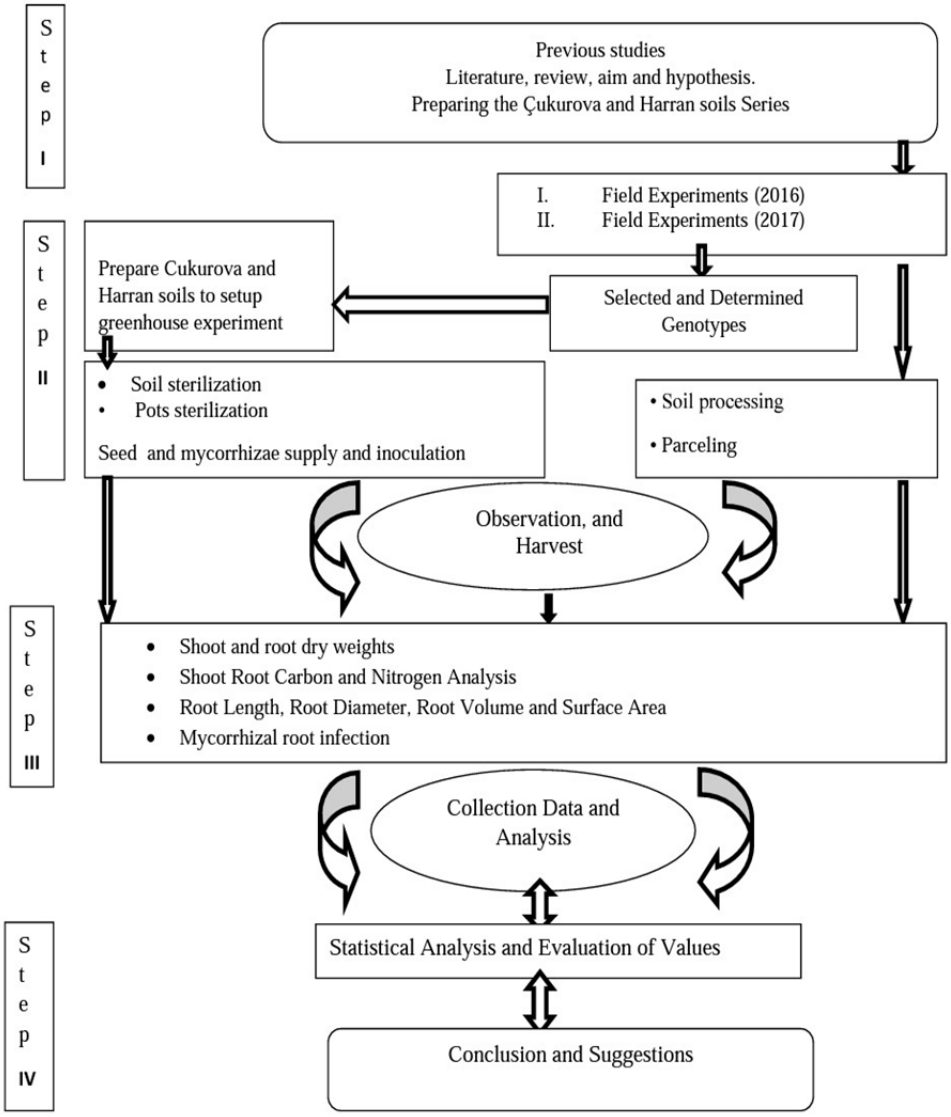

Figure 3.2. Flow of the Method and Work Performed in the Research

3.3.1. Field Experiment Design

The experiment in both trial sites (locations were Adana and Şanlıurfa) were conducted in summer seasons (June to October) in Turkey in the year of 2016 and 2017. Sixteen sweet sorghum genotypes were evaluated as randomized complete block design with four replications. Each plot contained 4 lines. In both trial sites, each experimental had plot sizes 2.8 × 5 m (14 m^2). The line to line distance was 70 cm. The plant to plant distance was 15 cm. The experimental designs were 2 locations × 16 genotypes × 2 years.

3.3.1.1. Field Experiment Management

The 16 sweet sorghum lines were sown; initial seeding rates of both two-year experiments were 95,000 seeds ha^{-1}. At both locations sowing was done by hand putting of seeds with 3 seeds per hill. The plants were thinned two weeks after planting when the plants were completely established.

Before sowing, 50 kg ha^{-1} pure nitrogen and phosphorus were applied to the experimental plots as basal fertilizers. Dressing fertilizers were applied manually when the plants reached to heights of 40-50 cm as to have 50 kg ha^{-1} pure nitrogen. 20:20 composite was used as a phosphorus and nitrogen fertilizer source; Urea was applied as a nitrogen (46 %N) fertilizer source. At a rate was applied as split fertilizer dose.

The experiments at both locations were rainfed and supplemented by irrigation. The trials at both locations were kept weed free by hand dig up. During the period of vegetation, spraying was applied 4 times against the stalk worm. The plant was harvested at 98-144 DAS at flowering stage in both years.

3.3.1.2. Harvest and Root Samples Collection Procedure

At harvest, shoot and root parts of genotypes were taken separately. Root samples were collected according to monolith root sampling techniques (Riedell and Osborne 2017). Monolith sampling was used to remove a soil block as randomized complete block design with three replications (20 cm long by 10 cm wide by 30 cm deep) in which root length was measured after grid sampling. Soil–root monoliths were taken on the same dates as roots were dug using standard techniques. Roots were separated from soil manually and washed by tap water initially Figure 3.3.

Figure 3.3. Field Experiment root samples collection Şanlıurfa location 2017

3.3.2. Greenhouse Experimental Design

Çukurova and Harran Soils were collected from 0 to 30 cm soil depth at both locations in Adana and Şanlıurfa. Çukurova soils taken from experiment area of the Eastern Mediterranean Agriculture Research Institute, Adana, Turkey. The collected Çukurova soil series was Arıklı. Global positioning system (GPS) location of collected soil site is 36°51' 35" K and 35° 20' 43". Harran soils taken from experiment area of the GAP Agriculture Research Institute, Akçakale/Şanlıurfa, Turkey (Şanlıurfa, 360

42’ K, 380 58’ D) the Soils were sieved through a 2- mm screen and placed in 3 kg -plastic pots. The soils were sterilized in an autoclave at 121 °C, 1 atm for 2 hours. Soils initial basic chemical and physical properties of soil were measured and shown in (Table 3.4).

This experiment was conducted in greenhouse at the University of Çukurova, Department of Soil Science and Plant Nutrition, Adana, Turkey. In the experiment, a total of 2 soil series 2 mycorrhizae (with mycorrhizae and without mycorrhiza) and the most effective determined in the field denomination of 16 sorghum genotypes and three replications for the cultivation of the total (2 x 2 x 16 x 3 = 192) 192 pots used.

Figure 3.4. Greenhouse experiment the different sweet sorghum genotypes with and without mycorrhizae

3.3.2.1. Greenhouse Experiment Management

Plants were grown under natural photoperiods with 10 hours’ light at 33/21°C (day night^{-1}) on 65% humidity in Greenhouse. Mycorrhizal treatments received 100 g of indigenous mycorrhizae half of it mixed with soil in pot and half of it was placed about 30 mm below the seed. The plants were watered every second day to maintain at 75% of field capacity throughout the experiment to avoid any possible loss of applied fertilizer

through de-nitrification in excessive moisture. Initially 5 pre-germinated seeds were sown in each pot, after that thinned to 2 plants at 10 days after sowing (DAS). The NH_4NO_3 was used as N source. An 80 kg N ha^{-1} and 50 P_2O_5 kg ha^{-1} was used as a basal dose.

Initial AMF spores were 45 per 10 g soil in Adana soil and 35 per 10 g soil in Şanlıurfa soil. Indigenous mycorrhizae inoculums were produced for two months with onion and alfalfa plants. The AMF spores for indigenous mycorrhizae inoculums were 250 per 10 g soil. Each pot was re-positioned during experiment period to avoid positional error. The experiment was harvested at 8 weeks after sowing and befor the boot stage (Undersander et al. 1990).

Figure 3.5. Sweet sorghum growth response during experiment period was differentiated.

3.3.3. Root Morphological Characteristics Measurement

At harvest the roots were separated from the shoots. The separated roots were washed 3-4 times with deionized water. Then, the whole root system was scanned by a root-system scanner. Root morphological characteristics was measured using the software WinRHIZO image analysis system (WIN MAC, Regent Instruments Inc., Quebec, Canada, http://www.regentinstruments.com/) (Arsenault et al. 1995).

3.3.4. Root Biomass and Trait Measurements

The root samples were first passed through a 2 mm sieve with water to loosen the soil particles ensuring all water was collected. Root material was dried in a fan forced oven at 65°C for at least 48 h until constant weight. Root dry weights were converted to an equivalent mass per hectare of soil surface kg ha^{-1} using the cross-sectional surface area of the soil core. Carbon accumulation kg ha^{-1} in above ground biomass and roots was determined by multiplying dry matter weight by total C concentration. Annual C inputs from the rooting systems of sweet sorghum were estimated to determine how it may compensate for the removal of aboveground biomass. For convert of aboveground and belowground carbon to carbon dioxide calculator: One ton of carbon equals 44/12 = 3.67 tons of CO_2.

3.3.4.1. Root Colonization

Roots were separated from the core soil by the method of (Ortas et al. 1996a). The shoots were separated from the roots at 0.5 cm above the soil surface. Following which, they were separated from the soil by washing with running tap water and distilled water. Furthermore, the roots were then cut into 1 cm segments and stored in 70% ethanol at 4°C for further analysis of mycorrhizal infection and root morphological analysis. The small proportion of the roots were stained as described by Koske and Gemma (1989), to examine the presence and degree of mycorrhizal infection according to (Giovannetti and Mosse 1980).

3.3.5. Soil Analysis

Soil reaction was determined using a ratio 1:2.5 soil to water by pH meter. Electric conductivity (EC) was determined with an Orion model 115A plus conductivity meter bridge (Schlichting and Blume 1966). The

lime content of the soil was measured by Scheibler calcimetres and the results were calculated as $CaCO_3$ percentage. Organic Carbon was determined according to modified Walkley-Black method and results were calculated as % (Nelson and Sommers 1982). Soil structure, the texture of the soil was determined according to (Bouyoucos 1962). Mycorrhizae spores were separated and isolated from soil by wet sieving method (Gerdemann and Nicolson 1963). Soil bulk density was measured by collecting a known volume of soil using a metal ring pressed into the soil (intact core), and determining the weight after drying (McKenzie et al. 2004).

3.3.6. Soil Organic Carbon Analysis

Loss-on-ignition (LOI) procedure for SOM following (Wang et al. 1996) and (Wang et al. 2011), were first place 5.000 g soil in a quartz glass and heated at 105 ° C for 12 hours to remove soil moisture, then combust soil in a programmable muffle furnace at 375 °C for 17 hours. Soil organic matter is calculated as the weight loss between 105 ° C and 375 ° C, Calculate % OM and % OC using the following equation:

$$OM\ \% = \frac{(\text{weight } 105\ ^{o}C - \text{weight } 375\ ^{o}C) \times 100}{\text{Weight } 105\ ^{o}C}$$

$$OC\% = \frac{OM\%}{1.724}$$

3.3.7. Plant and Root Analysis

Sweet Sorghum was harvested at dough stage (89 days after planting). Root samples was taken (30 cm long, 15 cm wide, and 30 cm deep) from soil monolith. The monolith soil sampler (Buman et al. 1994), was modified from the design of (Walker and Coventry 1976). Roots were

separated from the soil manually and were washed with distilled water and oven-dried at 65°C for 48 hours, ground top truss through 0.5 mm sieve and stored prior to total nitrogen and carbon analysis. Plant and root samples collected for estimation of dry matter accumulation at 89 days after planting, total carbon (TC) and nitrogen (N) content of the plant and root samples determined by combustion using a Thermo Fisher Scientific FLASH 2000 Series CN Elemental Analyzer (Thermo Fisher Scientific, Waltham, USA).

3.3.8. Dry Matter Accumulation and Plant Nutrient Analysis

As aforementioned, the Sorghum was harvested at dough stage (98-134 days after planting). Randomly selected above ground samples were washed with distilled water and oven-dried at 65°C for 48-hour, ground to pass through 0.5 mm sieve and stored prior to chemical analysis. Plant and root samples collected for estimation of dry matter accumulation at 98-134 days after planting, total carbon (TC) and nitrogen (N) content of the plant and root samples determined by combustion using a Thermo Fisher Scientific FLASH 2000 Series CN Elemental Analyzer (Thermo Fisher Scientific, Waltham, USA).

Total uptake of N/C was calculated separately by the following formula:

$$\text{Uptake of N/C (kg ha}^{-1}\text{)} = \frac{\text{N\% C\% X dry matter (kg ha}^{-1}\text{)}}{100}$$

3.3.9. Mycorrhizal Dependency

Mycorrhizal dependency (MD) was determined by expressing the difference between the shoot dry weight (SDW) of the mycorrhizal plant

and the shoot dry weight of the non-mycorrhizal plant as a percentage of the shoot dry weight of the mycorrhizal plant (Plenchette et al. 1983).

$$\text{Mycorrhizal dependency} = \frac{\text{SDW}(+\text{M}) - \text{SDW}(-\text{M})}{\text{SDW}(+\text{M})} \times 100$$

Where +M = Mycorrhizae plant and –M = Non-mycorrhizae plant

3.3.10. Statistical Analysis

Both experiments (field and greenhouse experiments as randomized complete block design with three replications) results were analyzed by two-way analysis of variance (ANOVA) using the Statistical Analysis System (SAS 9.1.3). In order to investigate the effect of mycorrhizae on shoot dry weight, root dry weight, root colonization, mycorrhizal dependency, C and N dynamics data were analyzed using the Statistical Analysis System (SAS 9.1.3) package program. All the statistical testing was performed based on $P \leq 0.05$ as the critical level for the significance of Turkey.

Tables, graph bars of data were carried out using Excel Office 2016 product (Microsoft Software Inc. USA). Data is presented as means and standard deviation.

Dendogram and Principal Components Analysis (PCA) were completed by using Minitab computer program. The major trends across multivariate data-set of 16 evaluated parameters related to sweet sorghum genotypes were summarized using a PCA on centered and standardized data's.

4. RESULTS AND DISCUSSION

4.1. Field Experiment

4.1.1. Sweet Sorghum Genotypes Growth Response Plant Height (cm)

Growth responses of sweet sorghum varied in between two soil locations, years and genotypes and their statistical signification were presented in Tables 4.2, 4.3, 4.4, 4.5 and 4.6. A higher plant height average was observed in Şanlıurfa location than in Adana location. In the year 2016, the plant height in Adana varied from 325 cm to 437 cm (Table 4.2 Figure 4.1). The highest plant height was obtained from the UNL. hybrid-3 genotype while the lowest plant height was obtained from the Gulşeker genotype (Table 4.2). Similarly, in the year 2017, in the same location, the plant height varied from 313 cm to 425 cm and the plant height of 16 genotypes recorded an average of 372 cm while the highest plant height was observed in UNL. hybrid-3 and the lowest plant height was recorded from Roma genotype (Tables 4.2). Observably, for the 2016 period in the Sanlıurfa location, it was noted that the plant height means of sixteen sweet sorghum genotypes recorded a 384 cm height (Table 4.2). Notably, the Grassi, PI575753 and UNL. hybrid-3, have the highest plant height in comparison to the average of sixteen sweet sorghum genotypes. Similarly, in the same Şanlıurfa location for the year of 2017, plant height changed in between 333 cm to 427 cm and the average of sixteen sweet sorghum genotypes was 381 cm (Table 4.2). Lekgari and Dweikat (2014) previously reported that sweet sorghum was grown up to 4.5 m in cultivation period under appropriate conditions.

In this research, the plant height Tables 4.2 was constant due to the environmental conditions which prevailed during the growth period. The genotypic variations were attributed to the genetic background for most of the trails evaluated among the tested sixteen sweet sorghum genotypes.

Thus, the sweet sorghum is adapted and can be grown under a wide range of cultivation conditions in marginal areas such as salt (Shakeri and Emam 2017). In addition, a one year field study was conducted to evaluate sweet sorghum and sorghum × Sudan grass hybrids as feed stocks for ethanol production (Tew et al. 2008) and they found that yield of Theis sweet sorghum genotype was the highest among all five sweet sorghum genotypes evaluated in their study (Tew et al. 2008). This one-year study also suggested that choice of sweet sorghum type would depend on environment condition.

Figure 4.1. Sweet Sorghum Genotypes growth under at Adana location in 2017

4.1.2. Biomass yield in Sweet Sorghum Genotypes

At harvest the above ground shoot dry weight (SDW) was determined. Generally, on average, shoot dry weight was higher in 2016 than in 2017 for both locations (Table 4.3). The shoot dry weight of the genotypes varies from 29.10 Mg ha^{-1} to 49.2 Mg ha^{-1} and 31.27 Mg ha^{-1} to 65.02 Mg ha^{-1} in the year 2016 and 2017, respectively in Adana location (Table and 4.3). The shoot dry weight varies 29.97 Mg ha^{-1} to 42.76 Mg ha^{-1} and 31.68 Mg ha^{-1} to 54.51 Mg ha^{-1} in the year 2016 and 2017 respectively in Sanliurfa location (Table 4.3).

4.1.3. Root Dry Weight

At the time of harvest, the root's fresh and dry weight was determined as indicated. The root dry weight (RDW) was significantly ($p<0.05$) different among sweet sorghum genotypes. A summation of the data collected and recorded showed that the dry root weight (DRW) was higher in 2016 than it was in 2017 in the Adana location for the various sweet sorghum genotypes (Table 4.4). In the year 2016, the highest DRW was obtained from the UNL.hybrid-3 genotype with 8.12 Mg ha^{-1} and the lowest was obtained from the Ramada genotype with 5.51 Mg ha^{-1}. Similarly, the other genotypes recorded a lower DRW in 2016. As for 2017, the highest recorded DRW was obtained from the Topper 76 genotype which weighed 7.88 Mg ha^{-1} while the lowest recorded was the Williams genotype with a weight of 4.94 Mg ha^{-1}. In the Şanlıurfa location, the 2016 showed that the highest DRW was obtained from the Theis genotype with a weight of 7.12 Mg ha^{-1} whilst the lowest record was obtained from the Nebraska sugarcane genotype with a weight of 4.51 Mg ha^{-1} (Table 4.4). 2017 recorded a high DRW in the UNL.hybrid-3 genotype which indicated a 7.62 Mg ha^{-1} and the lowest being recorded from the Ramada genotype with a weight of 5.12 Mg ha^{-1} (Table 4.5). Other

genotypes varied between these values and from 4.51 to 7.98 Mg ha^{-1} in both locations in the year 2016 and 2017, respectively.

4.1.4. Total Dry Weight

Total dry weight was determined and it has been found that in generally genotypes grown in Adana location for both years proceed more biomass than the same genotypes grown in Şanlıurfa location. The total dry weight (Total biomass) in Adana location average for year 2016 is 43.74 Mg ha^{-1} and for the year of 2017 is 54.32 Mg ha^{-1}. However, for Şanlıurfa location was 40.99 Mg ha^{-1} and 48.66 Mg ha^{-1} respectively, also more yield was determined in year 2017 than the year of 2016 (Table 4.5).

4.1.5. Shoot/Root Ratio

Shoot and root ratio is one of the very important parameters of plant growth. In present work, sweet sorghum genotypes were grown in Adana Location have higher shoot/root ration than Şanlıurfa location for both years. Shoot/root ration is also affected under the soil and climate conditions. Shoot/root ratio was determined to be significantly ($p<0.05$) different among sweet sorghum genotypes in both Adana and Şanliurfa location. The average shoot/root ratio for the sweet sorghum genotypes is 5.9 – 8.0 in Adana location in year 2016 and 2017 respectively (Table 4.6). Similarly, mean shoot/root ratio was 5.7- 6.6 in years 2016 and 2017 in Şanliurfa location (Tables 4.6).

Overall results shown that locations have significant effect on root growth parameters (Tables 4.1). Since Adana location have high rainfed than Şanlıurfa location that it is affected by soil water content. As a results plant growth in Adana location is higher than that in Şanlıurfa location. It has been indicated that under water stress conditions the root/shoot ratio was improved (Younis et al. 2000). Also Clark and Reinhard (1991)

reported that sorghum Genotypes differed in most growth traits, especially dry matter yields, root lengths, and leaf areas.

Table 4.1. Level of significance for the main and interactive effect on plant height, shoot biomass, Root biomass and Total biomass of the sweet sorghum genotypes in years 2016 and 2017 at Adana and Şanlıurfa Locations.

Sources of variations	**Plant height**	**Shoot. D.W**	**Root. D.W**	**Total Biomass**
Genotypes	***	***	***	***
Location	n.s.	n.s.	***	n.s.
Genotypes X Location	***	***	***	***
Year	***	n.s.	***	n.s.
Genotypes X Year	***	***	***	***
Location X Year	n.s.	***	**	***
Geno X Location X Year	*	***	***	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.2. Average of plant height in years 2016 and 2017 at Adana and Şanlıurfa Locations.

Genotype	Plant height (cm)											
	2016		2017		Mean		2016		2017		Mean	
	Adana location						Şanlıurfa location					
Cowley	338	±13hi	367	±15c-e	353	±14.5d-f	352	±24g	380	±5b-d	366	±14.0e-g
Grassi	393	±6dc	389	±8.0b-d	391	±2.0bc	**446**	**±14a**	**413**	±6ba	430	±16.5a
M81-E	422	±8ba	410	±26ba	416	±6.0ab	379	±5.0b-e	383	±24b-d	381	±2.0c-g
Neb. sugarcane	368	±8ef	393	±15bc	381	±12.5b-d	380	±5.0b-e	358	±18d-f	369	±11.0d-g
PI 575753	347	±6hg	337	±8.0f-h	342	±5.0ef	**442**	**±13a**	405	±23ba	424	±18.5a
Ramada	363	±6gf	373	±15c-e	368	±5.0c-e	388	±8.0b	380	±17b-d	384	±4.0b-e
Roma	337	±15hi	**313**	±15h	325	±12.0f	367	±8.0d-g	368	±19c-f	368	±0.5d-g
Smith	367	±13ef	352	±24e-g	360	±7.5c-f	365	±.2.0e-g	383	±25b-d	374	±9.0c-g
Theis	408	±16bc	412	±15ba	410	±2.0ab	**352**	**±8.0g**	338	±13ef	345	±7.0g
Topper 76	377	±8d-f	365	±15ed	371	±6.0c-e	370	±5.0c-f	**333**	±12f	352	±18.5e-g
Tracy	335	±5hi	372	±13c-e	354	±18.5d-f	383	±4.0b-d	**423**	±46a	403	±20.0a-d
UNL. hybrid-3	**437**	±15a	**425**	±15a	**431**	±6.0a	**437**	**±15a**	400	±13a-c	419	±18.5ab
Williams	330	±10hi	325	±25hg	328	±2.5f	365	±5.0e-g	398	±24a-c	382	±16.5c-f
No91	427	±18a	407	±19ba	417	±10.0ab	375	±15b-e	363	±16d-f	369	±6.0d-g
No5	383	±12de	360	±10ef	372	±11.5c-e	355	±5.0gf	340	±10ef	348	±7.5fg
Gülşeker	**325**	±5i	352	±10e-g	339	±13.5ef	386	±8.0cb	**427**	±25a	407	±20.5a-c
Mean	**371**	**±10.1**	**372**	**±16**	**372**	**±0.5B**	**384**	**±9.0**	**381**	**±18**	**382**	**±1.6A**
P≤0.05		**0.0001**		**0.0001**				**0.0001**		**0.0001**		

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.3. Average of shoot dry weight in years 2016 and 2017 at Adana and Şanlıurfa Locations.

Genotype	Shoot Dry Weight (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana location						Şanlıurfa location					
Cowley	32.4	±1533d-g	36.7	±489hg	34.6	±2.2ef	35.5	±2101c-f	46.0	±394b-d	40.8	±5.2a-c
Grassi	34.7	±7451d-g	54.2	±344dc	44.5	±9.7cd	31.0	±1716gf	43.2	±357c-f	37.1	±6.1a-d
M81-E	34.8	±885d-g	57.1	±952b-d	46.0	±11.2cd	36.9	±2066bc	43.0	±118d-f	39.9	±3.1a-d
Neb. sugarcane	37.9	±3474c-e	43.5	±263fe	40.7	±2.8c-e	40.8	±5054ba	43.0	±100d-f	41.9	±1.1ab
PI 575753	29.4	±859fg	37.7	±130f-g	33.5	±4.1ef	32.1	±1666d-g	**31.7**	±234g	31.9	±0.2d
Ramada	35.7	±3249c-f	59.1	±955a-d	47.4	±11.7bc	32.9	±3164c-g	34.3	±536g	33.6	±0.7cd
Roma	32.8	±3268d-g	61.0	±952ba	46.9	±14.1bc	34.1	±1933c-g	38.9	±143d-g	36.5	±2.4a-d
Smith	42.1	±1403bc	45.2	±810e	43.6	±1.5cd	32.7	±3042c-g	54.0	±822ba	43.4	±10.6a
Theis	30.6	±571fg	57.9	±7748b-d	44.2	±13.7cd	34.6	±666c-g	39.0	±727d-g	36.8	±2.2a-d
Topper 76	**49.2**	±7164a	**65.0**	±4782a	57.1	±7.9a	**42.8**	**±1763a**	38.2	±714d-g	40.5	±2.3a-c
Tracy	31.8	±935e-g	31.3	±3906g	31.5	±0.3f	**30.0**	**±1243g**	39.7	±212d-g	34.8	±4.9b-d
UNL. hybrid-3	48.6	±3636ba	59.8	±144a-c	54.2	±5.6ab	36.6	±3408b-d	51.3	±286a-c	43.9	±7.4a
Williams	**29.1**	±476g	**31.9**	±130h	30.5	±1.4f	34.7	±1769c-f	44.5	±320c-e	39.6	±4.9a-d
No91	41.8	±1049c	52.4	±952d	47.1	±5.3bc	36.4	±3883b-d	36.3	±588fg	36.3	±0.1a-d
No5	38.7	±6280cd	35.9	±518hg	37.3	±1.4d-f	31.9	±1224f-g	37.3	±618e-g	34.6	±2.7b-d
Gülşeker	48.5	±7146ba	42.3	±453e-g	45.4	±3.1cd	33.8	±4096c-g	**54.5**	±654a	44.1	±10.4a
Mean	**37.4**	**±3086**	**48.2**	**±1471**	**42.8**	**±5.4A**	**34.8**	**±2425.3**	**42.2**	**±426**	**38.5**	**±3.7A**
P≤0.05	**0.0001**		**0.0001**				**0.0001**		**0.0001**			

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.4. Average of Root dry weight in years 2016 and 2017 at Adana and Şanlıurfa Locations.

Genotype	Root Dry Weight (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana location						Şanlıurfa location					
Cowley	6.40	±272cb	6.17	±596c-e	6.29	±0.12b-d	6.70	±205a-d	7.58	±496a	7.14	±0.44a
Grassi	7.58	±559a	**7.51**	±305a	7.55	±0.04a	6.08	±154d-f	7.46	±300a	6.77	±0.69a-c
M81-E	5.52	±175d	5.27	±214fg	5.40	±0.13d	6.14	±233c-f	6.23	±656dc	6.19	±0.05a-d
Neb. sugarcane	6.16	±431b-d	5.99	±419c-f	6.08	±0.09b-d	**4.51**	**±113h**	5.83	±119c-e	5.17	±0.66e
PI 575753	6.17	±79b-d	5.85	±305d-f	6.01	±0.16b-d	6.81	±48ba	5.56	±182de	6.18	±0.63a-d
Ramada	**5.51**	±180d	5.45	±140eg	5.48	±0.03cd	5.70	±251gf	**5.12**	±833e	5.41	±0.29de
Roma	5.67	±208d	5.29	±212fg	5.48	±0.19cd	5.91	±553ef	5.87	±718c-e	5.89	±0.02c-e
Smith	6.78	±1102b	6.59	±171bc	6.69	±0.10a-c	5.14	±424gh	**7.54**	±248a	6.34	±1.20a-d
Theis	5.67	±189d	5.40	±324fg	5.54	±0.14cd	**7.12**	**±304a**	6.51	±300bc	6.81	±0.31a-c
Topper 76	**7.98**	±208a	7.88	±309a	7.93	±0.05a	6.28	±238b-f	5.95	±357dc	6.12	±0.16b-e
Tracy	6.19	±717b-d	6.22	±754dc	6.21	±0.01b-d	6.73	±380a-c	7.10	±451ba	6.92	±0.19ab
UNL. hybrid-3	8.12	±208a	**7.34**	±428a	7.73	±0.39a	6.66	±305a-d	**7.62**	±238a	7.14	±0.48a
Williams	5.58	±136d	**4.94**	±61g	5.26	±0.32d	6.13	±370c-f	7.26	±119ba	6.70	±0.57a-c
No91	5.67	±208d	5.51	±202d-g	5.59	±0.08cd	6.50	±974a-e	6.27	±364dc	6.39	±0.12a-c
No5	5.99	±236cd	5.64	±286d-g	5.82	±0.18b-d	6.19	±392b-f	5.56	±861de	5.87	±0.32c-e
Gülşeker	6.78	±258b	7.16	±128ba	6.97	±0.19ab	6.67	±240a-d	6.21	±262dc	6.44	±0.23a-c
Mean	**6.36**	**±323**	**6.14**	**±303**	**6.2**	**±0.11B**	**6.20**	**±324**	**6.5**	**±406**	**6.5**	**±0.14A**
P≤0.05	**0.0001**		**0.0001**				**0.0001**		**0.0001**			

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.5. Average of total biomass in years 2016 and 2017 at Adana and Şanlıurfa Locations.

Genotype	Total Biomass (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana location						Şanlıurfa location					
Cowley	38.78	±1263e-i	42.9	±1009fg	40.8	±2.1d-e	42.23	±2010b-d	53.58	±3447a-c	47.9	±5.7a-d
Grassi	42.31	±6909d-g	61.74	±3463bc	52.0	±9.7b	37.03	±1813fe	50.7	±3583c-e	43.9	±6.8a-f
M81-E	40.34	±977e-i	62.42	±741bc	51.4	±11.0bc	42.99	±2276bc	49.21	±1112c-e	46.1	±3.1a-f
Neb. sugarcane	44.03	±3661c-f	49.51	±1797fe	46.8	±2.7b-d	45.27	±5119ba	48.85	±1062c-e	47.1	±1.8a-e
PI 575753	35.57	±930i	43.50	±997fg	39.5	±4.0d-e	38.93	±1687c-f	**37.24**	±2167g	38.1	±0.8f
Ramada	41.22	±3412d-h	64.50	±9202bc	52.9	±11.6b	38.62	±3415c-f	39.41	±4845fg	39.0	±0.4ef
Roma	38.46	±3465e-i	66.24	±866ba	52.4	±13.9b	39.98	±2374c-f	44.76	±715d-g	42.4	±2.4b-f
Smith	48.88	±303bc	51.77	±1403de	50.3	±1.4bc	37.87	±2957d-f	**61.54**	±8407a	49.7	±11.8a-c
Theis	36.25	±736g-i	63.31	±7447bc	49.8	±13.5bc	41.69	±527b-e	45.49	±7566c-f	43.6	±1.9a-f
Topper 76	**57.16**	±6964a	**72.89**	±4956a	65.0	±7.9a	**49.04**	**±1527a**	44.18	±7195d-g	46.6	±2.4a-e
Tracy	37.97	±1612f-i	37.49	±4361g	37.7	±0.2e	**36.70**	**±1281f**	46.79	±1670c-f	41.7	±5.0c-f
UNL. hybrid-3	56.72	±3818a	67.12	±1526ba	61.9	±5.2a	43.23	±3713bc	58.89	±3054ba	51.1	±7.8a
Williams	**34.63**	±340i	**36.84**	±1281g	35.7	±1.1e	40.86	±2108b-f	51.8	±3164b-d	46.3	±5.5a-f
No91	47.51	±849dc	57.89	±755dc	52.7	±5.2b	42.91	±4291bc	42.52	±6185e-g	42.7	±0.2a-f
No5	44.65	±6178c-e	41.57	±5585g	43.1	±1.5c-e	38.06	±1414d-f	42.89	±7006e-g	40.5	±2.4d-f
Gülşeker	55.32	±7392ba	49.48	±4502fe	52.4	±2.9b	40.45	±4163c-f	**60.71**	±6498a	50.6	±10.1ab
Mean	**43.7**	**±7465**	**54.3**	**±11605**	**49.03**	**±5.3A**	**41.0**	**±3281**	**48.7**	**±7259**	**44.8**	**±3.8B**
P≤0.05		**0.0001**		**0.0001**				**0.0004**		**0.0001**		

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.6. Average of Shoot/Root in years 2016 and 2017 at Adana and Şanlıurfa Locations.

Genotype	Shoot/Root (Ratio)											
	2016		2017		Mean		2016		2017		Mean	
	Adana location						Şanlıurfa location					
Cowley	5.1	±0.5d-f	6.0	±0.5fe	3.7	0.45de	5.3	±0.4b-d	6.1	±0.9b-d	3.8	±0.4b-e
Grassi	**4.6**	±1.4f	7.2	±0.5de	3.9	1.30de	5.1	±0.2ed	5.8	±0.5cd	3.6	±0.4b-e
M81-E	6.3	±0.2a-d	10.9	±0.6ba	5.7	2.30a	6.0	±0.2b-d	7.0	±0.9cb	4.3	±0.5b-e
Neb. sugarcane	6.2	±0.5a-d	7.3	±0.9de	4.5	0.55a-e	**9.0**	**±1.0a**	7.4	±0.2b	5.5	±0.8a
PI 575753	4.8	±0.1f-e	6.5	±0.6e	3.8	0.85de	4.7	±0.2ed	**5.7**	±0.6d	3.5	±0.5de
Ramada	6.5	±0.4a-d	10.9	±1.8ba	5.8	2.20a	5.8	±0.3b-d	6.9	±1.8b-d	4.2	±0.6b-e
Roma	5.8	±0.4c-f	**11.5**	±0.6a	5.8	2.85a	5.8	±0.4b-d	6.7	±1.1cb	4.2	±0.5b-e
Smith	6.4	±1.4a-c	7.0	±1.2e	4.5	0.30a-e	6.4	±0.9cb	7.1	±0.9b	4.5	±0.4a-c
Theis	5.4	±0.1d-f	10.8	±2.0ba	5.4	2.70a-c	4.9	±0.3ed	6.0	±0.9b-d	3.6	±0.6c-e
Topper 76	6.2	±1.1b-e	8.3	±0.5dc	4.8	1.05a-d	6.8	±0.5b	6.4	±1.2b-d	4.4	±0.2b-d
Tracy	5.2	±0.5d-f	**5.0**	±0.6f	3.4	0.10e	**4.5**	**±0.3e**	5.6	±0.6cd	3.4	±0.6e
UNL. hybrid-3	6.0	±0.3b-e	8.2	±0.5dc	4.7	1.10a-e	5.5	±0.3b-d	6.7	±0.3cb	4.1	±0.6b-e
Williams	5.2	±0.2fe	6.5	±0.2e	3.9	0.65de	5.7	±0.1b-d	6.1	±0.5b-d	3.9	±0.2b-e
No91	**7.4**	±0.5a	9.5	±0.5bc	5.6	1.05ab	5.7	±0.9b-d	5.8	±0.7cd	3.8	±0.0b-e
No5	6.5	±1.2a-d	6.4	±0.8e	4.3	0.05c-e	5.2	±0.3c-e	6.7	±0.4b-d	4.0	±0.8b-e
Gülşeker	7.1	±0.8ba	5.9	±0.6fe	4.3	0.60b-e	5.1	±0.6ed	**8.8**	±1.2a	4.6	±1.9ab
Mean	**5.9**	**±0.6**	**8**	**±0.8**	**4.64**	**1.05A**	**5.7**	**±0.4**	**6.6**	**±0.8**	**4.09**	**±0.5B**
P≤0.05		**0.0025**		**0.0001**				**0.0001**		**0.0015**		

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

4.1.6. Effect of Climatic and Soil Condition on Sweet Sorghum Growth Response

Sweet sorghum genotypes growth response was significantly ($p<0.05$) different in between the two locations. Genotypes growth parameters were better in Adana location than those recorded in Şanlıurfa location. The climatic conditions in the Adana location are mild. The precipitation levels are usually 650 mm per year (Ortas and Coskan 2016a) and the soil nutrients are rich as indicated in the soil properties Table 3.2. Given such, this contributed to the sweet sorghum genotypes growth parameters recorded in the location. Regardless of the sweet sorghum's drought resistant properties, the mild climatic conditions were an additive to the better growth results obtained. As accordingly, Laopaiboon et al. (2009) reported that sweet sorghum varieties differ widely in their adaptation to various soil and climatic conditions. Similarly, the study of Gnansounou et al. (2005) showed that sweet sorghum can be adapted to widely differing climatic and soil conditions. In the same vein, other studies also speculated that climate has a significant impact on sweet sorghum plant biomass productivity (Clarke et al. 1997).

4.1.7. Root Morphological Characteristics

Root morphological characteristics of sixteen sweet sorghum genotypes vary among the genotypes, locations as well as genotype× locations interaction (Tables 4.7).

4.1.7.1. Root Diameter

The highest root diameter was found 0.662 mm for Grassi genotype and the lowest was 0.553 mm for Williams sweet sorghum genotype in year 2016 at Adana location (Table 4.8).

The highest root diameter recorded was 0.746 mm for PI 575753 sweet sorghum genotype in the year 2016 at Şanliurfa location Table 4.6 and lowest root diameter recorded was for the Theis sweet sorghum genotypes in the year 2017 at Şanlıurfa location Table 4.8 with a 0.448 mm root diameter. Root diameter differ significantly ($p<0.05$) among sweet sorghum genotypes (Table 4.7).

4.1.7.2. Total Root Length

Total root length differed significantly ($p<0.05$) among genotypes as well as locations × genotypes interactions (Tables 4.7). The total root length of the sweet sorghum genotypes was higher in Şanlıurfa than Adana location in the years 2016 and 2017 except Nebraska sugarcane, PI575753, UNL-Hybrid 3, USDA No91 and Gülşeker genotypes. It has been determined that the mean of total root length 62.8 to 62.7 km ha^{-1} in the year 2016 and 2017 in Adana location respectively (Table 4.9). The Cowley had the lowest total root length 46.7 km ha^{-1}, and the UNL-Hybrid 3 have the highest total root length 92.5 km ha^{-1} in 2016 year in Adana location (Table 4.9). Similarly, the total root length of the sweet sorghum genotypes average between 62.2- 63.2 km ha^{-1} in the year 2016 and 2017 in Şanliurfa location respectively (Tables 4.9). The total root length varies 37.7 to 80.5 and 43.2 to 81.2 kg ha^{-1} in the year 2016 and 2017 respectively for Şanliurfa location.

4.1.7.3. Root surface area

Root surface area differed significantly ($p<0.05$) among genotypes as well as locations × genotypes interactions (Tables 4.7). Root surface area of the sweet sorghum genotypes was higher in Adana than Şanlıurfa except for the Cowley sweet sorghum genotypes (Table 4.10). Interestingly, the root volume differs significantly ($p<0.05$) between

locations among genotypes as well as locations and genotypes interactions. The highest and lowest root volume for UNL-Hybrid 3 and Williams's sweet sorghum genotypes were 0.028 and 0.01 m^3 ha^{-1} respectively in the year 2016 at Adana location (Table 4.10). Likewise, the highest and lowest root volume were (0.012 - 0.026 m^3 ha^{-1} in the year 2016 and 0.011-0.026 m^3 ha^{-1} in year 2017 respectively at Şanlıurfa location (Table 4.11).

Table 4.7. Level of significance for the main and interactive effect on root morphological characteristics of sixteen sweet sorghum genotypes in Adana and Sanliurfa Locations.

Sources of variations	**Root Diameter**	**Total Root length**	**Root Surface Area**	**Root Volume**
Genotypes	***	***	***	***
Location	***	n.s.	*	***
Genotypes X Location	**	***	***	***
Year	**	n.s.	n.s.	n.s.
Genotypes X Year	***	***	***	***
Location X Year	n.s.	n.s.	n.s.	n.s.
Geno X Location X Year	***	*	**	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.
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Table 4.8. Average of Root diameter of the sweet sorghum genotypes at Adana and Şanlıurfa locations in years 2016 and 2017

Genotype	Root Diameter (mm)											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	0.647	±0.01a	0.572	±0.03a-c	0.406	±0.04ab	0.619	±0.04c-e	0.654	±0.01a	0.424	±0.018a-c
Grassi	**0.662**	±0.03a	0.592	±0.01ab	0.418	±0.04a	0.651	±0.03b-d	0.637	±0.03a	0.429	±0.007a-c
M81-E	0.631	±0.07a	0.506	±0.01e	0.379	±0.06a-c	0.572	±0.09ed	0.563	±0.11b-d	0.378	±0.005bc
Neb. sugarcane	0.641	±0.02a	0.533	±0.02c-e	0.391	±0.05a-c	**0.711**	±0.01ab	0.588	±0.02a-c	0.433	±0.062ab
PI 575753	**0.461**	±0.02d	0.566	±0.04a-c	0.342	±0.05d	0.746	±0.03a	0.61	±0.06a-c	0.452	±0.068a
Ramada	0.559	±0.01c	0.508	±0.02de	0.356	±0.03cd	0.554	±0.04e	0.551	±0.04c-e	0.368	±0.002c
Roma	0.574	±0.02bc	**0.499**	±0.02e	0.358	±0.04a-c	0.596	±0.05c-e	0.568	±0.02b-d	0.388	±0.014a-c
Smith	0.559	±0.04c	0.528	±0.02c-e	0.362	±0.02b-d	**0.538**	±0.05e	0.542	±0.01c-e	0.360	±0.002c
Theis	0.632	±0.01a	0.565	±0.04a-d	0.399	±0.03ab	0.583	±0.03c-e	0.448	±0.05f	0.344	±0.068c
Topper 76	0.650	±0.03a	0.593	±0.05ab	0.414	±0.03a	0.613	±0.01c-e	**0.656**	±0.02a	0.423	±0.022a-c
Tracy	0.650	±0.04a	0.540	±0.03b-e	0.397	±0.06ab	0.659	±0.03bc	0.641	±0.03a	0.433	±0.009a-c
UNL. hybrid-3	0.620	±0.03ba	0.609	±0.03a	0.410	±0.01a-c	0.573	±0.13ed	0.629	±0.05ba	0.401	±0.028bc
Williams	0.553	±0.02c	0.572	±0.06a-c	0.375	±0.01a-c	0.541	±0.03e	**0.485**	±0.01ef	0.342	±0.028c
No91	0.617	±0.01ba	**0.617**	±0.06a	0.411	±0.00a-c	0.648	±0.02b-d	0.551	±0.02c-e	0.400	±0.049a-c
No5	0.643	±0.01a	0.604	±0.02a	0.416	±0.02a	0.618	±0.03c-e	0.511	±0.01d-f	0.376	±0.054a-c
Gülşeker	0.568	±0.03c	0.537	±0.04b-e	0.368	±0.02b-d	0.586	±0.03c-e	0.649	±0.02a	0.412	±0.032a-c
Mean	**0.604**	**±0.05**	**0.559**	**±0.04**	**0.388**	**±0.02A**	**0.613**	**±0.06**	**0.58**	**±0.06**	**0.398**	**±0.017A**
P≤0.05	**0.0001**		**0.001**				**0.0003**		**0.0001**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.9. Average of tatal root length of the sweet sorghum genotypes at Adana and Şanlıurfa locations in years 2016 and 2017

Genotype	Total Root Length (km ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	46.7	±7f	63.4	±5d	55.1	±8.4d-g	**80.5**	±29a	67.9	±10a-c	74.2	±6.3ab
Grassi	61.8	±6c-e	80.6	±4ba	71.2	±9.4a-d	53.4	±4c-e	56.5	±6c-e	55.0	±1.6a-c
M81-E	49.9	±3ef	49.2	±9e-g	49.6	±0.3fg	50.0	±1de	53.9	±12c-e	52.0	±2.0bc
Neb. sugarcane	48.7	±5ef	55.7	±12d-g	52.2	±3.5fg	**37.7**	±4e	60.9	±7b-e	49.3	±11.6bc
PI 575753	57.4	±4d-f	58.2	±13d-f	57.8	±0.4d-g	49.5	±1de	**43.2**	±4e	46.4	±3.2c
Ramada	54.2	±3ef	60.1	±3de	57.2	±3.0d-g	54.5	±10c-e	59.4	±15b-e	57.0	±2.5a-c
Roma	60.3	±15c-f	46.7	±11gf	53.5	±6.8fg	77.8	±23ba	58.7	±6c-e	68.3	±9.5a-c
Smith	50.9	±8ef	66.5	±8dc	58.7	±7.8c-g	52.9	±6c-e	72.3	±19a-c	62.6	±9.7a-c
Theis	74.6	±13bc	77.9	±6bc	76.3	±1.7ab	75.7	±4ba	80.6	±25a	78.2	±2.5a
Topper 76	57.8	±13d-f	**92.0**	±4a	74.9	±17.1a-c	67.9	±4a-d	69.8	±4a-c	68.9	±0.9a-c
Tracy	81.3	±13ba	57.2	±4d-f	69.3	±12.1a-e	77.2	±4ba	66.3	±11a-c	71.8	±5.5ab
UNL. hybrid-3	**92.5**	±7a	58.4	±6d-f	75.5	±17.1ab	62.4	±15a-d	45.7	±6de	54.1	±8.4a-c
Williams	**46.2**	±5f	**43.0**	±4g	44.6	±1.6g	51.1	±6de	**81.2**	±11a	66.2	±15.1a-c
No91	70.4	±13b-d	55.6	±1d-g	63.0	±7.4b-f	73.4	±6ba	63.7	±11a-d	68.6	±4.9a-c
No5	70.8	±6b-d	55.9	±10d-g	63.4	±7.5b-f	60.3	±4b-d	54.0	±5c-e	57.2	±3.2a-c
Gülşeker	80.8	±12ba	82.3	±12ba	81.6	±0.8a	70.9	±14a-c	77.7	±7ba	74.3	±3.4ab
Mean	**62.8**	**±14.11**	**62.7**	**±13.80**	**62.7**	**±0.0A**	**62.2**	**±12.86**	**63.2**	**±11.4**	**62.7**	**±0.5A**
P≤0.05	**0.0001**		**0.0001**				**0.0007**		**0.0038**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.10. Average of root surface area of the sweet sorghum genotypes at Adana and Şanlıurfa locations in years 2016 and 2017

Genotype	Root Surface Area (m ha^{-2})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	9487	±1478f-h	11412	±1440c-e	10450	±963b-e	**15444**	±4876a	13915	±1903a-c	14680	±765a
Grassi	12848	±1556c-e	14974	±734ab	13911	±1063a	10917	±1217c-f	11275	±990c-e	11096	±179a-d
M81-E	9864	±865f-h	7812	±1307fg	8838	±1026e	8959	±1120d-f	9272	±723fe	9116	±157d
Neb. sugarcane	9807	±1340f-h	9336	±2237efg	9572	±236c-e	8423	±920f	11243	±1410c-f	9833	±1410cd
PI 575753	8307	±806gh	10311	±2139ef	9309	±1002c-e	11589	±569b-e	**8224**	±167f	9907	±1683cd
Ramada	9505	±464f-h	9583	±483efg	9544	±39c-e	9392	±975d-f	10364	±3067d-f	9878	±486cd
Roma	10866	±2631e-g	**7297**	±1709g	9082	±1785de	14337	±3366ab	10494	±1254d-f	12416	±1922a-d
Smith	8869	±721gh	11047	±1689e	9958	±1089c-e	8884	±226d-f	12351	±3446b-d	10618	±1734a-d
Theis	14809	±2683bc	13857	±2043b-d	14333	±476a	13851	±1280a-c	11102	±2173c-f	12477	±1375a-d
Topper 76	11712	±2076d-f	**17081**	±981a	14397	±2685a	13066	±722a-c	14379	±738ba	13723	±657a-c
Tracy	16967	±3557ab	9717	±1071e-g	13342	±3625ab	15956	±963a	13365	±2435a-d	14661	±1296a
UNL. hybrid-3	**17959**	±**876a**	11137	±932ed	14548	±3411a	10920	±2058c-f	9091	±1799fe	10006	±915cd
Williams	8023	±1044h	7699	±907fg	7861	±162e	**8669**	±981fe	12388	±1764b-d	10529	±1860a-d
No91	13630	±2513cd	10786	±1287e	12208	±1422a-d	14902	±808a	11000	±1564c-f	12951	±1951a-d
No5	14308	±1290cd	10635	±2081e	12472	±1837a-c	11690	±706b-d	8655	±782fe	10173	±1518b-d
Gülşeker	14354	±134b-d	13970	±3055bc	14162	±192a	12952	±1820a-c	**15823**	±1520a	14388	±1436ab
Mean	**11957**	**±3107.25**	**11041**	**±1506**	**11499**	**±458A**	**11872**	**±2567**	**11434**	**±2163**	**11653**	**±219A**
P≤0.05	**0.0001**		**0.0001**				**0.0001**		**0.003**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.11. Average of Root Volume of the sweet sorghum genotypes at Adana and Şanlıurfa locations in years 2016 and 2017

Genotype	Root Volume (m ha^{-3})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	0.015	±0.003d-f	0.016	±0.003cde	0.016	±0.001b-e	0.024	±0.007ba	0.023	±0.003ba	0.024	±0.001a
Grassi	0.021	±0.003c	0.022	±0.001ab	0.022	±0.000a	0.018	±0.003c-e	0.018	±0.002b-d	0.018	±0.000a-d
M81-E	0.016	±0.003d-f	**0.010**	±0.002g	0.013	±0.003e	0.013	±0.004f	0.013	±0.003d-f	0.013	±0.000d
Neb. sugarcane	0.016	±0.003d-f	0.012	±0.003e-g	0.014	±0.002c-e	0.015	±0.002fe	0.017	±0.002c-e	0.016	±0.001b-d
PI 575753	**0.010**	±0.001h	0.015	±0.003d-f	0.013	±0.003e	0.022	±0.002a-c	0.013	±0.001ef	0.018	±0.005a-d
Ramada	0.013	±0.001f-h	0.012	±0.001e-g	0.013	±0.001e	0.013	±0.000f	0.014	±0.005d-f	0.014	±0.001d
Roma	0.016	±0.004e-g	0.009	±0.002g	0.013	±0.004e	0.021	±0.004a-c	0.015	±0.002d-f	0.018	±0.003a-d
Smith	0.012	±0.000e-h	0.015	±0.003d-f	0.014	±0.002de	0.012	±0.001f	0.017	±0.005c-e	0.015	±0.003d
Theis	0.023	±0.004dc	0.020	±0.004bc	0.022	±0.002ab	0.020	±0.003b-e	0.012	±0.002ef	0.016	±0.004b-d
Topper 76	0.019	±0.002c-e	**0.025**	±0.004a	0.022	±0.003a	0.020	±0.001b-d	**0.024**	±0.001a	0.022	±0.002a-c
Tracy	**0.028**	±0.007ab	0.013	±0.002e-g	0.021	±0.008ab	**0.026**	±0.003a	0.021	±0.005a-c	0.024	±0.003a
UNL. hybrid-3	**0.028**	±0.001a	0.017	±0.001c-e	0.023	±0.006a	0.016	±0.005d-f	0.014	±0.004d-f	0.015	±0.001cd
Williams	0.011	±0.002gh	0.011	±0.002fg	0.011	±0.000e	**0.012**	±0.002f	0.015	±0.002d-f	0.014	±0.002d
No91	0.021	±0.004c	0.017	±0.004c-e	0.019	±0.002a-d	0.024	±0.001ba	0.015	±0.002d-f	0.020	±0.005a-d
No5	0.023	±0.002c	0.016	±0.004c-e	0.020	±0.004a-c	0.018	±0.001c-e	**0.011**	±0.001f	0.015	±0.004d
Gülşeker	0.020	±0.001dc	0.019	±0.006b-d	0.020	±0.001a-c	0.019	±0.002c-e	0.026	±0.003a	0.023	±0.004ab
Mean	**0.018**	**±0.006**	**0.016**	**±0.003**	**0.017**	**±0.001A**	**0.018**	**±0.004**	**0.017**	**±0.005**	**0.018**	**±0.000A**
P≤0.05	**0.0001**		**0.0001**						**0.0001**			

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

4.1.8. Genotypic Responses to Root Morphological Characteristics

Root surface area and root volume among genotypes, location as well as location × genotypes interactions significantly ($p<0.05$) differed at depth of 0-30 cm (Tables 4.7). The sweet sorghum genotypes responded differently in term of root morphological characteristics. The root volume was lowest in Roma sweet sorghum genotypes for both sites and locations in the year 2017 (Table 4.11). The study showed that root length (0-30 cm) of sixteen sweet sorghum genotypes at both locations varies from 37.7 to 92.5 km ha^{-1} (Table 4.7). Likewise a study found that root length in 0-30 cm soil depth for sweet sorghum genotypes varies from 31 to 46 m g^{-1} (Thivierge et al. 2014).

Furthermore, root diameter influences the decomposition and turnover of roots. Whereas, smaller fine roots (<2 mm diameter) have a faster decomposition and turnover (Pacaldo et al. 2014). The ratio of root length to root dry mass is a widely used indicator which facilitate the ability of crops to compete for below ground nutrients (Zegada-Lizarazu et al. 2012).

Since nutrient are got up by plant roots and/or mycorrhizae it is sound to search the relationship in between root parameters and nutrient uptake and plant growth. Present research was mainly concentrated on this issue. The results are shown that genotypes and locations are significantly effects root parameters. And data are partly support our hypothesis that genotypes root growth parameters are different than each other's.

4.1.9. Soil Organic Carbon (0-30 cm)

Soil organic carbon (SOC) is known to be a sensitive indicator of soil quality and necessary for the functioning of agricultural ecosystems as it affects many chemical, physical and biological parameters of soil. Soil conditions are a determinant for how best the overall plant grows.

After harvest, soil samples were taken from the Adana and Şanlıurfa locations in both 2016 and 2017 and soil organic carbon concentration was determined and results are presented in (Tables 4.13). These samples were taken from an average of 0-30 cm in depth across strategic points in the plots. On average, the soil samples showed that there is an existence of soil carbon in the fields. The soil organic carbon (SOC) average of the sweet sorghum genotypes 77.5 – 62.02 Mg ha^{-1} at Adana location in year 2016 and 2017 respectively (Table 4.13). Similarly, the soil organic carbon average 50.4 – 54.4 t ha^{-1} at Şanlıurfa in year 2016 and 2017 respectively (Table 4.13).

4.1.10. Soil Total Nitrogen (0-30 cm)

When compared to nitrogen in the atmosphere, the amount of N in the soil is very low. The total N content of most mineral soils ranges from 0.02% to 0.5%, with an average amount of 0.15% (Mengel and Kirkby 1987). A large part of the soil nitrogen is in organic form. Under normal conditions, 2-3% of organic nitrogen is only mineralized every year. The nitrogen content detected in soil samples taken from 0-30 cm depth showed a significant difference between the two years at both locations (Table 4.12). In Adana location, the average soil total nitrogen contains (TN) in 2016 is 0.381 and in year 2017 is 0.287 Mg ha^{-1}. The highest soil total nitrogen was obtained from the Cowley genotype grown soil as 0.416 Mg ha^{-1} and the lowest total soil nitrogen was obtained from the No5 USDA genotype grown soil as 0.319 Mg ha^{-1} in year 2016 at Adana location (Table 4.14).

Table 4.12. Level of significance for the main and interactive effect on soil C stock and soil total N (0-30 cm) of sixteen sweet sorghum genotypes in Adana and Şanlıurfa Locations in years 2016 and 2017.

Sources of variations	**Soil C Stock (Mg ha^{-1})**	**Soil Total N (Mg ha^{-1})**
Genotypes	***	n.s.
Location	***	**
Genotypes X Location	***	n.s.
Year	***	***
Genotypes X Year	***	n.s.
Location X Year	***	*
Geno X Location X Year	***	n.s.

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.13. Average of organic carbon stock in soil samples (0-30 cm) of the sweet sorghum genotypes at Adana and Şanlıurfa locations in years 2016 and 2017

Genotype	Organic Carbon (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	**92**	±4.2a	65	±0.8ba	78.5	±14a	52.4	±1.5a	53.8	±1.2c-g	53.1	±0.7a-d
Grassi	86	±3.6a-c	64	±3.6a-c	75.0	±11ab	**53.6**	±2.4a	53.7	±0.6c-g	53.7	±0.1a-c
M81-E	81	±3.4b-e	64	±1.9bc	72.5	±9a-c	52.6	±1.3a	52.8	±1.6d-g	52.7	±0.1a-d
Neb. sugarcane	75	±1.3e-g	64	±1.2bc	69.5	±6bc	52.9	±2.5a	54.6	±1.1b-e	53.8	±0.9a-c
PI 575753	67	±8.6hg	63	±1.9bc	65.0	±2cd	52.9	±0.7a	54.5	±2.7b-f	53.7	±0.8a-c
Ramada	68	±1.8f-h	65	±0.9ba	66.5	±2cd	53.1	±0.5a	56.4	±2.7a-c	54.8	±1.7ab
Roma	76	±2.2d-f	**67**	±2.4a	71.5	±5a-c	53.1	±1.3a	**58.2**	±1.2a	55.7	±2.6a
Smith	72	±0.9e-g	64	±1.0ba	68.0	±4bc	51.7	±2.5ba	56.8	±1.4ba	54.3	±2.6ab
Theis	73	±2.7e-g	64	±0.8ba	68.5	±5bc	51.8	±1.4a	55.3	±0.1b-d	53.6	±1.8a-c
Topper 76	76	±2.5d-f	62	±2.9b-d	69.0	±7bc	51.2	±6.3a-c	54.3	±1.3b-f	52.8	±1.6a-d
Tracy	90	±2.2a	61	±1.1b-d	75.5	±15ab	**45.6**	±4.0d	55.9	±0.9a-c	50.8	±5.2b-d
UNL. hybrid-3	77	±1.4de	62	±1.4b-d	69.5	±8bc	47.3	±3.3dc	55.1	±2.0b-d	51.2	±3.9a-d
Williams	87	±3.5ba	61	±1.9dc	74.0	±13ab	47.2	±1.5dc	54.1	±2.3b-f	50.7	±3.5cd
No91	**60**	±16.2h	60	±1.8d	60.0	±0d	46.6	±3.0d	51.8	±1.4e-g	49.2	±2.6cd
No5	83	±2.1a-d	**59**	±2.1d	71.0	±12a-c	47.2	±1.6dc	51.8	±2.0fg	49.5	±2.3cd
Gülşeker	78	±1.4c-e	60	±1.7d	69.0	±9bc	46.7	±2.1d	**51.1**	±2.1g	48.9	±2.2d
Mean	**78**	**±3.6**	**63**	**±1.7**	**70.2**	**±8A**	**50.4**	**±2.2**	**54.4**	**±1.5**	**52.4**	**±2.0B**
P≤0.05	**0.0001**		**0.0008**				**0.0007**		**0.0006**			

Data were means of three replicates ±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.14 Average of total nitrogen stock in soil samples (0-30 cm) of the sweet sorghum genotypes Adana and Şanlıurfa locations in years 2016 and 2017

Genotype	Total Nitrogen (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	0.408	±49.57ba	0.310	±13a	0.36	±0.05a	0.192	±9.5a-d	0.218	±14	0.205	±0.01
Grassi	0.393	±39.28a-c	0.278	±21b	0.34	±0.06a-c	0.186	±8.7b-d	0.213	±17	0.200	±0.01
M81-E	0.360	±14.31b-d	**0.275**	±10b	0.32	±0.04bc	**0.181**	±3.8d	0.208	±17	0.195	±0.01
Neb. sugarcane	0.384	±28.87a-c	0.278	±6b	0.33	±0.05a-c	0.183	±2.2dc	0.208	±4	0.196	±0.01
PI 575753	0.391	±21.82a-c	0.287	±8ba	0.34	±0.05a-c	0.193	±6.5a-c	0.214	±6	0.204	±0.01
Ramada	0.374	±37.23a-c	0.278	±15b	0.33	±0.05a-c	0.184	±4.4b-d	0.210	±12	0.197	±0.01
Roma	0.403	±21.82ba	0.294	±6ba	0.35	±0.05ab	0.185	±3.8b-d	0.213	±9	0.199	±0.01
Smith	0.345	±30.55dc	**0.289**	±8ba	0.32	±0.03bc	0.189	±3.8a-d	0.218	±9	0.204	±0.01
Theis	0.388	±24.30a-c	0.295	±19ba	0.34	±0.05a-c	0.185	±6.5b-d	0.218	±8	0.202	±0.02
Topper 76	0.367	±16.48a-d	0.292	±17ba	0.33	±0.04a-c	0.195	±7.5ba	0.212	±8	0.204	±0.01
Tracy	0.396	±34.92a-c	0.295	±26ba	0.35	±0.05ab	0.186	±8.7b-d	0.212	±4	0.199	±0.01
UNL. hybrid-3	0.406	±53.64ba	0.278	±15b	0.34	±0.06a-c	**0.198**	±8.7a	0.219	±10	0.209	±0.01
Williams	**0.416**	±37.80a	0.286	±19ba	0.35	±0.06ab	0.184	±7.9b-d	**0.223**	±8	0.204	±0.02
No91	0.373	±37.29a-d	0.285	±13b	0.33	±0.04a-c	0.189	±3.8a-d	**0.207**	±9	0.198	±0.01
No5	**0.319**	±7.87d	0.286	±10ba	0.30	±0.02c	0.184	±8.7b-d	0.210	±8	0.197	±0.01
Gülşeker	0.379	±35.93a-c	0.284	±17b	0.33	±0.05a-c	0.189	±3.8a-d	0.217	±9	0.203	±0.01
Mean	**0.381**	**±30.7**	**0.286**	**±13.9**	**0.33**	**±0.05A**	**0.187**	**±6.1**	**0.213**	**±9.4**	**0.201**	**±0.01B**
P≤0.05	**0.093**		**0.432**				**0.1737**		**0.818**			

Data were means of three replicates ±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

In Şanlıurfa location, the recorded average TN content, was 0.187 – 0.213 Mg ha^{-1} in year 2016 and 2017 respectively (Table 4.14). All genotypes in year 2017 are not significantly different among each other (Table 4.14). Compare to year 2016, in year 2017 more TN content was measured.

In generally for both years, the treatments have significant effects on soil carbon content. However, genotypes have no effects on soil nitrogen content. Since nitrogen is so mobile and converted to in another N for it may have less effects. Sweet sorghum is not fixing nitrogen and plant tissue N concentration compare to carbon is less. As a result, may be less nitrogen is remained in soil as a residue.

4.1.11. Carbon and Nitrogen Stocks in Soil (0-30 cm) By Sweet Sorghum

The study found that the sweet sorghum genotypes on soil N stocks varies 0.183 to 0.416 N Mg ha^{-1} (Table 4.14). Likewise, other studies conducted in similar situations found sorghum plant N stock in soil to be 2.47 N Mg ha^{-1} (Das et al. 2016).

Furthermore, shoot C input was ten times higher than root C input. Also, the sweet sorghum genotypes sequester too much C in soil as compared to N stock in soil. Besides their specific function in N uptake, very fine roots could also play a key role in soil C accumulation and C sequestration. This study confirmed that the sweet sorghum genotypes have the ability to C sink in soil. The amount of C stock in soil by the sweet sorghum genotypes depends on land-use change and management practices of the sweet sorghum cultivation (Tolbert et al. 2002). This has been a contributing factor in this study. Sweet sorghum genotypes have high shoot N concentration than root N concentration (Table 4.14). Shoot N varies from 1.3 to 2.10% and root N varies from 0.81 to 1.33%. This difference could be related to the stronger ability of sweet sorghum roots

to secrete nitrification inhibitors that likely helped in competing for soil N and may have compensate lower root N than shoot N (Tesfamariam et al. 2014).

4.1.12. Root N Concentration

Root N% was higher in Şanlıurfa than Adana location with some exceptions noted in the (Table 4.17). The maximum root N% was found 1.29 for the Tracy genotype in the year 2016 and minimum root N% was found 0.81 for Gülşeker sweet sorghum genotype in the year 2017 at Sanlıurfa location (Table 4.17). The maximum root N% was 1.33 for Theis genotypes and minimum root N% was 0.86 for No91 Genotype at Adana location. Root N% differed significantly ($p<0.05$) among genotypes as well as locations × genotypes interactions (Tables 4.15).

4.1.13. Shoot N Concentration

The research confirmed that shoot N% was higher in Adana than Şanliurfa location in the 16 sweet sorghum genotypes (Table 4.19). It was determined that the sweet sorghum genotypes tested in 2016 and 2017 in Şanlıurfa and Adana locations differed significantly in term of above ground plant nitrogen content depending on the genotypes. The mean above ground nitrogen content of the sweet sorghum was found to be 1.55-1.88% and 1.10 - 1.80% in year 2016 and 2017 at Adana and Şanlıurfa locations respectively (Table 4.19). The maximum shoot N% was 2.1 % in Williams and minimum was 1.3% in Theis sweet sorghum genotype at Adana location (Table 4.19). Likewise, the maximum shoot N% was 2.2% for PI575753 and the minimum was 0.7% for Ramada genotype in Şanlıurfa location (Table 4.19). Shoot N% differed significantly ($p<0.05$) between locations as well as location X genotypes interactions (Tables 4.15).

Table 4.15. Level of significance for the main and interactive effect on root C%, . root N% shoot C% and shoot N% of the sweet sorghum genotypes in Adana and Şanlıurfa Locations in years 2016 and 2017.

Sources of variations	**Shoot C%**	**Root C%**	**Root N%**	**Shoot N%**
Genotypes	***	***	***	***
Location	***	***	n.s.	***
Genotypes X Location	**	***	**	***
Year	***	***	***	***
Genotypes X Year	***	***	***	***
Location X Year	***	***	***	***
Geno X Location X Year	n.s.	***	***	***

Where n.s. ** and ***represents probability of ≤0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.16. Average of root carbon content % in the sweet sorghum genotypes that grown in two years at Adana and Şanlıurfa locations.

Genotype	Root Carbon Concentration (%)											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	50.3	±1.1a	44.7	±1.5b-f	47.5	±2.8a-d	46.8	±0.3ef	47.9	±0.5ba	47.4	±0.6a-c
Grassi	48.3	±0.6bc	44.2	±1.3d-f	46.3	±2.1a-e	48.1	±0.6cd	46.0	±1.1a-d	47.1	±1.1a-c
M81-E	48.3	±1.1bc	**43.1**	±1.0f	45.7	±2.6c-e	49.2	±0.3b	46.2	±0.6a-d	47.7	±1.5a-c
Neb. sugarcane	46.4	±1.1d	46.6	±0.6ba	46.5	±0.1a-e	49.1	±0.8cb	47.6	±1.4a-c	48.4	±0.8ab
PI 575753	49.8	±1.0a	45.3	±1.6b-e	47.6	±2.3a-d	48.0	±0.5d	**43.4**	±2.3e	45.7	±2.3c
Ramada	47.5	±0.4dc	**47.9**	±0.5a	47.7	±0.2a-c	47.9	±1.0d	44.6	±1.2de	46.3	±1.7bc
Roma	**46.3**	±0.2d	44.7	±0.9b-f	45.5	±0.8e	46.9	±0.2ef	44.3	±1.3de	45.6	±1.3c
Smith	48.1	±0.7bc	43.7	±1.5fe	45.9	±2.2b-e	47.5	±0.5d-f	45.9	±1.2b-d	46.7	±0.8a-c
Theis	47.2	±0.3dc	44.0	±1.3d-f	45.6	±1.6de	47.8	±0.6ed	47.5	±1.1a-c	47.7	±0.1a-c
Topper 76	**50.4**	±1.4a	45.5	±0.6b-e	48.0	±2.5a	**46.5**	±0.5f	47.0	±1.0a-c	46.8	±0.3a-c
Tracy	50.2	±1.0a	45.0	±0.6b-f	47.6	±2.6a-d	49.3	±1.1b	48.0	±0.5ba	48.7	±0.6ab
UNL. hybrid-3	47.7	±0.2c	43.9	±0.9d-f	45.8	±1.9c-e	46.7	±0.3ef	47.4	±2.0a-c	47.1	±0.3a-c
Williams	49.3	±0.7ba	46.4	±1.3a-c	47.9	±1.5ab	49.6	±1.0b	**48.0**	±1.1a	48.8	±0.8a
No91	48.2	±0.2bc	45.9	±1.0a-d	47.1	±1.2a-e	47.1	±0.5d-f	45.7	±1.4dc	46.4	±0.7bc
No5	48.0	±0.1c	44.4	±1.8c-f	46.2	±1.8a-e	47.1	±0.4d-f	**42.7**	±0.9e	44.9	±2.2a-c
Gülşeker	48.4	±0.3bc	43.6	±1.4fe	46.0	±2.4a-e	**51.1**	±0.7a	**48.1**	±1.2a	49.6	±1.5a-c
Mean	**48.4**	**±0.7**	**44.9**	**±1.1**	**46.7**	**±1.8A**	**48**	**±0.6**	**46.3**	**±1.2**	**47.2**	**±0.9B**
P≤0.05	**0.0001**		**0.0015**				**0.0001**		**0.0001**			

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.17. Average of root nitrogen content % in the sweet sorghum genotypes that grown in two years at Adana location and Şanlıurfa locations.

Genotype	Root Nitrogen Content (%)											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	0.92	±0.1ed	1.12	±0.1c	1.02	±0.10bc	**0.82**	±0.1e	0.89	±0.0bc	0.86	±0.04e
Grassi	1.03	±0.2b-e	1.29	±0.1ba	1.16	±0.13ab	1.05	±0.0cb	0.97	±0.1a-c	1.01	±0.04b-e
M81-E	1.01	±0.1b-e	1.13	±0.0c	1.07	±0.06bc	0.98	±0.1b-d	0.97	±0.2a-c	0.98	±0.01c-e
Neb. sugarcane	1.24	±0.1a	1.18	±0.0bc	1.21	±0.03ab	0.96	±0.1cd	0.93	±0.0a-c	0.95	±0.02c-e
PI 575753	1.12	±0.0a-c	1.22	±0.1a-c	1.17	±0.05ab	0.96	±0.1cd	0.99	±0.1ba	0.98	±0.02b-e
Ramada	1.03	±0.1b-e	1.15	±0.0c	1.09	±0.06a-c	1.01	±0.1b-d	0.89	±0.2bc	0.95	±0.06c-e
Roma	0.98	±0.0c-e	1.21	±0.1a-c	1.10	±0.12a-c	1.08	±0.1cb	0.97	±0.1a-c	1.03	±0.06a-d
Smith	1.09	±0.2a-d	1.28	±0.1ba	1.19	±0.10ab	0.97	±0.1b-d	0.91	±0.1a-c	0.94	±0.03c-e
Theis	1.21	±0.2ba	**1.33**	±0.1a	1.27	±0.06a	1.06	±0.0cb	0.95	±0.1a-c	1.01	±0.06b-e
Topper 76	1.07	±0.2a-e	1.12	±0.0c	1.10	±0.03a-c	1.29	±0.1a	**1.07**	±0.1a	1.18	±0.11a
Tracy	0.94	±0.0c-e	1.32	±0.1a	1.13	±0.19ab	1.29	±0.0a	0.97	±0.0a-c	1.13	±0.16ab
UNL. hybrid-3	**1.25**	±0.1a	1.17	±0.1bc	1.21	±0.04ab	0.91	±0.0ed	0.89	±0.0bc	0.90	±0.01de
Williams	1.10	±0.2a-d	1.12	±0.0c	1.11	±0.01a-c	**1.24**	±0.1a	0.95	±0.1a-c	1.10	±0.15a-c
No91	**0.86**	±0.0e	1.31	±0.1a	1.09	±0.23a-c	1.08	±0.0cb	0.87	±0.0bc	0.98	±0.11b-e
No5	0.95	±0.1c-e	1.20	±0.1a-c	1.08	±0.13bc	1.10	±0.1b	0.97	±0.2a-c	1.04	±0.07a-d
Gülşeker	0.93	±0.1c-e	**0.93**	±0.1d	0.93	±0.00c	1.09	±0.1cb	**0.81**	±0.0c	0.95	±0.14c-e
Mean	**1.05**	**±0.118**	**1.19**	**±0.103**	**1.12**	**±0.07A**	**1.06**	**±0.131**	**0.938**	**±0.060**	**1**	**±0.06B**
P≤0.05	**0.0077**		**0.0001**				**0.0001**		**0.441**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.18. Average of shoot carbon content % in the sweet sorghum genotypes that grown in two years at Adana and Şanlıurfa locations.

Genotype	Shoot Carbon Content (%)											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	47.9	±0.9b-f	44.3	±0.6ba	46.1	±1.8	50.6	±0.6c-e	44.3	±1.8a-d	47.5	±3.2a-d
Grassi	48.2	±0.7b-d	44.3	±0.9ba	46.3	±2.0	50.9	±0.8bc	43/0	±1.3c-e	47/0	±4.0a-d
M81-E	48.3	±0.5b-d	43.3	±0.9a-c	45.8	±2.5	50.1	±0.3c-e	43.4	±0.9b-e	46.8	±3.4a-e
Neb. sugarcane	47.9	±0.9b-f	43.9	±1.6ba	45.9	±2.0	**47.3**	±0.3f	42.2	±1.4ed	44.8	±2.6e
PI 575753	**49.7**	±1.7a	43.9	±0.4ba	46.8	±2.9	51.9	±0.4a	45.8	±1.2ba	48.9	±3.1a
Ramada	48.8	±0.7a-c	**44.7**	±1.4a	46.8	±2.1	50.4	±0.4c-e	**41.4**	±0.5e	45.9	±4.5de
Roma	**47.5**	±0.5d-f	43/0	±0.0a-c	45.3	±2.3	50.8	±0.3dc	**46.0**	±1.0a	48.4	±2.4ab
Smith	46.9	±0.1fe	43.4	±0.7a-c	45.2	±1.8	51.0	±0.9bc	42.4	±1.6ed	46.7	±4.3a-e
Theis	48.6	±1.1a-d	44.4	±1.3ba	46.5	±2.1	50.0	±0.1de	42.3	±1.5ed	46.2	±3.9b-e
Topper 76	48.8	±0.9a-c	43/0	±1.3a-c	45.9	±2.9	52.2	±0.5a	44.0	±1.0a-d	48.1	±4.1a-d
Tracy	47.6	±0.4c-f	**41.3**	±3.4c	44.5	±3.2	51.7	±0.8ba	44.9	±1.2a-c	48.3	±3.4a-c
UNL. hybrid-3	48.2	±0.4b-e	42.6	±0.9a-c	45.4	±2.8	51.8	±0.6ba	42/0	±1.7ed	46.9	±4.9a-e
Williams	48.7	±0.5a-d	44.4	±2.0ba	46.6	±2.2	49.8	±0.3e	44.2	±1.6a-d	47/0	±2.8a-d
No91	46.9	±0.2f	42.3	±1.5bc	44.6	±2.3	50.2	±0.4c-e	42.4	±1.3ed	46.3	±3.9b-e
No5	48.2	±0.8b-d	43.1	±1.2a-c	45.7	±2.6	52.0	±0.8a	43.7	±2.0a-e	47.9	±4.2a-d
Gülşeker	49.1	±0.9ba	42.5	±1.3a-c	45.8	±3.3	**52.1**	±0.5a	43.1	±1.9c-e	47.6	±4.5a-d
Mean	**48.2**	**±0.7**	**43.4**	**±1.2**	**45.8**	**±2.4A**	**50.8**	**±0.5**	**43.4**	**±1.4**	**47.1**	**±3.7B**
P≤0.05	**0.0059**		**0.251**				**0.0001**		**0.00097**			

Data were means of three replicates ±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.19. Average of shoot nitrogen % in the sweet sorghum genotypes that grown in two years at Adana and Şanlıurfa locations.

Genotype	Shoot Nitrogen Content (%)											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	1.54	±0.06b-f	1.85	±0.01cf	1.7	±0.15a-c	1.03	±0.08e-g	1.87	±0.02ed	1.45	±0.42c-f
Grassi	1.5	±0.14d-f	1.87	±0.03b-f	1.68	±0.19a-c	1.10	±0.10de	1.99	±0.03b	1.55	±0.45b-d
M81-E	1.42	±0.09e-g	1.88	±0.02a-f	1.65	±0.23a-c	0.95	±0.04gf	2.04	±0.06b	1.49	±0.55b-f
Neb. sugarcane	**1.76**	±0.09a	1.91	±0.01b-e	1.84	±0.08ab	1.21	±0.07cd	1.93	±0.06cd	1.57	±0.36bc
PI 575753	1.5	±0.18c-f	1.87	±0.03b-f	1.69	±0.18a-c	0.71	±0.04h	**2.15**	±0.05a	1.43	±0.72c-g
Ramada	1.69	±0.06a-c	1.86	±0.08b-f	1.78	±0.08ab	1.38	±0.03b	1.86	±0.01d-f	1.62	±0.24b
Roma	**1.77**	±0.19a	1.84	±0.24c-f	1.81	±0.03ab	1.18	±0.02cd	1.48	±0.03h	1.33	±0.15fg
Smith	1.63	±0.03a-d	1.98	±0.04ba	1.81	±0.18ab	**0.93**	±0.09g	1.86	±0.02d-f	1.40	±0.46d-g
Theis	**1.28**	±0.06g	**1.77**	±0.03f	1.53	±0.24c	0.99	±0.01e-g	1.63	±0.03g	1.31	±0.32fg
Topper 76	1.4	±0.06gf	1.81	±0.06d-f	1.61	±0.21bc	1.00	±0.09e-g	1.7	±0.09g	1.35	±0.35e-g
Tracy	1.71	±0.26ba	1.79	±0.07fe	1.75	±0.04a-c	1.12	±0.08de	1.79	±0.04f	1.46	±0.33c-f
UNL. hybrid-3	1.53	±0.03b-f	1.95	±0.10a-c	1.74	±0.21a-c	1.08	±0.03d-f	1.80	±0.03ef	1.44	±0.36c-f
Williams	1.7	±0.06ba	**2.07**	±0.06a	1.89	±0.18a	1.03	±0.07e-g	2.04	±0.06b	1.53	±0.50b-d
No91	1.38	±0.15gf	1.95	±0.05a-c	1.67	±0.29a-c	1.04	±0.12e-g	**1.53**	±0.08h	1.29	±0.25g
No5	1.49	±0.10d-f	1.85	±0.09c-f	1.67	±0.18a-c	**2.03**	±0.21a	1.83	±0.03ef	1.93	±0.10a
Gülşeker	1.6	±0.06a-e	1.94	±0.05a-d	1.77	±0.17ab	1.29	±0.03cb	1.83	±0.06ef	1.56	±0.27bc
Mean	**1.56**	**±0.1**	**1.89**	**±0.1**	**1.72**	**±0.17A**	**1.13**	**±0.1**	**1.83**	**±0.0**	**1.48**	**±0.35B**
P≤0.05	**0.0001**		**0.0074**				**0.0001**		**0.0001**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

4.1.14. Root Carbon Input in the Sweet Sorghum Genotypes

Root carbon uptake by the Sweet sorghum genotypes differ significantly ($p<0.05$) in between locations as well as in locations × genotypes interactions (Tables 4.20). However, root C inputs did not differ among the sweet sorghum genotypes (Table 4.21). The highest root C input was found 4.03 Mg ha^{-1} in Topper 76 sweet sorghum genotypes and lowest root C input was found 2.4 Mg ha^{-1} in Smith in the year 2017 at Adana location (Table 4.21). Likewise, the highest root C input was 3.73 Mg ha^{-1} for Tracy sweet sorghum genotype in the year 2017 and lowest root C input was found 2.2 Mg ha^{-1} in Nebraska Sugarcane sweet sorghum genotypes in the year 2016 at Şanlıurfa location (Table 4.21).

4.1.15. Shoot Carbon Uptake from the Sweet Sorghum Genotypes

The shoot carbon uptake by sixteen sweet sorghum differ among genotypes as well as locations × genotypes interaction (Table 4.20). Naturally, the carbon binding capacity will be different when the biomass produced by the plant is also different. More carbon binding of plants increases the amount of carbohydrate in the plant and this increases the amount of soil and soil residues in the soil with the residual soil and plant residues. In general, two-year average shoot C uptake were double in Adana locations than Şanlıurfa locations with some exceptions (Table 4.22). Shoot C inputs significantly ($p<0.001$) differed between the two locations. The highest shoot C uptake was found 27.9 Mg ha^{-1} for Topper 76 sweet sorghum genotypes and lowest shoot C was found 12.8 Mg ha^{-1} for Tracu genotypes at Adana locations in year 2017 (Table 4.22). However, shoot C uptake varies 14.2 to 23.5 Mg ha^{-1} in the sweet sorghum genotypes in the year 2017 at Şanlıurfa locations (Table 4.22).

4.1.16. Plant Fixed Carbon Equal to CO_2

After determined an average, plant biomass production and carbon concentration, total carbon fixation was calculated by multiplying total biomass with tissue C%. After being calculation of total carbon data was converted in to CO_2. The plant fixed CO_2 varied 61.9-102.9 and 69.8-112.1 Mg ha^{-1} in the year 2016 and 2017, respectively at Adana location (Table 4.24). In Adana location, it has been found that CO_2 concentration was higher in 2017 than in year 2016 (Tables 4.24). The plant fixed CO_2 varied 68.6-92.6 and 60.5-96.1 Mg ha^{-1} in year 2016 and 2017, respectively at Şanlıurfa location (Tables 4.24). In general, plant fixed CO_2 was higher in 2017 than 2016 in Şanlıurfa location as well (Tables 4.24).

Table 4.20. Level of significance for the main and interactive effect on root C uptake, shoot C uptake and plant fixed CO_2 of sixteen sweet sorghum genotypes at Adana and Şanlıurfa Locations in years 2016 and 2017.

Sources of variations	**Shoot Carbon uptake**	**Root Carbon uptake**	**Plant fixed CO_2**
Genotypes	***	***	***
Location	***	***	***
Genotypes X Location	***	***	***
Year	*	***	***
Genotypes X Year	***	***	**
Location X Year	***	***	***
Geno X Location X Year	***	***	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.21. Average of root carbon uptake by the sweet sorghum genotypes that grown in years 2016 and 2017 at Adana and Şanlıurfa locations.

Genotype	Root Carbon Uptake (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	3.2	±193cb	2.8	±223ef	3.0	±0.20cd	3.1	±82a-c	**3.6**	±206a	3.4	±0.25b-d
Grassi	3.7	±313a	3.3	±208ba	3.5	±0.20ab	2.9	±91c-e	3.4	±189ba	3.2	±0.25ab
M81-E	2.7	±48f	2.3	±96h	2.5	±0.20d	3.0	±107b-e	2.9	±269dc	3.0	±0.05b-d
Neb. sugarcane	2.9	±268c-f	2.8	±225d-f	2.9	±0.05a-d	**2.2**	±36g	2.8	±132c-e	2.5	±0.30d
PI 575753	3.1	±103b-e	2.6	±83e-g	2.9	±0.25b-d	3.3	±59ba	2.4	±127fe	2.9	±0.45b-d
Ramada	**2.6**	±98f	2.6	±76e-h	2.6	±0.00cd	2.7	±178ef	2.3	±438f	2.5	±0.20cd
Roma	**2.6**	±86f	2.4	±133hg	2.5	±0.10cd	2.8	±264ed	2.6	±272d-f	2.7	±0.10b-d
Smith	3.3	±561b	2.9	±559c-d	3.1	±0.20a-c	2.4	±227gf	3.5	±192ba	3.0	±0.55b-d
Theis	2.7	±102f	2.4	±192hg	2.6	±0.15b-d	**3.4**	±129a	3.1	±169bc	3.3	±0.15ab
Topper 76	**4.0**	±184a	3.6	±111a	3.8	±0.20ab	2.9	±131c-e	2.8	±229c-e	2.9	±0.05ab
Tracy	3.1	±407b-d	2.8	±307d-f	3.0	±0.15b-d	3.3	±122ba	3.4	±250ba	3.4	±0.05a
UNL. hybrid-3	3.9	±81a	3.2	±124bc	3.6	±0.35a	3.1	±158a-c	**3.6**	±263a	3.4	±0.25a-c
Williams	2.7	±70d-f	2.3	±58h	2.5	±0.20d	3.0	±243b-e	3.5	±140ba	3.3	±0.25ab
No91	2.7	±111ef	2.5	±60f-h	2.6	±0.10cd	3.1	±469b-d	2.9	±80dc	3.0	±0.10b-d
No5	2.9	±111c-f	2.5	±165f-h	2.7	±0.20cd	2.9	±164c-e	2.7	±463d-f	2.8	±0.10b-d
Gülşeker	3.3	±121b	3.1	±69b-o	3.2	±0.10cd	3.4	±134a	2.6	±128d-f	3.0	±0.40b-d
Mean	**3.08**	**±0.45**	**2.75**	**±0.390**	**2.9**	**±0.17A**	**2.98**	**±0.326**	**3.01**	**±0.44**	**3.0**	**±0.01B**
P≤0.05	**0.0001**		**0.0001**				**0.0001**		**0.0001**			

Data were means of three replicates ±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.22. Average of shoot carbon uptake by the sweet sorghum genotypes that grown in years 2016 and 2017 at Adana and Şanlıurfa locations.

Genotype	Shoot Carbon Uptake (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	15.5	±454c-f	16.3	±20f-h	15.9	±0.4ef	18	±975b-d	20.4	±2079a-d	19.2	±1.2a-d
Grassi	16.7	±3343b-f	24	±159bc	20.4	±3.6b-d	15.8	±1051ed	18.6	±1854c-f	17.2	±1.4a-e
M81-E	16.8	±544b-f	24.7	±733bc	20.8	±4.0a-d	18.5	±968cb	18.6	±167c-f	18.6	±0.1a-d
Neb. sugarcane	18.2	±1925b-d	19.1	±370fe	18.7	±0.5c-e	19.3	±2316b	18.1	±834c-g	18.7	±0.6ab
PI 575753	14.6	±914fe	16.5	±551f-h	15.6	±1.0f	16.7	±839c-e	14.5	±787gh	15.6	±1.1e
Ramada	17.4	±1372b-e	26.4	±418ba	21.9	±4.5a-c	16.6	±1704c-e	**14.2**	±2126h	15.4	±1.2b-e
Roma	15.6	±1502c-f	26.2	±423ba	20.9	±5.3a-c	17.3	±866b-e	17.9	±890c-h	17.6	±0.3c-e
Smith	19.7	±691b	19.6	±274de	19.7	±0.0a-d	16.7	±1271c-e	22.8	±2744ba	19.8	±3.1ab
Theis	14.9	±615fe	25.8	±412ba	20.4	±5.4c-f	17.3	±360b-e	16.4	±2648e-h	16.9	±0.5c-e
Topper 76	**24**	±3840a	27.9	±133a	26.0	±2.0a	**22.3**	±697a	16.9	±3488d-h	19.6	±2.7b-e
Tracy	15.1	±586d-f	12.8	±515i	14.0	±1.2f	**15.5**	±416e	17.8	±1364c-h	16.7	±1.2b-e
UNL. hybrid-3	23.4	±1869a	25.5	±156ba	24.5	±1.1a	18.9	±1732b	21.5	±1721a-c	20.2	±1.3ab
Williams	**14.1**	±116f	14.2	±114ih	14.2	±0.0ef	17.3	±980b-e	19.7	±926b-e	18.5	±1.2a-c
No91	19.6	±544b	22.1	±585dc	20.9	±1.3a-c	18.3	±1952cb	15.4	±2634f-h	16.9	±1.5de
No5	18.7	±3248cb	15.4	±196g-i	17.1	±1.7c-e	16.6	±862c-e	16.4	±3493e-h	16.5	±0.1ab
Gülşeker	23.8	±3163a	18	±176e-g	20.9	±2.9a-c	17.6	±2167b-e	**23.5**	±3787a	20.6	±3.0a
Mean	**18.02**	**±3.32**	**20.91**	**±4.98**	**19.5**	**±1.4A**	**17.66**	**±1.63**	**18.29**	**±2.75**	**18**	**±0.3B**
P≤0.05	**0.0001**		**0.0001**				**0.0002**		**0.0002**			

Data were means of three replicates ±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.23. Average of total carbon uptake by the sweet sorghum genotypes that grown in years 2016 and 2017 at Adana and Şanlıurfa locations.

Genotype	Total Carbon Uptake (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	18.7	±270d-g	19.0	±2254gf	18.9	±0.2e-g	21.1	±934b-e	24.0	±1916a-c	22.6	±1.5ab
Grassi	20.4	±3034b-f	27.3	±219bc	23.9	±3.0c	**18.7**	±1136f	22.0	±1743b-e	20.4	±1.7a-d
M81-E	19.5	±586c-g	27.0	±1469bc	23.3	±3.8cd	21.5	±1067cb	21.5	±327b-f	21.5	±0.0a-d
Neb. sugarcane	21.0	±2023b-e	21.9	±637d-f	21.5	±0.4c-f	21.5	±2311cb	20.9	±855c-f	21.2	±0.3a-d
PI 575753	17.7	±1009fg	19.2	±324gf	18.5	±0.8fg	19.9	±855b-f	16.9	±822gh	18.4	±1.5cd
Ramada	20.0	±1464b-g	29.0	±481ba	24.5	±4.5bc	19.3	±1882c-f	**16.5**	±1824h	17.9	±1.4d
Roma	18.2	±1577e-g	28.6	±4169ba	23.4	±5.2cd	20.1	±1089b-f	20.5	±630c-g	20.3	±0.2a-d
Smith	23.0	±130b	22.5	±341de	22.8	±0.3c-e	19.1	±1229d-f	**26.3**	±2826a	22.7	±3.6ab
Theis	17.5	±708fg	28.2	±393b	22.9	±5.4cd	20.7	±260b-f	19.5	±2807d-h	20.1	±0.6a-d
Topper 76	**28.0**	±3712a	31.5	±3931a	29.8	±1.8a	**25.2**	±566a	19.7	±3512d-h	22.5	±2.8a-c
Tracy	18.2	±974e-g	15.6	±1388h	16.9	±1.3g	18.8	±432fe	21.2	±1132c-f	20.0	±1.2a-d
UNL. hybrid-3	27.3	±1934a	28.7	±784ba	28.0	±0.7ab	22.0	±1890b	25.2	±1984ba	23.6	±1.6a
Williams	**16.9**	±47g	16.5	±276hg	16.7	±0.2g	20.4	±1205b-f	23.2	±853a-d	21.8	±1.4a-d
No91	22.3	±439cb	24.7	±1082dc	23.5	±1.2cd	21.3	±2148b-d	18.2	±2694f-h	19.8	±1.6a-d
No5	21.5	±3215b-d	18.0	±625hg	19.8	±1.8d-g	19.5	±919c-f	19.1	±3939e-h	19.3	±0.2b-d
Gülşeker	27.1	±3267a	21.1	±2122ef	24.1	±3.0bc	21.0	±2254b-f	26.2	±3691a	23.6	±2.6a
Mean	**21.1**	**±3.62**	**23.66**	**±5.07**	**22.4**	**±1.3A**	**20.64**	**±1.60**	**21.31**	**±3.05**	**21**	**±0.3B**
P≤0.05	**0.0001**		**0.0001**				**0.0002**		**0.0001**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.24. Average of plant fixed carbon equal to CO_2 by the sweet sorghum genotypes that grown in years 2016 and 2017 at Adana and Şanlıurfa locations.

Genotype	Plant Fixed Carbon Equal to CO_2 (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	68.7	±1.0d-g	69.9	±0.8gf	69.3	±0.6e-g	77.5	±3.4b-e	88.2	±7.0a-c	82.9	±5.4ab
Grassi	74.8	±11.1b-f	100.3	±5.4bc	87.6	±12.8c	**68.6**	±4.2f	80.8	±6.4b-e	74.7	±6.1a-d
M81-E	71.5	±2.1c-g	99.1	±2.3bc	85.3	±13.8cd	78.9	±3.9cb	79.0	±1.2b-e	79.0	±0.0a-d
Neb. sugarcane	77.2	±7.4b-e	80.3	±1.2d-f	78.8	±1.6c-f	78.8	±8.5cb	76.8	±3.1c-e	77.8	±1.0a-d
PI 575753	64.9	±3.7fg	70.4	±1.8gf	67.7	±2.8fg	73.2	±3.1b-f	62.0	±3.0fg	67.6	±5.6cd
Ramada	73.6	±5.4b-g	106.3	±15.3ba	90.0	±16.4bc	70.9	±6.9c-f	**60.5**	±6.7g	65.7	±5.2d
Roma	66.8	±5.8e-g	104.9	±1.2ba	85.9	±19.1cd	73.6	±4.0b-f	75.2	±2.3c-f	74.4	±0.8a-d
Smith	84.5	±0.5b	82.6	±1.4de	83.6	±1.0c-e	70.1	±4.5d-f	96.5	±10.4a	83.3	±13.2ab
Theis	**64.4**	±2.6fg	103.4	±14.4b	83.9	±19.5cd	75.9	±1.0b-f	71.7	±10.3d-g	73.8	±2.1a-d
Topper 76	102.9	±13.6a	115.5	±5.1a	109.2	±6.3a	**92.6**	±2.1a	72.1	±12.9d-g	82.4	±10.a-c
Tracy	67.0	±3.6e-g	57.3	±2.9h	62.2	±4.9g	69.1	±1.6fe	77.9	±4.2c-e	73.5	±a-d4.4
UNL. hybrid-3	**100.2**	±7.1a	105.3	±1.0ba	102.8	±2.6ab	80.9	±6.9b	**92.3**	±7.3ba	86.6	±5.7a
Williams	62.0	±0.2g	60.4	±4.0hg	61.2	±0.8g	74.7	±4.4b-f	85.0	±3.1a-d	79.9	±5.2a-d
No91	82.0	±1.6cb	90.5	±2.3dc	86.3	±4.3cd	78.3	±7.9b-d	67.0	±9.9e-g	72.7	±5.7a-d
No5	79.1	±11.8bb-d	65.9	±7.8hg	72.5	±6.6d-g	71.5	±3.4c-f	70.0	±14.5e-g	70.8	±0.8b-d
Gülşeker	99.4	±12.0a	77.4	±6.7ef	88.4	±11.0bc	77.1	±8.3b-f	96.1	±13.5a	86.6	±9.5a
Mean	**77.43**	**±13.29**	**86.84**	**±18.6**	**82.1**	**±4.7A**	**75.7**	**±5.89**	**78.19**	**±11.16**	**77.0**	**±1.2B**
P≤0.05	**0.0001**		**0.0001**				**0.0006**		**0.0001**			

Data were means of three replicates ±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

4.1.17. Root and Shoot Carbon Uptake

Besides their role in nutrient uptake, roots constitute a major source of C for soil (Ortas and Lal 2012; Rasse et al. 2005). Other study also pointed that root biomass might be a good indicator of crop C input to soil (Monti and Zatta 2009b).

Root diameter of the sweet sorghum genotypes were low and did not differ between location and location × genotype interaction (Table 4.7). Root biomass, root volumes were high in the sweet sorghum genotypes in this study. Root volume varies from 7.92 to 26.70 m^3 ha^{-1} in the sweet sorghum genotypes at both sites. Due to a minimum root diameter, chances are higher that this contributed to less C input in the sweet sorghum genotypes. A study speculated that roots become more numerous, longer, thicker and faster growing in crops exposed to high CO_2 with increased root length in many plant species (February et al. 2020). Branching and extension of roots under elevated CO_2 may lead to altered root architecture and ability of roots to acquire water and nutrients from the soil profile with exploration of the soil volume. Root turnover is important to the global C budget as well as to nutrient cycling in ecosystems and individual plants. Agricultural management practices have a greater impact on root growth than rising atmospheric CO_2 since management practices influence soil physical, chemical and biological properties of soil consequently affects root growth dynamics in the belowground (Madhu and Hatfield 2013). There is no information available about sweet sorghum root morphological characteristics that are required to estimate the contribution of soil C and N inputs. However, some sweet sorghum genotypes had coarse root diameter in both sites that may contribute to soil C input into soil. Likewise, the studies have suggested that sweet sorghum C inputs into the soil could be explained by their root system architecture (Ceotto et al. 2013). This research's finding

indicates scope for enhancing soil C sequestration by cultivating collected the USA sweet sorghum genotypes. Similarly, the longer and finer root system of sweet sorghum genotypes likely contributes to higher N uptake efficiency. Thus, not only higher N uptake efficiency but also morphological characteristics of roots should be taken into account when assessing C input from roots.

The study findings indicate that even though the sweet sorghum genotypes allocated less C into their root system than shoot (Tables 4.22, 4.23), they produce larger root volume (Table 4.11) which likely increased their competitiveness for nutrients. Likewise, a study speculated that smaller allocation of C to roots along with a high root length gives opportunity for greater investment of C to the shoot (Bonifas and Lindquist 2009). This could explain the high C in shoot of the sweet sorghum genotypes in the present study.

4.1.18. Shoot Nitrogen Uptake

Shoot N differed significantly ($P \geq 0.05$) between locations as well as location × genotypes interactions (Tables 4.25). Shoot nitrogen uptake was higher in Adana than Şanlıurfa location in sixteen sweet sorghum genotypes (Table 4.26). The maximum shoot N uptake was 1.179 Mg ha^{-1} in Topper genotype and minimum was 0.441 Mg ha^{-1} in PI 575753 sweet sorghum genotypes at Adana location (Table 4.26). Likewise, the maximum shoot N uptake was 1.003 Mg ha^{-1} for Smith genotype and minimum was 0.227 Mg ha^{-1} for PI 575753 genotype (Table 4.26).

4.1.19. Root Nitrogen Uptake

Root N uptake differed significantly ($p<0.05$) among genotypes as well as locations × genotypes interactions (Table 4.25). Root N uptake was higher in Adana than Şanlıurfa location with some exception (Table 4.27).

The maximum root N uptake was found 1.01 Mg ha^{-1} for UNL-hybrid-3 genotype and minimum root N uptake was found 0.049 Mg ha^{-1} for No 91 sweet sorghum genotype at Adana location in year 2016 (Table 4.27). The maximum root N uptake was. 0.087 for Tracy genotype and minimum root N uptake was 0.043 for Neb. Sugarcane genotypes at Şanlıurfa location in year 2016 (Table 4.27).

4.1.20. Total Nitrogen Uptake

Total N uptake differed significantly ($P < 0.05$) between locations as well as location × genotypes interactions (Tables 4.25). On average, N uptake by the sweet sorghum genotypes were higher in Adana than in Şanlıurfa locations (Table 4.28). The highest total N uptake was found in the Topper 76 sweet sorghum genotype with 1.27 Mg ha^{-1} in year 2017 and the lowest was found in PI575753 at 0.461 Mg ha^{-1} in year 2016 at Adana locations (Table 4.28). Likewise, the highest N uptake by Smith genotype was 1.07 Mg ha^{-1} in year 2017 and lowest N uptake by PI575753 genotype was 0.292 Mg ha^{-1} in year 2016 at Şanlıurfa location (Table 4.28).

Table 4.25. Level of significance for the main and interactive effect on root N uptake, shoot N uptake and total N of sixteen sweet sorghum genotypes in Adana and Sanliurfa Locations.

Sources of variations	**Shoot N uptake**	**Root N uptake**	**Total N uptake**
Genotypes	***	***	***
Location	n.s.	***	***
Genotypes X Location	***	***	***
Year	***	***	***
Genotypes X Year	***	***	***
Location X Year	***	*	*
Genotypes X Location X Year	***	***	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.26. Average of root nitrogen uptake by the sweet sorghum genotypes that grown in two years at Adana and Şanlıurfa locations.

Genotype	Root Nitrogen Uptake (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	0.059	±8e-g	0.069	±5ed	0.064	±0.005cd	0.055	±4ih	0.067	±5a-c	0.061	±0.006b-d
Grassi	0.079	±20bc	**0.097**	±4a	0.088	±0.009ab	0.064	±4e-h	**0.072**	±7a	0.068	±0.004ab
M81-E	0.056	±5fg	0.060	±4ef	0.058	±0.002d	0.060	±9f-h	0.060	±16a-e	0.060	±0.000b-d
Neb. Sugarcane	0.077	±14b-d	0.071	±6ed	0.074	±0.003a-d	**0.043**	±2j	0.054	±1d-f	0.049	±0.006d
PI 575753	0.069	±1b-f	0.071	±9ed	0.070	±0.001b-d	0.066	±7d-g	0.055	±4c-f	0.061	±0.006b-d
Ramada	0.057	±9fg	0.063	±1ef	0.060	±0.003cd	0.058	±8g-i	**0.046**	±13f	0.052	±0.006cd
Roma	0.055	±2fg	0.064	±7ef	0.060	±0.005cd	0.064	±7e-h	0.057	±13b-f	0.061	±0.004b-d
Smith	0.073	±11b-e	0.085	±18a-c	0.079	±0.006a-c	0.050	±2ij	0.069	±8ba	0.060	±0.010b-d
Theis	0.069	±12b-f	0.072	±7ed	0.071	±0.001b-d	0.075	±3b-d	0.062	±4a-e	0.069	±0.007ab
Topper 76	0.085	±14ba	0.088	±4ba	0.087	±0.001ab	0.081	±4ba	0.063	±7a-d	0.072	±0.009ab
Tracy	0.058	±8e-g	0.082	±6b-d	0.070	±0.012b-d	**0.087**	±5a	0.069	±3ba	0.078	±0.009a
UNL. hybrid-3	**0.101**	±10a	0.086	±12ba	0.094	±0.008a	0.061	±5f-h	0.068	±1ba	0.065	±0.004a-c
Williams	0.061	±11d-g	**0.055**	±1f	0.058	±0.003d	0.076	±7bc	0.069	±11ba	0.073	±0.004ab
No91	**0.049**	±2g	0.072	±2c-e	0.061	±0.012cd	0.070	±8c-f	0.054	±3d-f	0.062	±0.008b-d
No5	0.057	±6fg	0.068	±11ef	0.063	±0.006cd	0.068	±7c-f	0.053	±2d-f	0.061	±0.008b-d
Gülşeker	0.063	±6c-g	0.067	±6ef	0.065	±0.002cd	0.073	±2b-e	0.050	±3ef	0.062	±0.012b-d
Mean	**0.066**	**±8.6**	**0.073**	**±6.6**	**0.070**	**±0.004A**	**0.066**	**±5**	**0.061**	**±6**	**0.063**	**±0.003B**
P≤0.05	**0.0001**		**0.0001**				**0.0001**		**0.0027**			

Data were means of three replicates ±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.27. Average of shoot nitrogen uptake by the sweet sorghum genotypes that grown in two years at Adana and Şanlıurfa locations.

Genotype	Shoot Nitrogen Uptake (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	0.500	±26f-i	0.680	±12fe	0.590	±0.09ef	0.364	±6e-g	0.860	±71ba	0.612	±0.25a-d
Grassi	0.518	±13f-h	1.013	±50bc	0.766	±0.25b-d	0.341	±40gf	0.860	±59ba	0.601	±0.26a-e
M81-E	0.495	±21g-i	1.072	±9ba	0.784	±0.29a-d	0.348	±4gf	0.875	±2ba	0.612	±0.26a-d
Neb. sugarcane	0.665	±33b-e	0.833	±36de	0.749	±0.08c-e	0.494	±41b	0.831	±44bc	0.663	±0.17ab
PI 575753	**0.441**	±42ih	0.705	±17fe	0.573	±0.13f	**0.227**	±14h	0.682	±65de	0.455	±0.23e
Ramada	0.604	±36c-f	1.102	±28ba	0.853	±0.25a-c	0.454	±38cb	0.637	±67de	0.546	±0.09b-e
Roma	0.578	±11d-g	1.119	±46ba	0.849	±0.27a-c	0.403	±22c-f	0.575	±11de	0.489	±0.09c-e
Smith	0.688	±31a-c	0.896	±25dc	0.792	±0.10a-d	0.304	±12g	**1.003**	±60a	0.654	±0.35ab
Theis	0.392	±21i	1.024	±48bc	0.708	±0.32c-f	0.342	±7gf	0.637	±48de	0.490	±0.15c-e
Topper 76	0.684	±42a-d	**1.179**	±93a	0.932	±0.25ab	0.429	±37b-e	0.646	±65de	0.538	±0.11b-e
Tracy	0.546	±68f-h	**0.559**	±54f	0.553	±0.01f	0.336	±12gf	0.711	±51dc	0.524	±0.19b-e
UNL. hybrid-3	0.743	±47ba	1.166	±75ba	0.955	±0.21a	0.395	±43c-f	0.925	±53ba	0.660	±0.27ab
Williams	0.495	±11g-i	0.659	±8f	0.577	±0.08ef	0.357	±5e-g	0.907	±75ba	0.632	±0.28a-c
No91	0.577	±58d-f	1.023	±44bc	0.800	±0.22a-c	0.380	±60d-f	**0.553**	±71e	0.467	±0.09de
No5	0.576	±20e-g	0.666	±20f	0.621	±0.05ef	**0.650**	±50a	0.686	±54c-e	0.668	±0.02ab
Gülşeker	**0.776**	±32a	0.823	±11de	0.800	±0.02a-c	0.436	±61b-d	0.997	±43a	0.717	±0.28a
Mean	**0.58**	**±31.9**	**0.908**	**±36.0**	**0.744**	**±0.16A**	**0.391**	**±28**	**0.774**	**±52**	**0.583**	**±0.19B**
P≤0.05	**0.0001**		**0.0001**				**0.0001**		**0.0001**			

Data were means of three replicates ±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.28. Average of total nitrogen uptake by the sweet sorghum genotypes that grown in two years at Adana and Şanlıurfa locations.

Genotype	Total Nitrogen Uptake (Mg ha^{-1})											
	2016		2017		Mean		2016		2017		Mean	
	Adana Location						Şanlıurfa Location					
Cowley	0.558	±24c-f	0.749	±14fg	0.654	±0.10ef	0.419	±10ef	0.927	±66a-c	0.673	±0.25a-e
Grassi	0.597	±65c-e	1.110	±53b-d	0.854	±0.26b-d	0.404	±37ef	0.932	±65ba	0.668	±0.26a-e
M81-E	0.551	±16d-f	1.132	±5a-d	0.842	±0.29cd	0.408	±13ef	0.935	±15ba	0.672	±0.26a-e
Neb. Sugarcane	0.742	±33ba	0.903	±32fe	0.823	±0.08c-f	0.537	±42b	0.885	±43b-d	0.711	±0.17a-d
PI 575753	0.510	±41fe	0.776	±8fg	0.643	±0.13f	**0.292**	±19g	0.737	±64d-f	0.515	±0.22e
Ramada	0.660	±41bc	1.165	±28a-c	0.913	±0.25a-c	0.512	±45cb	0.684	±64ef	0.598	±0.09b-e
Roma	0.633	±12dc	1.184	±40a-c	0.909	±0.28a-c	0.467	±28b-e	**0.633**	±3ef	0.550	±0.08de
Smith	0.761	±30ba	0.981	±42de	0.871	±0.11bc	0.354	±13gf	**1.072**	±68a	0.713	±0.36a-c
Theis	**0.461**	±32f	1.096	±45dc	0.779	±0.32c-f	0.417	±10ef	0.698	±31ef	0.558	±0.14c-e
Topper 76	0.769	±65a	**1.267**	±47a	1.018	±0.25ab	0.510	±34b-d	0.709	±72ef	0.610	±0.10b-e
Tracy	0.604	±15c-e	**0.641**	±57g	0.623	±0.02f	0.423	±16ef	0.780	±49c-f	0.602	±0.18b-e
UNL. hybrid-3	**0.844**	±43a	1.253	±53ba	1.049	±0.20a	0.456	±45c-f	0.993	±54ba	0.725	±0.27ab
Williams	0.556	±5c-f	0.714	±8g	0.635	±0.08f	0.433	±11ed	0.977	±62ba	0.705	±0.27a-d
No91	0.626	±58dc	1.096	±45dc	0.861	±0.24bc	0.450	±85c-e	0.608	±72f	0.529	±0.08e
No5	0.633	±16dc	0.734	±34g	0.684	±0.05d-f	**0.718**	±67a	0.739	±24d-f	0.729	±0.01ab
Gülşeker	0.839	±37a	0.889	±18fe	0.864	±0.03bc	0.509	±63b-d	1.048	±40a	0.779	±0.27a
Mean	**0.647**	**±33**	**0.981**	**±33**	**0.814**	**±0.17A**	**0.456**	**±34**	**0.834**	**±50**	**0.646**	**±0.19B**
P≤0.05	**0.0001**		**0.0001**				**0.0001**		**0.0001**			

Data were means of three replicates ±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

4.2. Greenhouse Experiment

4.2.1. Growth Response of the Sweet Sorghum Genotypes

In other to determine the indigenous mycorrhiza on sorghum genotypes one pot experiment was conducted under greenhouse conditions. The soils were collected (0-30 cm) from both locations Adana location and Şanlıurfa location. Sterilized soils were inoculated with and without extracted ingenious mycorrhiza spore's inoculation. Non-inoculated pots got mycorrhizae free inoculum material. After harvest plant and soil parameters were analyzed.

In general shoot dry weight (SDW) was higher at mycorrhiza added treatment and non-mycorrhiza added treatment in Harran soils than Çukurova soils (Table 4.30). Statistically mycorrhizal inoculation was highly significantly ($P<0.001$) effected SDW compare to non-inoculated treatments. The shoot dry weight was found 56 to 62.3 g pot^{-1} at mycorrhiza added treatment and 46.8 to 56 g pot^{-1} non-mycorrhiza added treatment in Adana soils (Table 4.30). Similarly, in Şanlıurfa soils the SDW was found 56 g pot^{-1} to 90 g pot^{-1} for mycorrhiza added treatment and 37.7 g pot^{-1} to 58.7 g pot^{-1} for non-mycorrhiza added treatment (Table 4.30).

Root dry weight (RDW) of the sweet sorghum was determined as well and mycorrhiza inoculated soils were higher than in non-mycorrhizae inoculated Şanlıurfa soils (Table 4.31). In contrast, root dry weight of four sweet sorghums was higher in mycorrhiza inoculated soil than non-mycorrhiza inoculated in Adana soils (Table 4.31). These are Cowley, Grassi, Nebraska Sugarcane and Topper 76 respectively. The treatment × genotype interaction was highly significant ($P < 0.001$) (Table 4.29). Total biomass (dry weight) was calculated and it has been calculated that mycorrhizal inoculation resulted 15% and 25 % of more biomass in Adana and Şanlıurfa location respectively. It is very important for Şanlıurfa location in their water deficiency and fertility is lower than Adana

location. It is very important for Şanlıurfa location in their water deficiency and fertility is lower than Adana location.

Total plant biomass average, was higher in in mycorrhiza inoculated soil than non-mycorrhiza inoculated in Adana soils (Table 4.32). The total biomass varied 64.5-72.5 and 52.6- 64.3 Mg ha^{-1} in mycorrhiza inoculated and non-mycorrhiza inoculated, respectively at Adana soil (Table 4.32). In general, total biomass was higher in mycorrhiza inoculated than non-mycorrhiza inoculated in Şanlıurfa location (Table 4.32). The plant biomass varied 66.5-100.6 and 45.6-65.7 Mg ha^{-1} in in mycorrhiza inoculated and non-mycorrhiza inoculated, respectively in Şanlıurfa soil (Table 4.32).

Table 4.29. Level of significance for the main and interactive effect on plant hight, shoot biomass and root biomass of sixteen sweet sorghum genotypes that grown in (+M = Mycorrhizae and –M= Non-Mycorrhizae) in Adana and Şanlıurfafa soils.

Sources of variations	Total Biomass	Shoot D. W	Root D. W
Genotypes	***	***	***
Soil	***	***	***
Genotypes X Soil	***	***	***
Mycorrhizae	***	***	***
Genotypes X Mycorrhizae	***	***	***
Soil X Mycorrhizae	***	***	***
Geno X Soil X Mycorrhizae	***	***	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.30. Average of shoot dry weight of the sweet sorghum genotypes that grown in (+M and -M) Mycorrhiza in Adana and Şanlıurfa soils.

Genotype	Shoot Dry Weight (g pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	**62.3**	±2.42a	51.4	±1.18hi	56.9	±5.5a-c	**55.6**	±0.45mn	46.0	±1.00rs	50.8	±4.8h
Grassi	59.7	±1.39b-d	48.2	±0.49lm	54.0	±5.7c-f	69.0	±0.95d	50.4	±0.40pq	59.7	±9.3c-e
M81-E	57.1	±0.94ef	52.4	±1.40gh	54.8	±2.4c-e	67.9	±0.79ed	45.2	±1.06s	56.6	±11.4d-f
Neb. Sugarcane	58.5	±0.61de	50.7	±0.49i-k	54.6	±3.9c-f	65.9	±1.03e-g	46.4	±0.53rs	56.2	±9.7ef
PI 575753	59.9	±1.15b-d	50.3	±1.46i-k	55.1	±4.8b-e	**90.0**	±2.65a	48.3	±1.53rq	69.2	±20.9ab
Ramada	57.2	±1.31ef	49.0	±0.30lk	53.1	±4.1d-f	65.1	±0.95f-h	**37.7**	±1.10u	51.4	±13.7gh
Roma	56.6	±0.81ef	**46.8**	±0.17m	51.7	±4.9f	68.5	±1.32d	41.8	±0.50t	55.2	±13.4fg
Smith	58.5	±0.46de	50.8	±0.76h-j	54.7	±3.9c-f	61.0	±1.00kj	52.7	±3.06po	56.9	±4.2c-f
Theis	**56.0**	±0.87f	48.4	±0.75lm	52.2	±3.8ef	62.7	±1.53ji	51.6	±0.60p	57.2	±5.6c-f
Topper 76	59.2	±1.27cd	49.2	±1.26j-l	54.2	±5.0c-f	64.7	±2.52g-i	56.3	±1.53l-n	60.5	±4.2c
Tracy	61.2	±0.76ab	48.9	±1.01lk	55.1	±6.2c-f	67.7	±2.08d-f	52.3	±2.33p	60.0	±7.7c-e
UNL. hybrid-3	60.4	±2.38bc	49.4	±1.47j-l	54.9	±5.5c-f	63.0	±1.00h-j	56.1	±1.10mn	59.6	±3.5c-e
Williams	60.2	±0.85b-d	51.3	±0.58hi	55.8	±4.5a-d	76.6	±2.29c	**58.7**	±2.08kl	67.7	±8.9b
No91	58.9	±0.51cd	51.8	±0.72lhi	55.4	±3.6b-d	64.0	±1.00g-i	56.2	±1.26l-n	60.1	±3.9cd
No5	**62.3**	±0.58a	53.8	±0.72g	58.1	±4.3ab	66.0	±1.61e-g	55.0	±1.00on	60.5	±5.5c
Gülşeker	60.7	±0.61a-c	**56.7**	±0.58ef	58.7	±2.0a	86.0	±1.00b	58.0	±1.00ml	72.0	±14.0a
Mean	**59.3**	**±1.91**	**50.6**	**±2.41**	**54.9**	**±4.4B**	**68.4**	**±8.87**	**50.8**	**±6.10**	**59.6**	**±8.8A**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates ±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.31. Average of root dry weight of the Sweet sorghum genotypes that grown in (+M and -M) Mycorrhiza in Adana and Şanlıurfa soils.

Genotype	Root Dry Weight (g pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	**10.2**	±0.28a	6.4	±0.25j-l	8.3	±1.9a	10.9	±0.37b-d	8.6	±0.94ih	9.8	±1.2a-c
Grassi	8.2	±0.57bc	6.2	±0.13k-m	7.2	±1.0c-f	9.8	±0.49e-g	8.2	±0.53i-l	9.0	±0.8a-c
M81-E	7.5	±0.19e	6.2	±0.16l-n	6.9	±0.7e-h	10.6	±0.03b-f	7.5	±0.28ml	9.1	±1.6a-c
Neb. Sugarcane	7.9	±0.28cd	**7.8**	±0.43c-e	7.9	±0.1ab	10.5	±0.17c-f	8.5	±0.61ij	9.5	±1.0a-c
PI 575753	6.5	±0.21h-k	5.5	±0.20o	6.0	±0.5jk	10.6	±0.32c-f	7.9	±1.42i-m	9.3	±1.4a-c
Ramada	7.0	±0.31f	5.7	±0.17no	6.4	±0.7h-j	10.5	±0.27c-f	7.9	±0.86i-m	9.2	±1.3a-c
Roma	6.6	±0.22g-k	5.8	±0.14m-o	6.2	±0.4ij	9.8	±0.12fg	**7.0**	±0.29m	8.4	±1.4c
Smith	**5.7**	±0.07o	**5.6**	±0.26o	5.7	±0.1kl	10.3	±0.59d-g	7.4	±1.06ml	8.9	±1.5a-c
Theis	5.8	±0.34no	5.1	±0.07p	5.5	±0.4l	10.5	±0.53c-f	7.7	±0.37i-m	9.1	±1.4a-c
Topper 76	8.3	±0.45b	6.6	±0.18g-h	7.5	±0.9ab	11.6	±0.06ba	8.4	±0.89i-k	10.0	±1.6a
Tracy	6.8	±0.34f-i	7.0	±0.19f	6.9	±0.1d-h	11.4	±0.17a-c	8.0	±0.89i-l	9.7	±1.7a-c
UNL. hybrid-3	7.8	±0.16c-e	6.9	±0.14f-h	7.4	±0.5b-d	**12.0**	±0.35a	7.7	±0.43i-m	9.9	±2.2ab
Williams	6.9	±0.23fg	6.4	±0.12i-k	6.7	±0.3f-i	9.5	±0.05gh	7.5	±1.05k-m	8.5	±1.0bc
No91	7.7	±0.27de	6.4	±0.18i-l	7.1	±0.7c-f	9.9	±0.23e-g	7.7	±0.25j-m	8.8	±1.1a-c
No5	6.8	±0.05f-j	6.5	±0.27h-l	6.6	±0.1g-i	10.7	±0.18b-e	7.7	±0.30i-m	9.2	±1.5a-c
Gülşeker	6.8	±0.11f-h	7.7	±0.15de	7.3	±0.4c-e	10.5	±0.22c-f	7.7	±0.12i-m	9.1	±1.4a-c
Mean	**7.38**	**±1.09**	**6.4**	**±0.75**	**6.8**	**±0.5B**	**10.6**	**±0.67**	**7.8**	**±0.43**	**9.2**	**±1.4A**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates ±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.32. Average of total biomass of the Sweet sorghum genotypes that grown in (+M and -M) Mycorrhiza in Adana and Şanlıurfa Soils.

Genotype	Total Biomass (g pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	**72.5**	±2.61a	57.8	±1.37i-k	65.2	±7.3ab	66.5	±0.80j	54.6	±1.63on	60.6	±6.0g
Grassi	67.8	±1.87cb	54.4	±0.41m-o	61.1	±6.7d	78.8	±1.44d	58.6	±0.93m	68.7	±10.1c-e
M81-E	64.6	±1.14ed	58.6	±1.56ih	61.6	±3.0cd	78.5	±0.82ed	52.7	±0.79o	65.6	±12.9ef
Neb. Sugarcane	66.4	±0.34cd	58.5	±0.59ih	62.5	±4.0b-d	76.4	±0.91ef	54.9	±1.08on	65.7	±10.8ef
PI 575753	66.4	±1.16cd	55.8	±1.56lm	61.1	±5.3d	**100.6**	±2.54a	56.2	±1.11n	78.4	±22.2ab
Ramada	64.2	±1.02e	54.7	±0.47l-n	59.5	±4.8de	75.6	±0.70gf	**45.6**	±1.67q	60.6	±15.0g
Roma	63.1	±0.74ef	**52.6**	±0.32o	57.9	±5.3e	78.3	±1.27ed	48.8	±0.33p	63.6	±14.8fg
Smith	64.2	±0.45e	56.4	±0.72j-l	60.3	±3.9de	71.3	±0.59i	60.1	±2.37m	65.7	±5.6ef
Theis	61.8	±1.13gf	53.5	±0.68on	57.7	±4.2e	73.2	±1.07hi	59.3	±0.90m	66.3	±6.9d-f
Topper 76	67.5	±1.71cb	55.8	±1.28lm	61.7	±5.9cd	76.3	±2.57ef	64.7	±2.24j-l	70.5	±5.8c
Tracy	68.0	±1.08cb	55.9	±1.15k-m	62.0	±6.1cd	79.0	±1.93d	60.3	±1.95m	69.7	±9.3cd
UNL. hybrid-3	68.2	±2.44cb	56.3	±1.35k-m	62.3	±6.0b-d	75.0	±0.66f-h	63.7	±0.78kl	69.4	±5.7cd
Williams	67.1	±0.71c	57.8	±0.67i-k	62.5	±4.7b-d	86.0	±2.24c	66.2	±1.70j	76.1	±9.9b
No91	66.7	±0.67c	58.3	±0.74ij	62.5	±4.2b-d	73.9	±1.04hg	63.8	±1.11kl	68.9	±5.1c-e
No5	69.1	±0.54b	60.3	±0.90gf	64.7	±4.4a-c	76.7	±1.44d-f	62.7	±1.22l	69.7	±7.0cd
Gülşeker	67.5	±0.54cb	64.3	±0.46e	65.9	±1.6a	96.5	±0.79b	65.7	±0.91kj	81.1	±15.4a
Mean	**66.6**	**±2.58**	**56.9**	**±2.83**	**61.8**	**±4.9B**	**78.9**	**±8.74**	**58.6**	**±6.09**	**68.8**	**±10.2A**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates ±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test

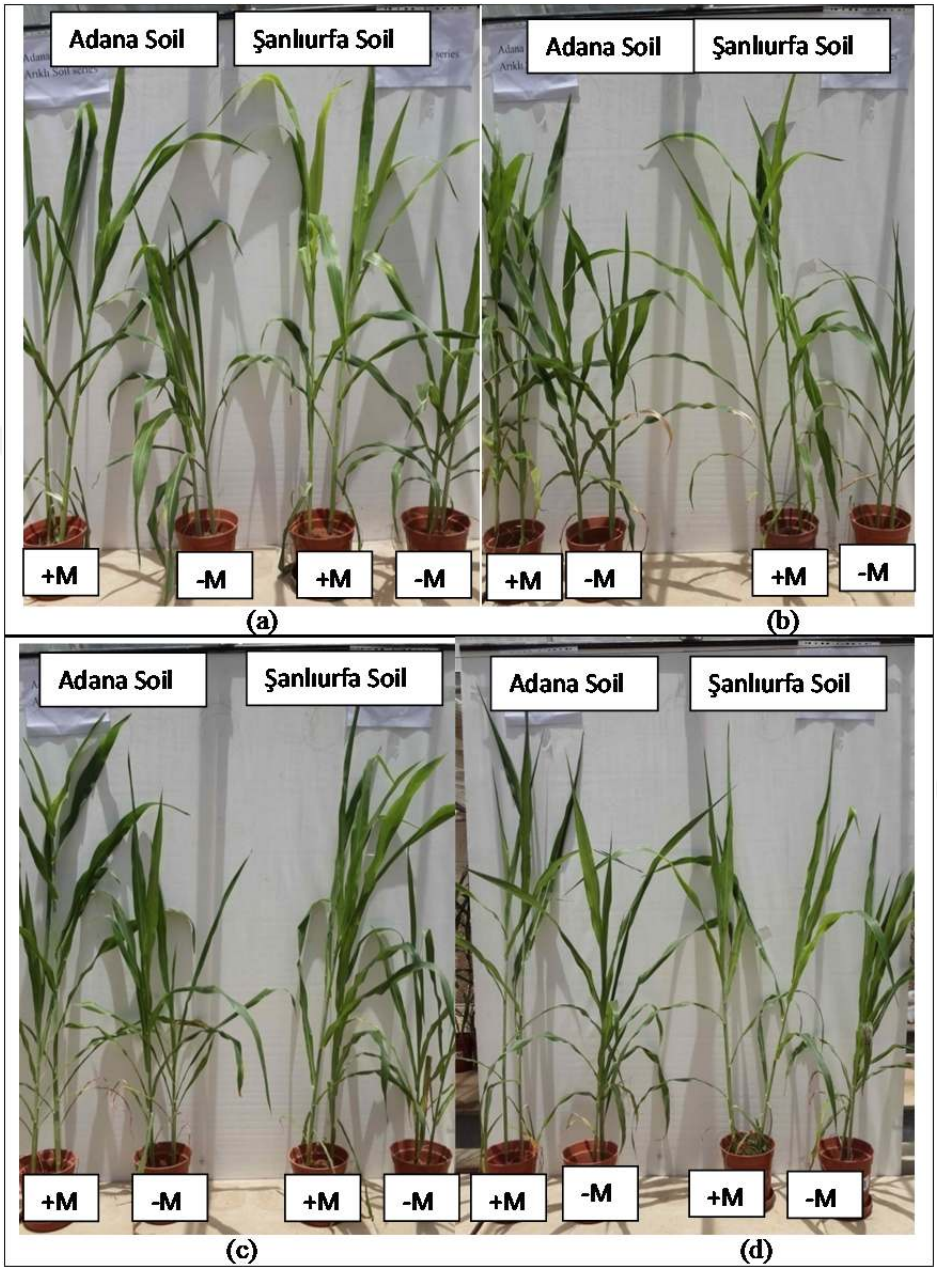

Figure 4.2. Plant height of sweet sorghum genotypes was highly significant ($p<0.001$) in mycorrhizal inoculated pots than non-mycorrhizal pots

4.2.2. Plant Height and Shoot/Root Ratio

Plant height of sweet sorghum genotypes was highly significant ($p<0.001$) in mycorrhizal inoculated pots than non-mycorrhizal pots (Table 4.33). In mycorrhiza amended Adana soil, plant height varies from 130 to 169 cm and in non-mycorrhiza inoculated pots plant height varies from 111 to 139 cm (Table 4.33). Likewise, in mycorrhiza inoculated Şanlıurfa soil the plant high varies from 118 to 166 cm and in non-mycorrhiza inoculated pots, plant height varies from 91 to 132 cm (Table 4.33 and Figure 4.3).

Shoot and root ratio of sweet sorghum genotypes was calculated for -M and +M mycorrhizal inoculation. In generally mycorrhizal inoculated plant have higher shoot/root ration than non-inoculated genotypes for both locations (Table 4.34).

Table 4.33. Average of plant height of the sweet sorghum genotypes that grown in (+M and -M) Mycorrhiza in Adana and Şanlıurfa soils.

Genotype	Plant Height (cm)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	137	±1.00e-i	115	±5.00n	126	±11.0f	146	±1.53d	104	±4.04p	125	±21.0e
Grassi	147	±2.65cd	125	±1.53m	136	±11.0c-e	159	±1.00b	122	±1.53ml	141	±18.5bc
M81-E	**130**	±2.00i-m	126	±1.00lm	128	±2.0ef	147	±1.53d	112	±2.52o	130	±17.5e
Neb. Sugarcane	142	±2.52de	128	±2.52lm	135	±7.0c-f	148	±3.21d	122	±2.08kl	135	±13.0d
PI 575753	135	±9.87g-k	118	±2.52n	127	±8.5f	133	±1.53hg	125	±2.08j-l	129	±4.0e
Ramada	138	±7.51e-h	127	±2.89lm	133	±5.5d-f	135	±2.08fg	103	±5.20p	119	±16.0f
Roma	137	±3.06e-h	129	±9.02k-m	133	±4.0d-f	157	±3.06cb	114	±0.58no	136	±21.5cd
Smith	152	±2.52bc	135	±4.36g-j	144	±8.5a-c	**166**	±1.00a	126	±1.00jk	146	±20.0a
Theis	140	±4.51e-g	**139**	±3.61e-g	140	±0.5b-d	145	±1.53d	131	±1.15hi	138	±7.0b-d
Topper 76	139	±0.58e-g	133	±7.00g-l	136	±3.0c-e	146	±1.15d	132	±1.53hg	139	±7.0b-d
Tracy	158	±2.52b	136	±7.81e-j	147	±11.0ab	154	±3.79c	127	±0.58ji	141	±13.5b
UNL. hybrid-3	**169**	±3.61a	134	±5.13f-k	152	±17.5a	160	±1.53b	118	±2.89m	139	±21.0b-d
Williams	141	±3.51d-f	126	±4.04m	134	±7.5d-f	138	±2.89fe	112	±2.65o	125	±13.0e
No91	138	±2.89e-g	115	±5.03n	127	±11.5f	132	±2.52hg	107	±1.53p	120	±12.5f
No5	148	±2.65cd	131	±2.08h-m	140	±8.5b-d	141	±1.15e	111	±1.15o	126	±15.0e
Gülşeker	148	±1.53cd	**111**	±1.73n	130	±18.5ef	117	±2.65nm	**91**	±1.53q	104	±13.0g
Mean	**144**	**±9.75**	**127**	**±8.27**	**135**	**±8.5A**	**144.3**	**±12.40**	**116**	**±11.37**	**131**	**±14.1B**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates ±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.34. Average of shoot/root ratio of the sweet sorghum genotypes that grown in (+M and -M) Mycorrhiza in Adana Şanlıurfa Soils.

Genotype	Shoot/Root (Ratio)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	**6.1**	±0.2p	5.1	±0.1j-l	5.6	±0.50h	5.1	±0.2p	5.4	±0.6n-p	5.3	±0.15f
Grassi	7.3	±0.4m-o	7.1	±0.3j-m	7.2	±0.10e-h	7.1	±0.2d-i	6.1	±0.3k-n	6.6	±0.47b-e
M81-E	7.7	±0.1l-n	6.4	±0.1f-i	7.1	±0.65de	6.4	±0.0h-l	6.0	±0.4k-o	6.2	±0.16c-f
Neb. sugarcane	7.4	±0.3m-o	6.3	±0.2p	6.9	±0.55h	6.3	±0.4j-m	5.5	±0.4m-p	5.9	±0.39d-f
PI 575753	9.2	±0.4cd	8.5	±0.4cd	8.9	±0.35ab	**8.5**	**±0.3a**	6.3	±1.2j-m	7.4	±1.10a-c
Ramada	8.1	±0.6h-k	6.2	±0.2f-h	7.2	±0.95cd	6.2	±0.2j-n	**4.8**	±0.5p	5.5	±0.69ef
Roma	8.6	±0.4e-g	7.0	±0.2j-l	7.8	±0.80cd	7.5	±0.2e-j	6.0	±0.3k-o	6.7	±0.77c-f
Smith	**10.2**	±0.2a	6.0	±0.4c-e	8.1	±2.10a	6.0	±0.5k-o	7.3	±1.3d-g	6.6	±0.65b-e
Theis	9.7	±0.5b	6.0	±0.4cb	7.9	±1.85a	6.0	±0.3k-o	6.7	±0.3e-k	6.3	±0.38c-f
Topper 76	7.1	±0.2o	5.6	±0.2m-o	6.4	±0.75gh	5.6	±0.3l-p	6.8	±0.6e-k	6.2	±0.58c-f
Tracy	9.0	±0.3d-f	6.0	±0.3p	7.5	±1.50d-f	6.0	±0.1k-o	6.6	±0.9f-k	6.3	±0.34c-f
UNL. hybrid-3	7.7	±0.3k-m	5.3	±0.2no	6.5	±1.20f-h	5.2	±0.3op	7.3	±0.6c-g	6.3	±1.05c-f
Williams	8.7	±0.4d-g	8.1	±0.3j-l	8.4	±0.30cd	8.1	±0.1a-c	7.9	±1.2a-d	8.0	±0.11a
No91	7.6	±0.2k-m	6.5	±0.2i-l	7.1	±0.55d-g	6.5	±0.3g-k	7.3	±0.4b-f	6.9	±0.42a-d
No5	9.2	±0.1cd	6.1	±0.2g-j	7.7	±1.55bc	6.2	±0.3j-n	7.1	±0.2d-h	6.7	±0.49b-e
Gülşeker	8.9	±0.2d-f	8.2	±0.3m-o	8.6	±0.35c-e	8.2	±0.2ab	7.5	±0.2b-e	7.8	±0.33ab
Mean	**8.3**	**±1.08**	**6.5**	**±1.04**	**7.4**	**±0.90A**	**6.4**	**±0.85**	**6.53**	**±0.86**	**6.5**	**±0.06B**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates ±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

4.2.3. Mycorrhizal Dependency

Since mycorrhizal dependency (MD) is a very important indication of response of mycorrhizae, the MD was calculated by using shoot dry weight. A wide variation was found among the sweet sorghum genotypes in term of MD. The highest MD was found to be 43.8% for PI575753 sweet sorghum genotypes in Adana soils and 46.1% for PI575753 sweet sorghum genotypes. The lowest was MD was found to be 17.5% for Smith sweet sorghum genotypes and 11.2% for UNL hybrid-3 sweet sorghum genotypes in Adana and Şanlıurfa soils respectively (Figure 4.3).

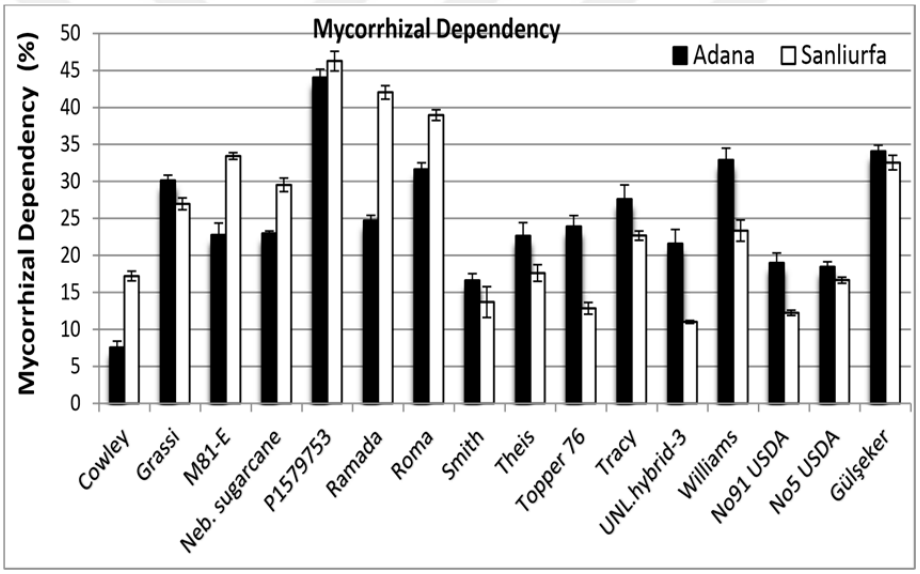

Figure 4.3. Mycorrhizae dependency in the sweet sorghum genotypes that grown in (+M= Mycorrhizae and –M=Non-Mycorrhiza) in two soils. Data were means of three replicates. Error bars means standard error. SE (±3).

4.2.3.1. Root Morphological Characteristics of the Sweet Sorghum Genotypes

Root morphological characteristics of the sweet sorghum varies between mycorrhiza and non-mycorrhiza treatment (Tables 4.36, 4.37, 4.38 and 4.39). On average, total root length was higher in non-mycorrhizae inoculated treatment than mycorrhizae inoculated treatment in two different soils (Table 4.37).

The root diameter data showed that root diameter was higher in non-mycorrhizae inoculated treatment than mycorrhiza inoculated treatment with the exception of NO5 sweet sorghum genotypes in Adana soils (Table 4.36). The root diameter of both mycorrhizae and non-mycorrhiza inoculated sweet sorghum genotypes vary from 0.230 to 0.339 mm in Şanlıurfa soils (Table 4.36). On average, root diameter of sixteen sweet sorghum genotypes was highly significant ($p<0.001$) (Table 4.35). In mycorrhiza inoculated pot, root diameter in sixteen sweet sorghum genotypes varies from 0.225 to 0.292 mm (Table 4.36). However, in non-mycorrhiza added pot varies from 0.231 to 0.288 mm in Adana soils (Tables 4.36). Likewise, the diameter varies 0.230 to 0.309 and 0.231 to 0.339 mm at mycorrhizae and non-mycorrhizae inoculated respectively in Şanlıurfa soils (Table 4.36).

In general, the total root length was higher at mycorrhiza inoculated treatment and non-mycorrhiza inoculated treatment in Şanlıurfa soils than in Adana soils (Table 4.37). The total root length of the sweet sorghum genotypes varies from 290.90 to 726.03 m pot^{-1} in mycorrhizae inoculated treatment. Whereas, the total root length of the sweet sorghum genotypes varies from 352.41 to 755.33 m pot^{-1} in non-mycorrhizae inoculated treatment (Table 4.37).

In both Adana and Şanlıurfa soils due mycorrhiza hyphae help to increase the surface area of the plant root system mycorrhizal inoculated plant some time have less root surface than non-mycorrhizae inoculated

sweet sorghum genotypes (Table 4.38). In mycorrhiza inoculated pots, the root surface area of the sweet sorghum genotypes in Adana soils varies from 2316 to 4441 cm^2 and in non-mycorrhiza inoculated treatment varies from 3155 to 5375 cm^2 (Table 4.38). In Şanlıurfa soils, the root surface area of the sweet sorghum genotypes varies from 2750 to 5609 cm^2 and in non-mycorrhiza inoculated treatment varies from 2698 to 5596 cm^2 (Table 4.38).

In Adana soils, total root volume of sixteen sweet sorghum genotypes varies 13 cm^3 pot^{-1} to 28 cm^3 pot^{-1} and 23.8 to 36 cm^3 pot^{-1} for mycorrhiza and non-mycorrhiza treatments, respectively (Table 4.39). Likewise, in Şanlıurfa soils the total root volume of the sweet sorghum genotypes varies from 19 to 36 cm^3 pot^{-1} and 14 to 37 cm^3 pot^{-1} for mycorrhiza and non-mycorrhiza treatments, respectively (Table 4.39). The root volume was higher in non-mycorrhiza inoculated treatment than mycorrhiza inoculated treatment with the exception of Roma and M81-E sweet sorghum genotypes in Adana soils (Table 4.39). The lowest root volume was 13 cm^3 pot^{-1} for Tracy sweet sorghum genotypes at mycorrhiza inoculated pots in Adana soils (Table 4.39). The highest root volume was 37 cm^3 pot^{-1} for M81-E sweet sorghum genotypes at non-mycorrhiza treatments in Şanlıurfa soils (Table 4.39).

Overall results shown in Tables 4.36, 4.37, 4.38 and 4.39 root diameter, root length, root surface and root volume data are higher under non-mycorrhizal inoculation than mycorrhizal inoculation. Since soil were sterilized and all soil organisms including indigenous mycorrhizae spores were eliminated, nutrient uptake was done my plant roots. As non-inoculated plant growth less than inoculated one, plant first increased root growth then shoot growth. This is supported by shoot/root ratio data which is important for healthy plant growth.

Table 4.35. Level of significance for the main and interactive effect on root morphological characteristics of sixteen sweet sorghum genotypesthat grown in (+M = With mycorrhizae and –M= Without mycorrhiza) in adana and Sanliurfa Soils.

Sources of variations	**Root Diameter**	**Root length**	**Root Surface**	**Root Volume**
Genotypes	***	***	***	***
Soil	***	***	***	***
Genotypes X Soil	***	***	***	***
Mycorrhizae	**	***	***	***
Genotypes X Mycorrhizae	***	***	***	***
Soil X Mycorrhizae	**	n.s.	**	***
Genotypes X Soil X Mycorrhizae	***	***	***	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.36. Average of root diameter of the sweet sorghum genotypes that grown in (+M and -M) mycorrhiza in Adana and Şanlıurfa soils.

Genotype	Root Diameter (mm)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	0.258	±0.01c-j	0.268	±0.01a-f	0.263	±0.005a-c	0.276	±0.01c-f	0.264	±0.01d-h	0.270	±0.006b-d
Grassi	0.273	±0.00a-e	0.288	±0.02ba	0.281	±0.007ab	0.256	±0.01f-j	0.272	±0.02c-f	0.264	±0.008c-e
M81-E	0.239	±0.02h-l	0.272	±0.04a-e	0.256	±0.017a-c	0.262	±0.01e-h	0.261	±0.01e-h	0.262	±0.001c-e
Neb. sugarcane	0.240	±0.01h-l	0.278	±0.01a-d	0.259	±0.019a-c	0.235	±0.01kj	0.267	±0.01d-g	0.251	±0.016c-e
PI 575753	0.253	±0.02d-j	0.252	±0.01e-j	0.253	±0.001a-c	0.239	±0.02i-k	0.248	±0.01g-k	0.244	±0.005de
Ramada	0.255	±0.01d-k	0.260	±0.03c-i	0.258	±0.003a-c	0.237	±0.01kj	0.245	±0.01h-k	0.241	±0.004de
Roma	0.253	±0.01d-k	0.259	±0.01c-i	0.256	±0.003a-c	0.238	±0.01i-k	0.246	±0.02g-k	0.242	±0.004de
Smith	0.237	±0.01i-l	0.266	±0.01b-g	0.252	±0.015a-c	0.275	±0.01c-f	0.265	±0.01d-h	0.270	±0.005b-d
Theis	0.245	±0.01f-l	0.260	±0.01c-i	0.253	±0.008a-c	0.265	±0.01d-h	**0.338**	±0.01a	0.302	±0.037a
Topper 76	**0.225**	±0.01l	0.261	±0.01c-i	0.243	±0.018c	**0.227**	±0.01k	0.248	±0.01g-k	0.238	±0.011e
Tracy	0.230	±0.02lk	0.265	±0.01b-h	0.248	±0.018dc	0.259	±0.01f-i	0.339	±0.02a	0.299	±0.040ab
UNL. hybrid-3	0.259	±0.02c-i	0.263	±0.02b-h	0.261	±0.002a-c	0.244	±0.01h-k	0.239	±0.02i-k	0.242	±0.003de
Williams	0.233	±0.01j-l	0.241	±0.01g-l	0.237	±0.004c	0.230	±0.02k	0.247	±0.02g-k	0.239	±0.008e
No91	0.252	±0.02e-k	0.281	±0.00a-c	0.267	±0.015a-c	0.292	±0.00cb	0.256	±0.01h-j	0.274	±0.018a-c
No5	**0.292**	±0.02a	0.273	±0.01a-e	0.283	±0.009a	0.309	±0.03b	0.284	±0.02cd	0.297	±0.013ab
Gülşeker	0.233	±0.01j-l	0.231	±0.00lk	0.232	±0.001c	0.282	±0.01c-e	0.231	±0.00k	0.257	±0.026c-e
Mean	**0.249**	**±0.02**	**0.264**	**±0.01**	**0.256**	**±0.008B**	**0.258**	**±0.02**	**0.266**	**±0.03**	**0.262**	**±0.004A**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.37. Average of total root length of the sweet sorghum genotypes that grown in (+M and -M) mycorrhiza in Adana and Şanlıurfa soils.

Genotype	Total Root Length (m pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	465.4	±6752f-h	579.5	±4950c	522.5	±57bc	515.9	±3524e-j	640.9	±2666a-d	578.4	±63ab
Grassi	380.3	±1552k-m	557.4	±4788c-e	468.8	±89c-e	481.6	±1476f-k	580.0	±10251c-g	530.8	±49a-e
M81-E	522.7	±5347c-g	402.3	±4628i-l	462.5	±60c-e	445.2	±1961h-l	650.0	±830a-d	547.6	±102a-d
Neb. sugarcane	527.5	±4760c-f	418.9	±1037i-l	473.2	±54cd	467.6	±4018e-j	616.2	±6753b-e	541.9	±74a-d
PI 575753	391.7	±6505kl	510.1	±2594d-g	450.9	±59c-f	512.4	±15353c-g	488.7	±1042f-k	500.6	±12b-e
Ramada	389.6	±2898kl	386.5	±750k-m	388.0	±2ef	572.5	±2464a-d	**755.3**	±2761a	663.9	±91a
Roma	370.3	±1449ml	439.8	±4457h-k	405.0	±35d-f	663.7	±2715k-m	589.3	±7343c-f	626.5	±37ab
Smith	458.1	±5131g-j	519.0	±3522c-g	488.5	±30cd	377.3	±932k-m	443.4	±2096i-l	410.4	±33de
Theis	415.5	±3795i-l	459.1	±5348g-j	437.3	±22d-f	380.8	±1964d-i	464.2	±18743g-l	422.5	±42c-e
Topper 76	511.3	±1076d-g	539.0	±4041c-e	525.1	±14bc	559.2	±7511d-i	561.3	±17053d-h	560.2	±1a-c
Tracy	321.8	±3144n	544.8	±5551c-e	433.3	±11d-f	689.0	±1725a-c	352.4	±2776lm	520.7	±168a-e
UNL. hybrid-3	**290.9**	±1036n	552.4	±4464c-e	421.7	±13d-f	726.0	±2729ba	448.5	±15042h-l	587.3	±139ab
Williams	525.0	±2547c-f	671.4	±5255b	598.2	±73ab	487.3	±701f-k	592.1	±11426c-f	539.7	±52a-d
No91	565.2	±5665dc	400.1	±1507j-l	482.6	±83cd	419.6	±2519j-l	356.2	±5995lm	387.9	±32e
No5	297.9	±1608n	441.0	±3270h-k	369.5	±72f	**298.5**	±1173m	484.1	±614f-k	391.3	±93e
Gülşeker	497.1	±3358e-h	**742.3**	±2447a	619.7	±123a	**295.3**	±1894m	**742.0**	±2736a	518.7	±223a-e
Mean	**433**	**±8803**	**510.22**	**±10019**	**472**	**±39B**	**493.24**	**±12776**	**548**	**±12101**	**521**	**±27A**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.38. Average of root surface of the sweet sorghum genotypes that grown in (+M and -M) Mycorrhiza in Adana and Şanlıurfa Soils.

Genotype	Root Surface Area (cm pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	3752	±337h-k	4879	±422a-d	4316	±564ab	4473	±227d-j	5306	±140a-d	4890	±417a
Grassi	3257	±101k-p	5027	±48a-c	4142	±885a-c	3877	±109h-l	4921	±621a-f	4399	±522ab
M81-E	3931	±632f-j	3444	±701i-o	3688	±244a-e	3660	±229j-m	**5596**	±321a	4628	±968ab
Neb. sugarcane	3969	±281f-i	3658	±194h-l	3814	±156a-e	3457	±355k-n	5158	±421a-e	4308	±851a-c
PI 575753	3095	±410n-p	4025	±83e-h	3560	±465b-e	3795	±883h-l	4662	±1432b-h	4229	±434a-c
Ramada	3114	±173m-p	3155	±281l-p	3135	±21e	4268	±322e-k	5535	±421ba	4902	±634a
Roma	2943	±43op	3592	±523h-n	3268	±325de	4678	±737b-h	4574	±179c-i	4626	±52ab
Smith	3415	±459j-o	4330	±278e-g	3873	±458a-e	3258	±124l-n	**2698**	±187n	2978	±280c
Theis	3183	±134l-p	3762	±641h-k	3473	±290c-e	3205	±384l-n	4243	±946f-k	3724	±519a-c
Topper 76	3607	±248h-n	4407	±301d-f	4007	±400a-d	3966	±389g-l	4322	±1154e-k	4144	±178a-c
Tracy	**2316**	±95q	4529	±495c-e	3423	±1107c-e	**5609**	±46a	3742	±115i-m	4676	±934ab
UNL. hybrid-3	2367	±113q	4546	±125b-e	3457	±1090c-e	5550	±164ba	3282	±719l-n	4416	±1134ab
Williams	3832	±76g-j	5081	±346ba	4457	±625a	3255	±213l-n	4798	±751a-g	4027	±772a-c
No91	4441	±208d-f	3529	±110h-n	3985	±456a-d	3843	±183h-l	2862	±495nm	3353	±491bc
No5	2728	±125qp	3789	±433g-k	3259	±531de	2750	±131n	4871	±686a-f	3811	±1061a-c
Gülşeker	3646	±334h-m	**5375**	±200a	4511	±865a	3199	±741l-n	5373	±122a-c	4286	±1087a-c
Mean	**3350**	**±589.24**	**4196**	**±671**	**3773**	**±423B**	**3928**	**±820.5**	**4496**	**±917.9**	**4212**	**±284A**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.39. Average of root volume of the sweet sorghum genotypes that grown in (+M and -M) Mycorrhiza in Adana and Şanlıurfa Soils.

Genotype	Root Volume (cm pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	24.1	±0.8d-i	32.7	±3.0ba	28.4	±4.3ab	31.0	±1.1b-d	35.0	±1.5ba	33.0	±2.0a
Grassi	22.2	±0.5f-j	**36.2**	±2.4a	29.2	±7.0a	25.0	±1.1g-i	33.0	±3.1ba	29.0	±4.0a-d
M81-E	23.6	±5.3e-i	23.8	±7.4e-i	23.7	±0.1a-c	24.0	±1.9g-i	**37.0**	±1.3a	30.5	±6.5ab
Neb. sugarcane	23.8	±2.1e-i	25.5	±2.1c-f	24.7	±0.9a-c	20.0	±2.7j-l	34.0	±1.9ba	27.0	±7.0b-e
PI 575753	19.5	±2.6i-k	25.3	±1.4c-f	22.4	±2.9a-c	22.0	±3.8i-l	24.0	±0.5g-j	23.0	±1.0e
Ramada	19.8	±1.1h-k	21.8	±4.7f-j	20.8	±1.0c	25.0	±2.8f-j	34.0	±1.5ba	29.5	±4.5a-c
Roma	18.6	±0.9kj	23.3	±4.5e-j	21.0	±2.3bc	28.0	±3.1d-g	27.0	±1.7e-h	27.5	±0.5b-e
Smith	20.3	±3.4g-j	28.8	±2.8b-d	24.6	±4.3a-c	22.0	±1.6i-l	**14.0**	±1.7m	18.0	±4.0f
Theis	19.4	±0.6i-k	24.6	±5.5d-h	22.0	±2.6a-c	21.0	±3.7i-l	32.0	±3.2b-d	26.5	±5.5b-e
Topper 76	20.3	±2.5g-j	28.7	±2.2b-d	24.5	±4.2a-c	22.0	±1.6i-l	27.0	±6.1e-h	24.5	±2.5c-e
Tracy	**13.3**	±0.9l	28.8	±2.3b-d	21.1	±7.8bc	**36.0**	±0.7a	32.0	±0.6b-d	34.0	±2.0a
UNL. hybrid-3	15.4	±1.8lk	30.0	±3.2bc	22.7	±7.3a-c	34.0	±1.9ba	19.0	±2.1lk	26.5	±7.5b-e
Williams	22.3	±0.3f-j	30.7	±2.7b	26.5	±4.2a-c	19.0	±0.8lk	29.0	±2.8c-f	24.0	±5.0de
No91	28.0	±3.4b-e	24.8	±0.8d-g	26.4	±1.6a-c	28.0	±1.0d-g	18.0	±3.3l	23.0	±5.0ef
No5	20.0	±2.5h-k	24.4	±2.4d-h	22.2	±2.2a-c	21.0	±3.1i-l	33.0	±0.9a-c	27.0	±6.0b-e
Gülşeker	21.3	±2.5f-g	31.0	±1.6b	26.2	±4.9a-c	23.0	±3.3h-k	31.0	±0.5b-e	27.0	±4.0b-e
Mean	**21.0**	**±3.5**	**28.0**	**±4.0**	**24.1**	**±3.5B**	**25**	**±5.0**	**29**	**±6.7**	**26.9**	**±2.0A**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Indigenous mycorrhiza had remarkable effect on growth response of sweet sorghum genotypes. Plant biomass was higher in indigenous mycorrhiza inoculated soil than non-mycorrhiza inoculated soil (Table 4.30 and Table 4.31). Previously shown that mycorrhiza inoculated sorghum significantly increased plant shoot dry weight. (Ortas et al. 1996b; Ortas et al. 2004; Sharif et al. 2011). They also speculated that inoculation of AMF may play a role in improving sorghum plant biomass production due to the reason that fungi significant the stimulation of the compatibility of the fungi and host plant species. Under greenhouse conditions it has been determined that sorghum plant is highly mycorrhizae dependent plant as well (Ortas et al. 1996b; Ortas et al. 2004; Ortaş and Harris 1996) Likewise, other study found that indigenous tropical AM fungi showed significantly better performance than the non-inoculated plants in terms of sweet sorghum plant height, root length and root dry weight (Ortas et al. 1996b; Ortas and Rowell 2004; Sarah and Burni 2013). The possible explanation of AM fungi on shoot dry matter growth of the genotypes may be due to the enhanced uptake of nutrient than non-inoculated one. Whereas, the higher root growth is due to higher nutrient supply on the AM fungus which competes with the roots for photosynthesis (Rydlová et al. 2011). Root growth was boosted by indigenous mycorrhizae probably because of C demand of indigenous mycorrhizae and due to the improved nutrition of mycorrhizal plants. It was argued that if the extension of root system by mycelia of AMF allows plants to have more roots that the C sink of AMF might be higher than C sink of “additional” roots of non-mycorrhizal plants (Jakobsen et al. 2003). The indigenous mycorrhizae can increase uptake of immobile nutrients like phosphorus (P) and Zinc (Zn) which could help to increase inoculated sweet sorghum plant biomass as compared to non-inoculated plant (Ortas et al. 2016; Ortas et al. 2018). Likewise, the indigenous mycorrhiza may

also help to enhance the competitive ability of the sweet sorghum genotypes to obtain the nutrients (Munns and Mosse 1980). Previously indicated that some phosphorus-efficient cultivars have a capacity to increase P arability for root uptake then the other cultivars (Rengel and Marschner 2005; Subramanian et al. 2009).

In addition, indigenous mycorrhiza also can develop extensive hyphae outside the sweet sorghum plant root. The intraradical and extraradical hyphae constitute a filamentous network that bridges rhizosphere and sweet sorghum plant roots and consequently facilitates the bidirectional nutrient transfer, where soil nutrients move to the plant and plant photosynthesis flow to the fungus (Smith et al. 2001). The results of Kamaei et al. (2019) shown that the highest rate of sorghum physiological growth indexes such as root area index and net assimilation rate were obtained with inoculation of mycorrhiza. Furthermore, mycorrhization of sorghum plants had a positive effect on plant growth that may be due to a more limited supply of nutrients to plants grown in pots inoculated with sterile inoculums.

4.2.4. Root Colonization

After harvest, root colonization of sub-samples was determined and results are presented in (Figure 4.5). The research showed that the sweet sorghum root colonization Figure 4.4 varies from 30 to 65% in Adana soils and 30 to 70% in Şanlıurfa soil among the sweet sorghum genotypes. The root colonization was 30% for No91 sweet sorghum in Adana soils and in Şanlıurfa soils the lowest root colonization was 30% for Williams genotype. Likewise, the highest root colonization was 65% for Roma and 70% for No5 genotype in Adana and Şanlıurfa soils, respectively (Figure 4.5).

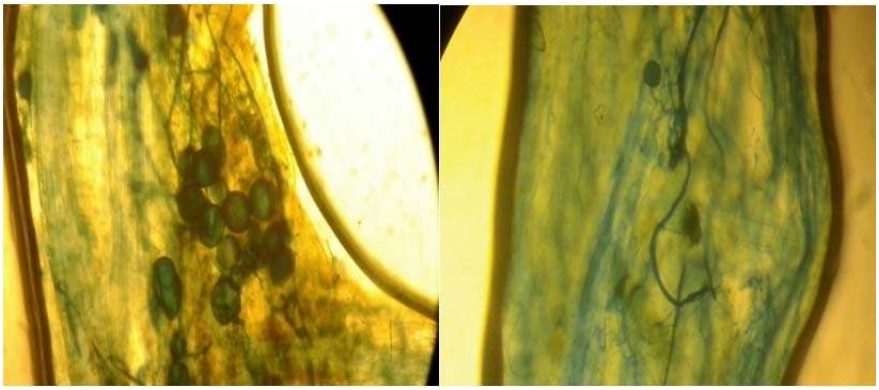

Figure 4.4. Sweet sorghum genotypes root infection

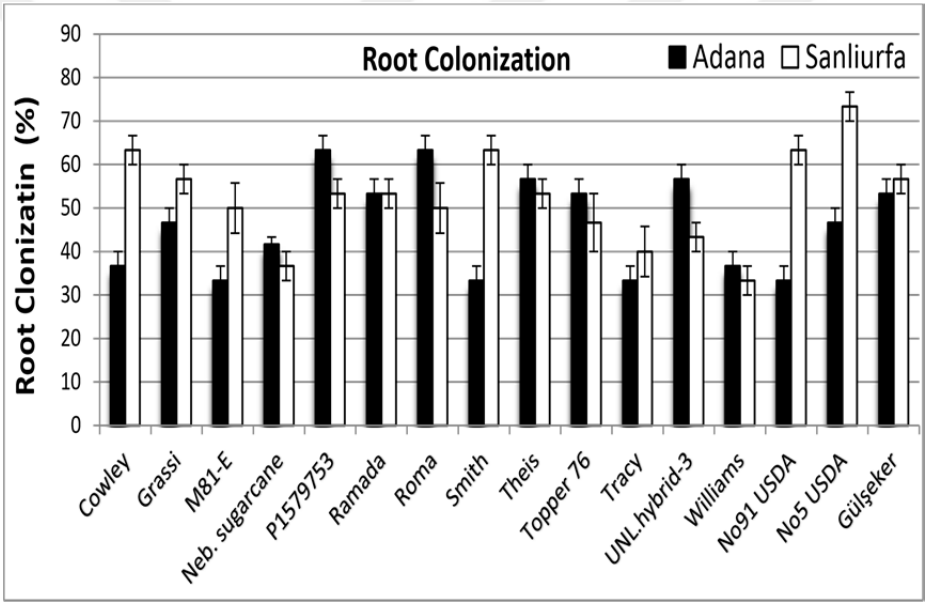

Figure 4.5. Root Clonization in the sweet sorghum genotypes that grown in (+M= mycorrhizae and –M=nNon-mycorrhiza) in two Soils. Data were means of three replicates. Error bars means standard error. SE (±3).

4.2.5. Bulk Soil Organic C and Total Nitrogen Concentration

The difference of bulk soil organic carbon (SOC) concentration was highly significant ($p < 0.001$) between indigenous mycorrhiza amendment and non-mycorrhiza amendment (Table 4.32). Mean bulk SOC concentration was 1.46% in Adana Soil and 2.31% in Şanlıurfa soil for

indigenous mycorrhiza amendment. Whereas, the mean bulk SOC concentration was 1.11% in Adana soil and 2.2% in Şanlıurfa soil for non-mycorrhiza amendment (Table 4.32). These findings indicate that indigenous mycorrhiza has the ability to input C in the soil by the sweet sorghum genotypes for Adana soil such as Cowley, Grassi, M81-E, Nebraska Sugarcane and PI575753 and for Şanlıurfa soil genotypes M81-E and PI 575753 (Table 4.32).

In generally, mycorrhiza inoculate genotypes grown in Adana soil's average C concentration was 1.46% and in non-inoculated genotypes grown soils C % was 1.12%. It is that mycorrhiza inoculated plant root surface area has high carbon accumulate (Table 4.38). For Şanlıurfa soil, mycorrhiza inoculated genotypes average mean C % was 2.32% and in non-inoculated soils C concentration was 2.21% (Table 4.41).

In contrast, bulk soil total nitrogen was significantly ($p<0.001$) higher in non-mycorrhiza inoculated soil than mycorrhiza inoculated soil (Table 4.42). The bulk soil total nitrogen was 0.069 to 0.091% in Adana soil and 0.046 to 0.053%in Şanlıurfa soil for mycorrhiza and non-mycorrhiza treatments, respectively (Table 4.42).

Mean of nitrogen concentration in mycorrhizae inoculated genotypes grown Adana soils is 0.085% (Table 4.42). However, in not inoculated genotypes grown soils mean N concentration is 0.094%. For Şanlıurfa soil mycorrhiza inoculated genotypes mean N concentration is 0.050% and non-inoculated soils is 0.053% (Table 4.42). Most probably mycorrhiza inoculated soils rhizosphere organisms and plants are consuming more nitrogen than non-inoculated treatments.

Table 4.40. Level of significance for the main and interactive effect on soil organic carbon and total nitrogen of the sweet sorghum genotypes that grown in (+M= Mycorrhizae and –M= Non-mycorrhiza) in Adana and Sanliurfa soils.

Sources of variations	**Soil OC %**	**Soil Total N %**
Genotypes	**	*
Soil	***	***
Genotypes X Soil	***	***
Mycorrhizae	***	***
Genotypes X Mycorrhizae	***	***
Soil X Mycorrhizae	***	***
Geno X Soil X Mycorrhizae	***	**

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.41. Average of organic carbon content% in soil saemples (0-30cm) for the sweet sorghum genotypes that grown in (+M= with mycorrhiza and –M= without mycorrhiza) in Adana and Şanlıurfa soils.

Genotype	Organic Carbon (%)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	1.59	±0.04ab	1.06	±0.06j-m	1.33	±0.27a	2.25	±0.15b-g	2.12	±0.04ji	2.19	±0.06
Grassi	**1.63**	±0.07a	1.02	±0.07lm	1.33	±0.31a	2.30	±0.03a-e	2.11	±0.06ji	2.21	±0.10
M81-E	1.54	±0.14bc	1.08	±0.01j-l	1.31	±0.23ab	**2.40**	±0.03a	**2.03**	**±0.01j**	2.22	±0.19
Neb. sugarcane	1.47	±0.03c-e	1.02	±0.05k-m	1.25	±0.22ab	2.35	±0.01a-c	2.16	±0.01f-j	2.26	±0.10
PI 575753	1.49	±0.04dc	1.12	±0.06h-j	1.31	±0.18ab	2.38	±0.17ab	2.24	±0.04c-i	2.31	±0.07
Ramada	1.43	±0.03d-f	**0.98**	±0.05m	1.21	±0.22b	2.23	±0.02c-I	2.26	±0.06b-g	2.25	±0.01
Roma	1.46	±0.04c-f	1.09	±0.02j-l	1.28	±0.19ab	2.32	±0.07a-d	2.25	±0.04b-i	2.29	±0.03
Smith	1.42	±0.06d-f	1.12	±0.03ij	1.27	±0.15ab	2.24	±0.06c-I	2.18	±0.06e-i	2.21	±0.03
Theis	1.42	±0.01d-f	1.07	±0.04j-l	1.25	±0.17ab	2.29	±0.12a-f	2.26	±0.13b-g	2.28	±0.02
Topper 76	1.47	±0.02c-e	1.13	±0.02h-j	1.30	±0.17ab	2.35	±0.09a-d	2.29	±0.02a-e	2.32	±0.03
Tracy	1.41	±0.02d-f	1.19	±0.10g-i	1.30	±0.11ab	2.32	±0.09a-d	2.15	±0.07h-j	2.24	±0.09
UNL. hybrid-3	1.44	±0.02d-f	1.20	±0.04g-i	1.32	±0.12ab	2.30	±0.18a-e	2.32	±0.02a-d	2.31	±0.01
Williams	1.42	±0.01d-f	1.20	±0.01gh	1.31	±0.11ab	2.28	±0.06a-g	2.30	±0.06a-e	2.29	±0.01
No91	1.42	±0.00d-f	1.11	±0.12jk	1.27	±0.15ab	2.36	±0.12a-c	2.15	±0.07g-j	2.26	±0.11
No5	1.38	±0.01f	1.20	±0.04g-i	1.29	±0.09ab	2.33	±0.02a-d	2.22	±0.04d-i	2.28	±0.05
Gülşeker	1.39	±0.02ef	1.25	±0.03g	1.32	±0.07a	2.35	±0.13a-d	2.26	±0.03a-h	2.31	±0.05
Mean	**1.46**	**±0.07**	**1.12**	**±0.08**	**1.29**	**±0.17B**	**2.32**	**±0.050**	**2.21**	**±0.081**	**2.26**	**±0.05A**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates ±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.42. Average of total nitrogen content % in soil samples (0-30cm) for the sweet sorghum genotypes that grown in (+M= with mycorrhiza and –M= without mycorrhiza) in Adana and Şanlıurfa soils.

Genotype	Total Nitrogen (%)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	0.092	±0.003a-e	0.095	±0.002a-c	0.094	±0.002	0.049	±0.001i-k	**0.056**	±0.001a	0.053	±0.004ab
Grassi	0.090	±0.003a-f	0.093	±0.003a-d	0.092	±0.002	0.053	±0.001b-e	0.055	±0.001a-d	0.054	±0.001a
M81-E	0.081	±0.013fg	0.094	±0.004a-c	0.088	±0.007	0.051	±0.001f-i	0.054	±0.001a-c	0.053	±0.002ab
Neb. sugarcane	**0.069**	±0.013h	0.096	±0.004ab	0.083	±0.014	0.051	±0.001f-j	0.056	±0.001a	0.054	±0.003a
PI 575753	0.074	±0.024gh	**0.097**	±0.003a	0.086	±0.012	0.049	±0.001i-k	0.054	±0.001a-c	0.052	±0.003ab
Ramada	0.084	±0.002ef	0.094	±0.002a-c	0.089	±0.005	0.047	±0.001l-n	0.052	±0.001c-f	0.050	±0.003b-d
Roma	0.092	±0.004a-e	0.096	±0.002a-c	0.094	±0.002	0.049	±0.001i-k	0.054	±0.001a-c	0.052	±0.003ab
Smith	0.084	±0.003ef	0.094	±0.001a-c	0.089	±0.005	0.049	±0.001i-k	0.055	±0.001ba	0.052	±0.003ab
Theis	0.087	±0.004b-f	0.096	±0.001a-c	0.092	±0.005	0.048	±0.002k-m	0.054	±0.001a-c	0.051	±0.003a-c
Topper 76	0.087	±0.001b-f	0.095	±0.002a-c	0.091	±0.004	0.046	±0.003mn	0.046	±0.004nm	0.046	±0.000e
Tracy	0.086	±0.004c-f	0.095	±0.002a-c	0.091	±0.005	0.049	±0.00i-k	0.055	±0.002a-d	0.052	±0.003ab
UNL. hybrid-3	0.090	±0.003a-f	0.094	±0.001a-c	0.092	±0.002	0.05	±0.000h-k	0.055	±0.002ba	0.053	±0.003ab
Williams	0.090	±0.001a-f	0.092	±0.003a-e	0.091	±0.001	0.049	±0.001i-k	0.046	±0.001nm	0.048	±0.002de
No91	0.090	±0.003a-f	0.092	±0.002a-e	0.091	±0.001	0.051	±0.001g-j	0.053	±0.001b-e	0.052	±0.001ab
No5	0.085	±0.004d-f	0.092	±0.002a-e	0.089	±0.004	0.052	±0.002c-f	**0.045**	±0.002n	0.049	±0.004c-e
Gülşeker	0.086	±0.001c-f	0.093	±0.001a-d	0.090	±0.004	0.052	±0.001c-f	**0.056**	±0.000a	0.054	±0.002a
Mean	**0.085**	**±0.01**	**0.094**	**±0.01**	**0.090**	**±0.005A**	**0.05**	**±0.002**	**0.053**	**±0.004**	**0.051**	**±0.002B**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates ±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Bulk soil organic C was significantly ($p<0.05$) higher in mycorrhizae inoculated than non-mycorrhizae inoculated treatment/application (Table 4.41). Similarly, a study found that the net verifiable carbon accumulation in mycorrhizal soil was 10.14 kg ha^{-1} while un-inoculated soil had just 9.55 kg ha^{-1} (Krishnakumar et al. 2013). The soil C findings in this study suggested that there is an enormous potential for mycorrhizal fungi to sequester soil C through sweet sorghum genotypes. The study findings also demonstrated that indigenous mycorrhizae can accelerate soil C sequestration at least in the short term. The principal mechanism by which AMF are proposed to stimulate soil C efflux is through priming of decomposers that are a commonly observed soil biotic response to increased labile organic matter deposition (De Graaff et al. 2010). Another study found that mycorrhizae inoculated sweet sorghum genotypes translocated 20% to 30% of the assimilated C to the underground where mycorrhizal structures conserve soil C. They speculated that detrimental influences of mycorrhizal inoculations has great effect on soil C sequestration (Cheng et al. 2012). Therefore, these evidences suggested that indigenous mycorrhizae generally stimulate sweet sorghum genotypes to sequester C in bulk soil.

4.2.6. Tissue C and N Concentration of the Sweet Sorghum Genotypes

After harvest plant tissue N concentration was measured. The shoot N% was higher in mycorrhizae inoculated soil than non-mycorrhizae inoculated soil in both of Adana and Şanlıurfa soils (Table 4.45). Shoot N% varies from 2.08 to 3.89% in Adana soils and 1.80 to 2.42% in Şanlıurfa soils at mycorrhizae inoculated soils (Table 4.45). Likewise, shoot N% varies from 1.80 to 2.37% in Adana soils and 1.73 to 2.43 in Şanlıurfa soils at non-mycorrhizae inoculated soil (Table 4.45). In non-mycorrhizal inoculated treatments especially Ramada, Roma, Smith and

Thesis genotypes, they have a higher shoot N% than the other genotypes in Adana soils (Table 4.45). Those genotypes should need for further search for nitrogen use efficiency (NUE).

On average, shoot C% concentration was higher in mycorrhizae inoculated soil than non-mycorrhizae inoculated soil (Tables 4.44). Shoot C% were highly significant ($p<0.001$) between mycorrhizae and non-mycorrhizae amendment among genotypes and genotypes × treatments interaction (Table 4.43). In the mycorrhizae inoculated soil, the shoot C% concentration of sweet sorghum genotypes varies from 38.82 to 50.40% in Adana soils and 38.40 to 50.00% in Şanlıurfa soils (Table 4.44). In the non-mycorrhizae inoculated soil C concentration varies from 36.1 to 43 % in Adana soils and 36.1 to 40.4% in Şanlıurfa soils (Tables 4. 44).

In general, root C% of sixteen sweet sorghum genotypes was higher in Adana soils at both mycorrhizae and non-mycorrhizae inoculated soil than in Şanlıurfa soils (Table 4.46). Root C% were highly significant ($p<0.001$) between mycorrhizae and non-mycorrhizae amendment among genotypes and genotypes × mycorrhizae interactions (Table 4.43). In the mycorrhizae inoculated soil, the root C% of sweet sorghum genotypes varies from 32.4 to 45.3% in Adana soils and 35.0 to 43.9% in Şanlıurfa soils at the non-mycorrhizae inoculated soil (Table 4.46).

Root N% did not differ between mycorrhizae and non-mycorrhizae amendment (Table 4.46). However, root N% differ significantly ($p<0.001$) among sweet sorghum genotypes and there was a significantly ($p<0.001$) treatment × genotype interaction between treatments (Table 4.43). The root N% varies 0.95 to 1.76% in Adana soils and 1.07 to 1.62 in Şanlıurfa soils at mycorrhizae inoculated soil in sixteen sweet sorghum genotypes (Table 4.47). The root N% varies 0.94 to 1.52 in Adana soils Table 4.47 and 0.91 to 1.39% in Şanlıurfa soils at non-mycorrhizae inoculated treatment in the sweet sorghum genotypes (Table 4.47).

In generally on the average mean of data of shoot and root for both soils mycorrhiza inoculated plant tissue has higher N and C concentration than the non-inoculated treatments. This is very valuable founding for better nitrogen utilization and atmospheric carbon fixation. Since mycorrhiza is demanding more carbon for making more hyphae, plants are increasing their photosynthesis capacity by fixing more CO_2 from atmosphere than non-inoculated plants.

Table 4.43. Level of significance for the main and interactive effect on Organic carbon and Total Nitrogen in Shoot and Root of the sweet sorghum genotypes that grown in (+M= Mycorrhizae and –M= Non-mycorrhiza) in Adana And Sanliurfa Soils.

Sources of variations	**Shoot N %**	**Shoot C%**	**Root N%**	**Root N%**
Genotypes	***	***	n.s.	***
Soil	***	***	***	***
Genotypes X Soil	***	***	**	***
Mycorrhizae	***	***	*	***
Genotypes X Mycorrhizae	***	***	***	***
Soil X Mycorrhizae	***	***	n.s.	n.s.
Genotypes X Soil X Mycorrhizae	***	***	*	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.44. Average of shoot carbon % in the sweet sorghum genotypes that grown in (+M= mycorrhizae and –M= non-mycorrhiza) in Adana and Şanlıurfa soils.

Genotype	Shoot Carbon (%)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	43.5	±1.4f	38.9	±0.9i-l	41.2	±2.3d-g	**50.0**	±1.0a	38.9	±0.8h-j	44.5	±5.5a
Grassi	39.9	±1.9h-k	41.8	±1.8gf	40.9	±0.9e-g	40.5	±1.3c-f	40.4	±0.6d-g	40.5	±0.1bc
M81-E	38.9	±0.2i-l	37.8	±0.3ml	38.4	±0.6h	38.4	±0.5i-k	37.0	±1.0lk	37.7	±0.7f
Neb. sugarcane	38.8	±1.7j-l	39.6	±0.6h-k	39.2	±0.4gh	40.9	±0.8b-e	39.5	±0.8f-j	40.2	±0.7bc
PI 575753	41.8	±1.2gf	38.2	±0.7kl	40.0	±1.8f-h	41.2	±0.7b-d	38.4	±1.0i-k	39.8	±1.4b-d
Ramada	**50.4**	±1.2a	37.2	±1.4ml	43.8	±6.6bc	39.7	±0.7e-i	**36.1**	±1.1l	37.9	±1.8ef
Roma	47.0	±1.0c-f	**36.1**	±1.3m	41.6	±5.5d-f	40.0	±1.7d-h	38.8	±1.2g-j	39.4	±0.6e
Smith	49.7	±0.6ba	38.3	±1.1kl	44.0	±5.7bc	42.4	±1.6b	38.0	±1.0jk	40.2	±2.2bc
Theis	48.2	±0.9bc	39.3	±1.9i-l	43.8	±4.5bc	39.8	±0.6e-i	39.1	±0.5f-j	39.5	±0.3b-e
Topper 76	48.5	±0.7a-c	38.9	±1.1i-l	43.7	±4.8bc	38.0	±0.1jk	38.7	±0.6h-j	38.4	±0.4d-f
Tracy	47.7	±0.7dc	40.8	±0.8gh	44.3	±3.5a-c	42.1	±0.9cb	39.7	±0.6e-i	40.9	±1.2b
UNL. hybrid-3	50.0	±0.8ab	40.7	±0.6g-i	45.4	±4.6ab	41.0	±1.0b-e	39.8	±0.7e-i	40.4	±0.6bc
Williams	46.1	±0.6ed	40.3	±1.5g-j	43.2	±2.9cd	39.4	±0.6f-j	38.8	±0.4h-j	39.1	±0.3c-f
No91	45.7	±1.1e	40.1	±0.3h-k	42.9	±2.8c-e	40.0	±1.2d-h	39.7	±0.6e-i	39.9	±0.1b-d
No5	46.4	±0.1ed	40.9	±0.9g-i	43.7	±2.8bc	40.4	±0.8d-g	39.8	±0.7e-i	40.1	±0.3bc
Gülşeker	48.7	±0.3abc	43.4	±1.4f	46.1	±2.7a	38.8	±0.4h-j	39.2	±0.3f-j	39.0	±0.2c-f
Mean	**45.71**	**±3.9**	**39.52**	**±1.8**	**42.6**	**±3.1A**	**40.79**	**±2.7**	**38.87**	**±1.1**	**39.8**	**±1.0B**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.45. Average of shoot nitrogen content % in the sweet sorghum genotypes that grown in (+M= mycorrhizae and –M= non-mycorrhiza) in Adana soil and Şanlıurfa soils.

Genotype	Shoot Nitrogen (%)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	2.60	±0.2c-f	2.00	±0.1h-l	2.30	±0.30a-c	2.40	±0.1ba	2.23	±0.1c-e	2.32	±0.09ab
Grassi	2.30	±0.1e-k	2.00	±0.5h-l	2.15	±0.15bc	2.36	±0.0a-c	2.16	±0.1d-f	2.26	±0.10a-c
M81-E	2.20	±0.2f-l	2.10	±0.3g-l	2.15	±0.05c	2.10	±0.1e-g	2.00	±0.1gh	2.05	±0.05cd
Neb. sugarcane	2.10	±0.1f-l	2.10	±0.1f-l	2.10	±0.00c	2.23	±0.1c-e	2.10	±0.1e-g	2.17	±0.06b-d
PI 575753	2.50	±0.3p-i	2.20	±0.5f-l	2.35	±0.15a-c	2.06	±0.1gf	2.00	±0.1gh	2.03	±0.03cd
Ramada	**3.90**	±0.7a	2.10	±0.2f-l	3.00	±0.90a	2.26	±0.1b-d	2.06	±0.1gf	2.16	±0.10b-d
Roma	3.50	±0.4ba	2.20	±0.3f-l	2.85	±0.65a-c	2.34	±0.0a-c	2.26	±0.1b-d	2.30	±0.04ab
Smith	3.50	±0.7ba	2.00	±0.1lk	2.75	±0.75a-c	2.10	±0.1e-g	1.83	±0.1i	1.97	±0.14de
Theis	3.70	±0.4a	2.10	±0.4g-l	2.90	±0.80ab	2.10	±0.1e-g	2.13	±0.1d-g	2.12	±0.01b-d
Topper 76	3.00	±0.4b-d	2.40	±0.4f-l	2.70	±0.30a-c	2.13	±0.0d-g	**2.43**	±0.1a	2.28	±0.15ab
Tracy	2.60	±0.6d-h	2.00	±0.4i-l	2.30	±0.30a-c	1.86	±0.0ih	2.03	±0.2f	1.95	±0.08de
UNL. hybrid-3	2.70	±0.2c-e	**1.80**	±1.8l	2.25	±0.45a-c	**2.43**	±0.0a	2.40	±0.1ba	2.42	±0.02a
Williams	2.50	±0.1d-j	1.80	±0.1lk	2.15	±0.35c	1.83	±0.0i	1.80	±0.1i	1.82	±0.02e
No91	2.50	±0.2e-k	2.10	±0.4e-l	2.30	±0.20a-c	2.16	±0.2d-f	2.13	±0.2d-g	2.15	±0.02b-d
No5	2.60	±0.1c-g	2.00	±0.2j-l	2.30	±0.30a-c	2.33	±0.2a-c	**1.73**	±0.1i	2.03	±0.30cd
Gülşeker	3.10	±0.4bc	2.30	±0.2e-l	2.70	±0.40a-c	1.80	±0.1i	2.10	±0.1e-g	1.95	±0.15de
Mean	**2.83**	**±0.6**	**2.08**	**±0.2**	**2.45**	**±0.38A**	**2.16**	**±0.2**	**2.08**	**±0.2**	**2.12**	**±0.04B**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.46. Average of root Organic Carbon % in the sweet sorghum genotypes that grown in (+M= mycorrhizae and –M= non-mycorrhiza) in Adana soil and Şanlıurfa soils.

Genotype	Root Carbon (%)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	42.2	±1.7bc	**31.3**	±0.6n	36.8	±5.5d-h	40.0	±1.0b-d	34.2	±1.3l-n	37.1	±2.9a-d
Grassi	43.0	±2.1b	44.0	±1.0ba	43.5	±0.5a	41.0	±1.1b	34.0	±1.6m-o	37.5	±3.5a-c
M81-E	42.9	±0.1b	39.0	±1.0e-g	41.0	±2.0bc	40.2	±0.7b-d	32.5	±0.5op	36.4	±3.9b-e
Neb. sugarcane	39.9	±2.0de	31.7	±1.4n	35.8	±4.1e-h	40.7	±2.1cb	32.2	±1.7op	36.5	±4.3b-e
PI 575753	45.0	±1.0a	37.8	±0.7gh	41.4	±3.6ab	**43.9**	±1.7a	34.5	±0.6k-n	39.2	±4.7a
Ramada	37.5	±1.3gh	32.4	±0.5mn	35.0	±2.6gh	37.7	±1.5e-h	34.0	±1.0m-o	35.9	±1.9c-e
Roma	**45.3**	±0.6a	39.0	±1.0e-g	42.2	±3.2ab	43.3	±1.5a	**30.7**	±0.6p	37.0	±6.3a-d
Smith	36.6	±0.7h-k	38.2	±1.3f-h	37.4	±0.8d-f	37.7	±0.6e-h	35.9	±0.8h-l	36.8	±0.9b-d
Theis	39.6	±0.5d-f	35.1	±0.5j-l	37.4	±2.3d-g	36.2	±0.7h-k	39.5	±1.6b-e	37.9	±1.7a-c
Topper 76	40.8	±0.8dc	35.1	±1.2kl	38.0	±2.9de	35.0	±1.0k-n	33.3	±0.6on	34.2	±0.9e
Tracy	45.0	±1.1a	40.6	±0.3de	42.8	±2.2ab	34.3	±0.6l-n	35.3	±0.9j-m	34.8	±0.5de
UNL. hybrid-3	32.4	±1.6mn	37.3	±1.5g-i	34.9	±2.5h	37.3	±0.6f-i	39.3	±0.7b-e	38.3	±1.0ab
Williams	35.0	±1.0kl	33.9	±1.6ml	34.5	±0.6h	39.3	±1.1b-e	34.8	±0.3k-n	37.1	±2.3a-d
No91	40.3	±1.5de	37.3	±0.1h-j	38.8	±1.5cd	37.5	±0.5e-h	35.5	±0.8i-m	36.5	±1.0b-e
No5	35.4	±0.5j-l	38.0	±0.9f-h	36.7	±1.3d-h	35.8	±0.8i-m	39.1	±0.9c-f	37.5	±1.7a-c
Gülşeker	35.6	±0.6i-l	34.9	±0.9kl	35.3	±0.4f-h	37.0	±1.0g-j	38.5	±1.0d-g	37.8	±0.8a-c
Mean	**38.2**	**±4.01**	**36.6**	**±3.40**	**38.2**	**±0.8A**	**38.56**	**±2.80**	**35.2**	**±2.67**	**36.9**	**±1.7B**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.47. Average of root nitrogen concentration % in the sweet sorghum genotypes that grown in (+M= mycorrhizae and –M= non-mycorrhiza) in Sanliurfa soil.

Genotype	Root Nitrogen (%)											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	**1.76**	±0.2a	1.20	±0.1d-i	1.48	±0.28a-c	1.30	±0.1b-g	0.92	±0.2j	1.11	±0.19b
Grassi	1.61	±0.3a-c	1.38	±0.5b-g	1.50	±0.12ab	1.14	±0.1e-j	1.13	±0.1e-j	1.14	±0.01ab
M81-E	1.34	±0.1b-g	1.34	±0.4b-g	1.34	±0.00a-d	1.14	±0.1d-j	1.13	±0.2e-j	1.14	±0.01ab
Neb. sugarcane	1.22	±0.1d-i	1.28	±0.1b-h	1.25	±0.03a-d	1.46	±0.1ba	1.10	±0.1f-j	1.28	±0.18ab
PI 575753	1.68	±0.1ba	1.06	±0.1g-i	1.37	±0.31a-d	1.23	±0.1b-h	1.07	±0.2g-j	1.15	±0.08ab
Ramada	1.30	±0.3b-h	1.03	±0.2g-i	1.17	±0.14a-d	1.19	±0.1c-h	0.96	±0.2ij	1.08	±0.12b
Roma	1.50	±0.1a-e	1.52	±0.3a-d	1.51	±0.01a	1.23	±0.2b-h	**0.91**	±0.2j	1.07	±0.16b
Smith	1.33	±0.2b-g	1.24	±0.0d-i	1.29	±0.05a-d	1.33	±0.3b-f	1.02	±0.0h-j	1.18	±0.16ab
Theis	0.95	±0.5ih	1.11	±0.3f-i	1.03	±0.08d	**1.62**	±0.1a	1.26	±0.1b-g	1.44	±0.18a
Topper 76	1.04	±0.2g-i	1.20	±0.1d-i	1.12	±0.08a-d	1.28	±0.0b-g	1.12	±0.1e-j	1.20	±0.08ab
Tracy	1.44	±0.4a-f	1.26	±0.2c-i	1.35	±0.09a-d	1.18	±0.1c-h	1.30	±0.0b-g	1.24	±0.06ab
UNL. hybrid-3	1.07	±0.2g-i	1.06	±0.2g-i	1.07	±0.01b-d	1.07	±0.1g-j	1.34	±0.2b-e	1.21	±0.14ab
Williams	1.16	±0.3e-i	**0.94**	±0.1i	1.05	±0.11cd	1.38	±0.0b-d	1.21	±0.2c-h	1.30	±0.09ab
No91	1.24	±0.2d-i	1.25	±0.0d-i	1.25	±0.01a-d	1.16	±0.2c-h	1.35	±0.2b-e	1.26	±0.10ab
No5	1.11	±0.2f-i	1.19	±0.1e-i	1.15	±0.04a-d	1.22	±0.1c-h	1.39	±0.2a-c	1.31	±0.09ab
Gülşeker	1.26	±0.2c-i	1.29	±0.1b-h	1.28	±0.02a-d	1.17	±0.1c-h	1.20	±0.0c-h	1.19	±0.02ab
Mean	**1.25**	**±0.23**	**1.21**	**±0.15**	**1.23**	**±0.02A**	**1.26**	**±0.14**	**1.15**	**±0.15**	**1.21**	**±0.06B**
P≤0.05	**0.0013**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

4.2.7. Plant Biomass Nitrogen Uptake

In this research, the total N uptake in both soils Adana and Şanlıurfa was calculated by multiplying DSW and DRW with N% concentration and the data are presented in Table 4.45 and 4.47. In general, the total N uptake by the sweet sorghum genotypes was higher in Adana soils than in the Şanlıurfa soils. Sweet sorghum total N uptake was significantly ($p<0.001$) higher in mycorrhizae inoculated application / amendment than in non-mycorrhizae inoculated application. Sweet sorghum N uptake was also significant in mycorrhizae × genotype interaction (Table 4.48). In Adana soil, total N uptake by sixteen sweet sorghum genotypes varies from 1.32 to 2.31 g pot^{-1} and from 1.41 to 2 (g pot^{-1}) for mycorrhizae and non-mycorrhizae treatments respectively (Table 4.51). In Şanlıurfa soil, total N uptake by sixteen sweet sorghum genotypes varies 0.96 to 1.39 Mg ha^{-1} and 0.86 to 1.46 g pot^{-1} for mycorrhizae and non-mycorrhizae inoculation respectively (Table 4.51).

In the present work indigenous mycorrhizae helped to N uptake of sixteen sweet sorghum genotypes. Shoot N content of sixteen sweet sorghum genotypes was significantly ($P \leq 0.05$) higher in mycorrhizae inoculated pots than in non-mycorrhizae inoculated pots (Table 4.49). Similarly, total N uptake by the sweet sorghum genotypes was significantly ($p< 0.05$) higher in mycorrhizae inoculated pot than non-mycorrhizae inoculated pot (Table 4.48). However, total N uptake was higher in non-mycorrhizae inoculated bulk soil than mycorrhizae inoculated bulk soil (Tables 4.51). This could be due to the reason that indigenous mycorrhizae help to uptake N by the sweet sorghum genotypes that result the less availability of bulk soil N in the mycorrhizae inoculated pot. In generally, for both soils, mycorrhiza inoculated genotypes N uptake data of shoot, root and total biomass are higher than in non-inoculated genotypes (Tables 4.49, 4.50 and 4.51).

The findings demonstrated that local mycorrhizae stimulate N uptake by sixteen sweet sorghum genotypes. It appears that the mycorrhizal hyphae help to uptake N from the soil which is not normally available to non-mycorrhizal sweet sorghum genotypes. It might just be the result of the changed temporal or spatial pattern of N uptake from the soil. Some of the N absorbed from the soil by the mycorrhizal roots was derived from N sources other than the mineral N (Ibijbijen et al. 1996). The study findings display further evidence that AMF are directly involved in the transfer of mineralized inorganic N to the sweet sorghum genotypes. Other studies also found that arbuscular mycorrhizas can increase plant N uptake from soils (Smith and Smith 2011). Thus, there was no doubt that mycorrhizal hyphae can translocate N from soil to sweet sorghum plants. Also, the results are very important for nitrogen use efficiency which is very important for environmental protection. At present time nitrogen is one of the serious sources polluted ground water. It is very important for nitrogen use efficiency. In this reason, it better to have efficient genotypes can use soil nitrogen efficiently.

Table 4.48. Level of significance for the main and interactive effect on Shoot N uptake. Root N uptake and Total N uptake of sixteen sweet sorghum genotypes that grown in (+M= Mycorrhizae and –M= Non-Mycorrhiza) in Adana and Sanliurfa Soils.

Sources of variations	**Root N uptake**	**Shoot N uptake**	**Total N uptake**
Genotypes	***	***	***
Soil	***	***	***
Genotypes X Soil	***	***	***
Mycorrhizae	***	***	***
Genotypes X Mycorrhizae	***	***	***
Soil X Mycorrhizae	***	***	***
Genotypes X Soil X Mycorrhizae	***	***	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.49. Average of shoot nitrogen uptake by the sweet sorghum genotypes that grown that grown in (+M and –M) in Adana and Şanlıurfa soils.

Genotype	Shoot Nitrogen uptake (g pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	1.64	±0.2c-e	1.05	±0.1j-l	1.35	±0.30a-d	1.33	±0.04f-i	1.03	±0.03l-n	1.18	±0.15e
Grassi	1.40	±0.0e-i	0.98	±0.2kl	1.19	±0.21cd	1.63	±0.04b	1.10	±0.04j-l	1.37	±0.27a-d
M81-E	1.27	±0.2g-k	1.09	±0.1i-l	1.18	±0.09cd	1.43	±0.02d-g	0.90	±0.06no	1.17	±0.27e
Neb. sugarcane	1.22	±0.1g-l	1.07	±0.1j-l	1.15	±0.08d	1.46	±0.03c-f	0.97	±0.04l-n	1.22	±0.25c-e
PI 575753	1.52	±0.2d-g	1.11	±0.2i-l	1.32	±0.21a-d	**1.87**	±0.19a	0.97	±0.02l-n	1.42	±0.45ab
Ramada	**2.22**	±0.4a	1.04	±0.1j-l	1.63	±0.59a	1.47	±0.06c-f	**0.78**	±0.00o	1.13	±0.35e
Roma	1.96	±0.2ba	1.02	±0.1j-l	1.49	±0.47a-d	1.59	±0.03cb	0.95	±0.03m-o	1.27	±0.32a-e
Smith	2.04	±0.4ba	0.99	±0.1kl	1.52	±0.53a-d	1.27	±0.07g-i	0.97	±0.09l-n	1.12	±0.15e
Theis	2.08	±0.2ba	1.01	±0.2j-l	1.55	±0.54a-c	1.31	±0.05g-i	1.10	±0.02j-l	1.21	±0.11c-e
Topper 76	1.80	±0.3b-d	1.16	±0.2h-l	1.48	±0.32a-d	1.39	±0.08d-g	1.37	±0.03e-h	1.38	±0.01a-c
Tracy	1.59	±0.4c-f	0.97	±0.2kl	1.28	±0.31a-d	1.27	±0.07g-i	1.07	±0.13k-m	1.17	±0.10e
UNL. hybrid-3	1.65	±0.1c-e	**0.89**	±0.2l	1.27	±0.38a-d	1.52	±0.02b-e	1.35	±0.05e-h	1.44	±0.09a
Williams	1.50	±0.1d-g	0.92	±0.0l	1.21	±0.29b-d	1.35	±0.02e-h	1.06	±0.09k-m	1.21	±0.15de
No91	1.45	±0.2e-h	1.10	±0.2i-l	1.28	±0.18a-d	1.38	±0.12d-g	1.20	±0.11i-k	1.29	±0.09a-e
No5	1.61	±0.1c-f	1.05	±0.1j-l	1.33	±0.28a-d	1.54	±0.19b-d	0.97	±0.06l-n	1.26	±0.29b-e
Gülşeker	1.90	±0.2bc	1.29	±0.1f-j	1.60	±0.31ab	1.55	±0.11cb	1.22	±0.07h-j	1.39	±0.17a-c
Mean	**1.68**	**±0.295**	**1.05**	**±0.096**	**1.36**	**±0.32A**	**1.46**	**±0.16**	**1.06**	**±0.05**	**1.26**	**±0.20B**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.50. Average of root nitrogen uptake by the sweet sorghum genotypes that grown that grown in (+M and –M) in Adana Şanlıurfa soils.

Genotype	Root Nitrogen uptake (g pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	**0.180**	±0.03a	0.077	±0.01e-h	0.129	±0.052a	0.140	±0.02a-d	0.080	±0.01lm	0.110	±0.030ab
Grassi	0.130	±0.01b	0.085	±0.03d-g	0.108	±0.023ab	0.110	±0.01e-j	0.090	±0.01i-l	0.100	±0.010ab
M81-E	0.101	±0.00c-e	0.082	±0.02d-g	0.092	±0.010bc	0.120	±0.01d-h	0.090	±0.02j-m	0.105	±0.015ab
Neb. sugarcane	0.096	±0.00c-e	0.100	±0.00cd	0.098	±0.002a-c	0.150	±0.02ba	0.090	±0.01i-l	0.120	±0.030ab
PI 575753	0.109	±0.01cb	**0.058**	±0.00h	0.084	±0.026b-d	0.130	±0.01b-f	0.080	±0.01k-m	0.105	±0.025ab
Ramada	0.091	±0.02c-f	**0.059**	±0.01h	0.075	±0.016cd	0.130	±0.02c-g	0.080	±0.02lm	0.105	±0.025ab
Roma	0.098	±0.01c-e	0.090	±0.01c-f	0.094	±0.004bc	0.120	±0.02d-h	**0.060**	±0.01m	0.090	±0.030b
Smith	0.075	±0.01d-h	0.069	±0.00f-h	0.072	±0.003cd	0.140	±0.04b-d	0.080	±0.01lm	0.110	±0.030ab
Theis	0.055	±0.03h	**0.056**	±0.02h	0.056	±0.001d	**0.170**	±0.02a	0.100	±0.00h-l	0.135	±0.035a
Topper 76	0.090	±0.02c-g	0.078	±0.01e-h	0.084	±0.006b-d	0.150	±0.00a-c	0.090	±0.01h-l	0.120	±0.030ab
Tracy	0.098	±0.03c-e	0.090	±0.01c-g	0.094	±0.004bc	0.130	±0.01b-e	0.100	±0.01g-k	0.115	±0.015ab
UNL. hybrid-3	0.083	±0.01d-g	0.073	±0.01f-h	0.078	±0.005b-d	0.130	±0.01c-g	0.100	±0.02g-k	0.115	±0.015ab
Williams	0.080	±0.02d-h	**0.061**	±0.01gh	0.071	±0.009cd	0.130	±0.00b-f	0.090	±0.03i-l	0.110	±0.020ab
No91	0.095	±0.01c-e	0.080	±0.00d-h	0.088	±0.008b-d	0.110	±0.02e-i	0.100	±0.02g-k	0.105	±0.005ab
No5	0.075	±0.01e-h	0.077	±0.01e-h	0.076	±0.001b-d	0.130	±0.01b-e	0.110	±0.02f-k	0.120	±0.010ab
Gülşeker	0.090	±0.01c-g	0.098	±0.01c-e	0.094	±0.004bc	0.120	±0.01d-h	0.090	±0.00i-l	0.105	±0.015ab
Mean	**0.1**	**±0.027**	**0.08**	**±0.014**	**0.087**	**±0.010B**	**0.13**	**±0.00**	**0.09**	**±0.02**	**0.111**	**±0.020A**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.51. Average of total nitrogen uptake by the sweet sorghum genotypes that grown that grown in (+M and –M) in Adana Şanlıurfa soils.

Genotype	Total Nitrogen uptake (g pot^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	1.82	±0.1c-f	1.13	±0.1j-l	1.48	±0.35a-c	1.48	±0.03f-i	1.10	±0.04l-o	1.29	±0.19ef
Grassi	1.53	±0.0f-i	1.07	±0.2kl	1.30	±0.23a-c	1.74	±0.05b	1.19	±0.05k-m	1.47	±0.28a-e
M81-E	1.37	±0.2h-k	1.17	±0.1j-l	1.27	±0.10c	1.55	±0.02d-g	0.99	±0.04o	1.27	±0.28f
Neb. sugarcane	1.32	±0.1h-k	1.17	±0.1j-l	1.25	±0.08c	1.62	±0.02b-e	1.06	±0.05l-o	1.34	±0.28c-f
PI 575753	1.62	±0.2e-h	1.17	±0.2j-l	1.40	±0.23a-c	**2.00**	±0.20a	1.05	±0.03no	1.53	±0.48ab
Ramada	**2.31**	±0.4a	1.10	±0.1j-l	1.71	±0.61a	1.60	±0.05c-f	**0.86**	±0.02p	1.23	±0.37f
Roma	2.06	±0.2a-c	1.11	±0.1j-l	1.59	±0.48a-c	1.71	±0.02cb	1.01	±0.04o	1.36	±0.35b-f
Smith	2.12	±0.4a-c	1.06	±0.1lk	1.59	±0.53a-c	1.41	±0.10ji	1.04	±0.08no	1.23	±0.18f
Theis	2.13	±0.2ba	1.07	±0.2lk	1.60	±0.53a-c	1.48	±0.07e-i	1.20	±0.02kl	1.34	±0.14c-f
Topper 76	1.89	±0.3b-e	1.24	±0.2i-l	1.57	±0.33a-c	1.54	±0.08d-h	1.46	±0.03g-i	1.50	±0.04a-c
Tracy	1.68	±0.4d-g	1.05	±0.2lk	1.37	±0.32a-c	1.41	±0.08h-j	1.17	±0.12l-n	1.29	±0.12ef
UNL. hybrid-3	1.74	±0.1d-f	**0.96**	±0.2l	1.35	±0.39a-c	1.65	±0.02bd	1.45	±0.03g-i	1.55	±0.10a
Williams	1.58	±0.1e-h	0.98	±0.0l	1.28	±0.30bc	1.48	±0.01f-i	1.15	±0.09l-n	1.32	±0.17d-f
No91	1.55	±0.1f-i	1.18	±0.2j-l	1.37	±0.19a-c	1.49	±0.14e-i	1.30	±0.10kj	1.40	±0.10a-f
No5	1.69	±0.1d-g	1.13	±0.1j-l	1.41	±0.28a-c	1.67	±0.19b-d	1.08	±0.05m-o	1.38	±0.30a-f
Gülşeker	1.98	±0.2b-d	1.39	±0.1g-j	1.69	±0.29ab	1.67	±0.11b-d	1.31	±0.07kj	1.49	±0.18a-d
Mean	**1.77**	**±0.286**	**1.12**	**±0.102**	**1.45**	**±0.33A**	**1.59**	**±0.16**	**1.15**	**±0.07**	**1.37**	**±0.22B**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

4.2.8. Plant Biomass Carbon Fixation (Uptake)

Shoot C input also varied significantly ($p<0.05$) among genotypes as well as genotype × mycorrhizae interaction (Table 4.52). Plant tissue carbon fixation was calculated by multiplying C % with biomass weight. Shoot C input of the sweet sorghum genotypes were significantly ($p<0.001$) higher in mycorrhizae amendment soil than non-mycorrhizae amendment soil. The shoot C input varies from 13.99 to 19.04 Mg ha^{-1} and 10.60 to 15.50 Mg ha^{-1} in Adana soil Table 4.53 and from 15.50 to 23.4 Mg ha^{-1} and 10.20 to 14.30 Mg ha^{-1} in Sanliurfa soils Table 4.53 for mycorrhizae and non-mycorrhizae amendment respectively.

The study observed that the C input in soil by root biomass was higher in most of sweet sorghum genotypes on mycorrhizae inoculated soil than non-mycorrhizae inoculated soil (Tables 4.32). In Adana soils, root C input in soil of the sweet sorghum genotypes varies 1.30 to 2.72 Mg ha^{-1} and 1.12 to 1.71 Mg ha^{-1} for mycorrhizae and non-mycorrhizae treatments, respectively (Table 4.54). Likewise, in Sanliurfa soils root C input in soil of the sweet sorghum genotypes varies 2.30 to 2.90 Mg ha^{-1} and 1.40 to 1.98 Mg ha^{-1} for mycorrhizae and non-mycorrhizae treatments, respectively (Table 4.54).

4.2.9. Total Biomass Fixed Carbon Amount

Total carbon fixation (uptake) was determined and it has been found that in Adana soil mycorrhizae inoculated genotypes produce the highest C uptake (Tables 4.55). In Şanlıurfa soil, the highest C uptake was determined in PI 575753 genotype as found highest fixed CO_2 96.5 Mg ha^{-1} (Tables 4.56).

Table 4.52. Level of significance for the main and interactive effect on root C input. shoot C input and plant CO_2 of sixteen sweet sorghum genotypes that grown in (+M= Mycorrhizaeand –M= Non-Mycorrhiza) in Adana and Sanliurfa Soils.

Sources of variations	**Root C uptake**	**Shoot C uptake**	**Plant fixed CO_2**
Genotypes	***	***	***
Soil	***	***	***
Genotypes X Soil	***	***	***
Mycorrhizae	***	***	***
Genotypes X Mycorrhizae	***	***	***
Soil X Mycorrhizae	***	***	***
Geno types X Soil X Mycorrhizae	***	***	***

Where n.s. ** and ***represents probability of < 0.05. ≤ 0.01 and ≤ 0.001 respectively.

Table 4.53. Average of shoot carbon uptake by the sweet sorghum genotypes that grown in (+M=mycorrhizae and –M= non-mycorrhiza) in Adana and Şanlıurfa Soils

Genotype	Shoot Carbon uptake (Mg ha^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	17.1	±2.06d	12.6	±1.06i-k	14.83	±2.2d-f	17.5	±0.64d-f	11.3	±1.17n	14.4	±3.1c-f
Grassi	15.0	±0.71fg	12.7	±0.38ji	13.85	±1.2gh	17.6	±0.89ed	12.8	±1.75m	15.2	±2.4b-d
M81-E	14.0	±0.80h	12.5	±0.28i-k	13.25	±0.7h	16.4	±0.68hg	10.5	±1.54o	13.45	±3.0f
Neb. sugarcane	14.3	±1.96hg	12.7	±0.70i-k	13.51	±0.8h	17.0	±5.67e-g	11.5	±0.38n	14.25	±2.8d-f
PI 575753	15.8	±2.02e	12.1	±0.42j-l	13.94	±1.8f-h	**23.4**	±6.40a	11.7	±2.55n	17.55	±5.9a
Ramada	18.2	±1.42dc	11.5	±0.28l	14.83	±3.3d-f	16.3	±0.78g-i	**8.6**	±2.09p	12.45	±3.9g
Roma	16.8	±1.56d	**10.6**	±1.84m	13.68	±3.1gh	17.2	±1.66d-f	10.2	±3.07o	13.7	±3.5ef
Smith	18.3	±1.24b	12.3	±0.80jk	15.30	±3.0b-e	16.3	±0.94g-i	12.6	±1.07m	14.45	±1.9c-f
Theis	17.0	±1.10d	12.0	±0.94lk	14.51	±2.5e-g	15.7	±0.98ji	12.7	±1.06m	14.2	±1.5d-f
Topper 76	18.1	±0.57bc	12.1	±0.24j-l	15.08	±3.0c-e	15.5	±2.08j	13.7	±0.83lk	14.6	±0.9b-e
Tracy	18.4	±1.72ba	12.6	±0.77i-k	15.49	±2.9b-d	17.9	±1.90d	13.1	±0.28lm	15.5	±2.4b
UNL. hybrid-3	**19.0**	±1.13a	12.7	±0.98i-k	15.87	±3.2bc	16.3	±2.65g-i	14.1	±0.56k	15.2	±1.1b-d
Williams	17.5	±1.12dc	13.0	±0.39i	15.24	±2.2b-e	19.0	±1.93c	14.4	±0.68k	16.7	±2.3a
No91	17.0	±1.15d	13.1	±0.51i	15.04	±1.9c-e	16.1	±1.20h-j	14.1	±0.75k	15.1	±1.0b-d
No5	18.2	±0.41b	13.8	±0.76h	16.01	±2.2b	16.8	±3.83f-h	13.8	±0.51lk	15.3	±1.5cb
Gülşeker	18.6	±5.72ba	15.5	±1.09fe	17.06	±1.6a	21.0	±9.20b	14.3	±0.23k	17.65	±3.4a
Mean	**17.07**	**±1.55**	**12.61**	**±1.05**	**14.84**	**±2.2B**	**17.5**	**±2.08**	**12.46**	**±1.69**	**14.98**	**±2.5A**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at *P*≤0.05 based on the TUKEY test.

Table 4.54. Average of root carbon uptake by the sweet sorghum genotypes that grown in (+M=mycorrhizae and –M= non-mycorrhiza) in Adana and Şanlıurfa soils.

Genotype	Root Carbon uptake (Mg ha^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	**2.72**	±0.68a	1.27	±0.37qp	2.00	±0.73a	2.70	±0.45a-c	1.80	±0.22g-i	2.25	±0.45a-c
Grassi	2.21	±0.23b	1.71	±0.22hi	1.96	±0.25ab	2.50	±0.05c-f	1.80	±0.14g-i	2.15	±0.35a-d
M81-E	2.02	±0.22cd	1.51	±0.15k-n	1.77	±0.25c-e	2.70	±0.10b-d	1.50	±0.15jk	2.10	±0.60a-d
Neb. sugarcane	1.98	±0.25ed	1.56	±0.25i-l	1.77	±0.21c-e	2.70	±0.12b-d	1.70	±0.12g-j	2.20	±0.50a-d
PI 575753	1.85	±0.19gf	1.31	±0.10op	1.58	±0.27f-i	**2.90**	±0.45a	1.70	±0.24g-j	2.30	±0.60ab
Ramada	1.67	±0.17h-j	**1.17**	±0.21q	1.42	±0.25ij	2.50	±0.13d-f	1.70	±0.12h-j	2.10	±0.40a-d
Roma	1.88	±0.49e-g	1.44	±0.12m-o	1.66	±0.22d-g	2.70	±0.31b-e	**1.40**	±0.11k	2.05	±0.65cd
Smith	1.32	±0.15op	1.35	±0.19op	1.34	±0.02j	2.40	±0.25fe	1.70	±0.07h-j	2.05	±0.35b-d
Theis	1.44	±0.59l-o	1.12	±0.32q	1.28	±0.16j	2.40	±0.22f	1.96	±0.31g	2.18	±0.22a-d
Topper 76	2.14	±0.34cb	1.46	±0.39l-o	1.80	±0.34b-d	2.60	±0.06c-f	1.80	±0.23g-i	2.20	±0.40a-d
Tracy	1.93	±0.28d-f	1.79	±0.13hg	1.86	±0.07a-c	2.50	±0.45fe	1.82	±0.27g-i	2.16	±0.34a-d
UNL. hybrid-3	1.60	±0.17i-k	1.62	±0.22i-k	1.61	±0.01e-h	2.80	±0.38ba	1.98	±0.22g	2.39	±0.41a
Williams	1.52	±0.45k-n	1.38	±0.10n-p	1.45	±0.07h-j	2.30	±0.08f	1.70	±0.16ji	2.00	±0.30d
No91	1.96	±0.40d-f	1.51	±0.03k-n	1.74	±0.23c-f	2.30	±0.12f	1.71	±0.32g-j	2.01	±0.29cd
No5	1.51	±0.06k-n	1.56	±0.03i-l	1.54	±0.03g-i	2.40	±0.03f	1.91	±0.05hg	2.16	±0.25a-d
Gülşeker	1.53	±0.24j-m	1.68	±0.93hi	1.61	±0.08e-h	2.50	±0.69fe	1.90	±0.10hg	2.20	±0.30a-d
Mean	**1.83**	**±0.355**	**1.47**	**±0.191**	**1.65**	**±0.18B**	**2.56**	**±0.18**	**1.74**	**±0.15**	**2.16**	**±0.41A**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.55. Average of total carbon uptake by the sweet sorghum genotypes that grown in (+M=mycorrhizae and –M= non-mycorrhiza) in Adana and Şanlıurfa soils.

Genotype	Total Carbon uptake (Mg ha^{-1})											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	19.8	±2.67b	13.9	±1.11ih	16.9	±2.9b-d	20.3	±0.92ed	13.1	±0.98o	16.7	±3.6c-f
Grassi	17.2	±0.94e	14.4	±0.57h-l	15.8	±1.4e-h	20.1	±0.94ed	14.6	±1.89n	17.35	±2.8c-e
M81-E	16.0	±0.58gf	14.0	±0.21h-k	15.0	±1.0h	19.1	±0.60g-i	12.1	±1.70p	15.6	±3.5g
Neb. sugarcane	16.3	±1.76f	14.2	±0.94lm	15.3	±1.1h	19.6	±5.78e-g	13.3	±0.26o	16.45	±3.1d-g
PI 575753	17.6	±1.87e	13.4	±0.43no	15.5	±2.1gh	**26.3**	±6.84a	13.4	±2.78o	19.85	±6.5a
Ramada	19.8	±1.33b	12.7	±0.08o	16.3	±3.6d-g	18.8	±0.72hj	**10.3**	±1.98q	14.55	±4.3h
Roma	18.6	±1.10d	**12.1**	±1.72j-m	15.4	±3.3gh	19.9	±1.97d-f	11.6	±3.18p	15.75	±4.2fg
Smith	19.6	±1.20bc	13.6	±0.99j-m	16.6	±3.0c-f	18.7	±1.10h-k	14.3	±1.07n	16.5	±2.2d-g
Theis	18.5	±1.68d	13.1	±0.78nm	15.8	±2.7f-h	18.1	±1.00kj	14.6	±0.99n	16.35	±1.8e-g
Topper 76	20.2	±0.62ab	13.5	±0.60k-m	16.9	±3.3b-d	18.0	±2.10k	15.5	±0.96ml	16.75	±1.3c-e
Tracy	20.3	±1.61ba	14.4	±0.63ih	17.4	±3.0bc	20.4	±1.46d	14.8	±0.54mn	17.6	±2.8c
UNL. hybrid-3	**20.6**	±1.26a	14.3	±0.77h-j	17.5	±3.1bc	19.1	±2.29g-i	16.0	±0.61l	17.55	±1.6c
Williams	19.0	±0.90dc	14.4	±0.42ih	16.7	±2.3b-e	21.3	±2.00c	16.0	±0.55l	18.65	±2.7b
No91	18.9	±0.75dc	14.6	±0.54h	16.8	±2.1b-d	18.5	±1.13i-k	15.8	±0.94l	17.15	±1.4c-e
No5	19.7	±0.45b	15.4	±0.79g	17.6	±2.2b	19.2	±3.82f-h	15.7	±0.51l	17.45	±1.8cd
Gülşeker	20.1	±5.95ba	17.2	±2.00e	18.7	±1.5a	23.5	±9.88b	16.2	±0.14l	19.85	±3.7a
Mean	**18.9**	**±1.43**	**14.07**	**±1.16**	**16.5**	**±2.4B**	**20.07**	**±2.14**	**14.2**	**±1.77**	**17.13**	**±2.9A**
P≤0.05	**0.0001**						**0.0001**					

Data were means of three replicates±S.D. NS – not significant at $p < 0.05$ based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

Table 4.56. Average of plant fixed CO_2 by the sweet sorghum genotypes that grown in (+M=mycorrhizae and –M= nNon-mycorrhiza) in Adana and Şanlıurfa Soils.

Genotype	plant fixed CO_2											
	+M		-M		Mean		+M		-M		Mean	
	Adana Soil						Şanlıurfa Soil					
Cowley	72.6	±9.80b	50.9	±4.08h-k	61.8	±10.9b-d	74.3	±3.4ed	48.1	±3.58o	61.2	±13.1c-f
Grassi	63.2	±3.45e	53.0	±2.08h	58.1	±5.1e-h	73.9	±3.5ed	53.5	±6.95n	63.7	±10.2c-e
M81-E	58.7	±2.14gf	51.4	±0.77h-k	55.1	±3.7h	70.3	±2.2g-i	44.3	±6.23p	57.3	±13.0g
Neb. sugarcane	59.8	±6.47f	52.2	±3.44h-j	56.0	±3.8h	72.1	±21.2e-g	48.7	±0.94o	60.4	±11.7d-g
PI 575753	64.7	±6.86e	49.3	±1.56kl	57.0	±7.7gh	**96.5**	±25.1a	49.1	±10.21o	72.8	±23.7a
Ramada	72.8	±4.89b	46.5	±0.30mn	59.7	±13.2d-g	69.0	±2.6h-j	**37.7**	±7.25q	53.4	±15.7h
Roma	68.4	±4.05d	**44.3**	±6.31n	56.4	±12.1gh	73.0	±7.2d-f	42.5	±11.66p	57.8	±15.3fg
Smith	72.0	±4.39bc	49.9	±3.63i-l	61.0	±11.1c-f	68.7	±4.1h-k	52.4	±3.94n	60.6	±8.2d-g
Theis	67.7	±6.17d	48.1	±2.87ml	57.9	±9.8f-h	66.5	±3.7kj	53.7	±3.62n	60.1	±6.4e-g
Topper 76	74.1	±2.28ba	49.6	±2.19j-l	61.9	±12.3b-d	66.2	±7.7k	56.9	±3.51ml	61.6	±4.7c-e
Tracy	74.5	±5.89ba	52.7	±2.33h	63.6	±10.9bc	74.8	±5.4d	54.5	±1.97mn	64.7	±10.2c
UNL. hybrid-3	**75.7**	±4.63a	52.4	±2.83ih	64.1	±11.7bc	70.1	±8.4g-i	58.6	±2.23l	64.4	±5.8c
Williams	69.7	±3.29dc	52.9	±1.55h	61.3	±8.4b-e	78.3	±7.4c	58.7	±2.02l	68.5	±9.8b
No91	69.5	±2.75dc	53.6	±1.98h	61.6	±8.0b-d	67.8	±4.1i-k	57.9	±3.45l	62.9	±5.0c-e
No5	72.4	±1.66b	56.6	±2.89g	64.5	±7.9b	70.6	±14.0f-h	57.5	±1.88l	64.1	±6.6cd
Gülşeker	73.9	±21.85ba	63.1	±7.36e	68.5	±5.4a	86.1	±36.3b	59.5	±0.51l	72.8	±13.3a
Mean	**69.36**	**±5.26**	**51.64**	**±4.25**	**60.5**	**±8.9B**	**73.64**	**±7.85**	**52.1**	**±6.50**	**62.9**	**±10.8A**
P≤0.05			**0.0001**						**0.0001**			

Data were means of three replicates±S.D. NS – not significant at p < 0.05 based on ANOVA. Means followed by the same letter within a column are not significantly differed at $P \leq 0.05$ based on the TUKEY test.

4.2.10. Indigenous Mycorrhiza Fixes Carbon and Mitigated Atmospheric CO_2 by Sweet Sorghum Genotypes

Total fixed CO_2 amount determined by converting total C fixation in to CO_2. Indigenous mycorrhizal inoculated sweet sorghum genotypes had more plant biomass than non-mycorrhizal plants. Likewise, Şanlıurfa soils produce greater shoot and root dry matter than plant grown in Adana soils (Table 4.30 and 4.31). In Şanlıurfa soils, plant biomass fixed CO_2 on the sweet sorghum genotypes varies from 66.2 to 96.5 CO_2 Mg ha^{-1} for mycorrhizae inoculated soil. Whereas, plant biomass CO_2 fixation varies from 37.7 to 59.5 CO_2 Mg ha^{-1} for non-mycorrhiza inoculated soil (Tables 4.56). In Adana soil, plant biomass fixed CO_2 on sixteen sweet sorghum genotypes varies 58.7 to 75.7 and 44.3 to 66.0 CO_2 Mg ha^{-1} for mycorrhiza and non-mycorrhiza treatment, respectively (Tables 4.56).

The results are very promising about fixing more CO_2 from atmosphere to plant tissue through photosynthesis. Since mycorrhizal inoculation increase plant growth and also increase plant tissue % of C concentration it is sound to use mycorrhizae or management the indigenous mycorrhiza to fix more CO_2 form atmosphere (Ortaş et al. 2016).

Mycorrhizae inoculated sweet sorghum captured significantly ($p<0.001$) higher CO2 than non-mycorrhizal plant (Tables 4.44). A study found that sweet sorghum captured 3.2 to 13.8 Mg ha^{-1} C (Holou and Kindomihou 2017). In another study, data showed that the total above ground biomass of mycorrhizal treatment was produced 23.21 kg ha^{-1} C higher than in the non-mycorrhizae treatment produced 21.31 C kg ha^{-1} indicating excessive amount of C approximately 2000 kg ha^{-1} C gets sequestered in the presence of mycorrhizal inoculation. Similarly, another measurements of plant carbon allocation to mycorrhizal fungi have been

estimated to be 5-20% of total plant C uptake (Pearson and Jakobsen 1993).

The study findings proved that sweet sorghum can produce a significant amount of biomass, suggesting that their C capture was highest. Mycorrhizal strategies of C acquisition by sweet sorghum genotypes differentially affect shoot and root C as total carbon C uptake. Most remarkably, the study found that only AMF inoculated sweet sorghum plant reduced soil C pools relative to the non-inoculated plants. The reason could be that photosynthetic effect has occurred due to high temperature of sweet sorghum growing period. A study speculated that plants transfer as much as 4–16% of photo synthetically fixed C to mycorrhizae and rhizobia symbionts in order to maintain an extensive hyphal network and nodule growth (Kaschuk et al. 2009). Other studies found that AMF stimulated plant to mitigate CO_2 for their growth period (Antoninka et al. 2011). Thus, mycorrhizae have the ability to fix C within sweet sorghum plant tissue and mitigate atmospheric CO_2 from the atmosphere.

4.3. General Discussion

In order to analyses the all measured parameters related with sorghum genotypes, the principal component analysis (PCA) were done. At harvest 16 sweet sorghum genotypes were analyzed and 22 plant and soil parameters were measured. In this work, two PC were used and mainly PC1 and PC2 were considered. For each year of locations, Pearson correlation matrix were created, also similarity of genotypes was determined for each location and for year as well. Also, for both field and greenhouse experiment, genotypes effects were shown on dendrogram tree presentation (Figures 4.7, 4.8, 4.10, 4.11, 4.14 and 4.17).

4.3.1. Field Experiment

All parameters shown that plant shoot, root and total dry weigh data are significantly related with plant nitrogen and carbon concentration Also soil N is highly significantly correlated with plant tissue C and N content as well.

Table 4.57 and Table 4.58 show the correlation between the variables and the selected factors which was done on Adana location in years 2016 and 2017, based on their eigenvalue the cumulative variation that is explainable after the rotation was found to be around 80% PC1, PC2, PC3 and PC4 gave 37, 48%, 23.37%, 10.35% and 8.4% variation explanation respectively (Figure 4.6). According to the correlation between the PC's and the factors in PC1 soil nitrogen stock (SN), shoot carbon % (Sh. C), shoot nitrogen % (Sh. N) and total nitrogen uptake (TN up), in the second PC dry shoot weight (DSW), root nitrogen uptake (RN up), root carbon uptake (RC up), in PC3 dry root weight (DRW), total biomass (TB), shoot carbon uptake (Sh. C up), total carbon uptake (TC up) and carbon dioxide (CO_2) in PC4 total root length (TRL), root surface area (RSA) and root volume (RV) had the highest coefficient score that is above 70% (Figure 4.3).

According to the closeness of the observation to the axis of the PCs (G30) No91 genotype in year 2017, (G16) Gülşeker genotype in year 2016, (G28) UNL. hybrid-3 genotype in year 2017, is highly effected by (TN up) total nitrogen uptake, (TC) total carbon uptake, (CO_2) carbon dioxide, (Sh. C up) shoot carbon uptake, (Sh. N up) shoot nitrogen uptake, (TB) total biomass, (RDW) root dry weight and (shoot/root) shoot/root ratio in PC1 while in PC2 (G15) No5 USD genotype in year 2016, (G14) No91 USDA genotype in year 2016, (G12) UNL.hybrid-3 genotype in year 2016 and (G18) Grassi genotype in year 2017 is highly affected by variables close to the axis in PC2 taking a look at the dendrogram diagram for year 2016 (Adana location).

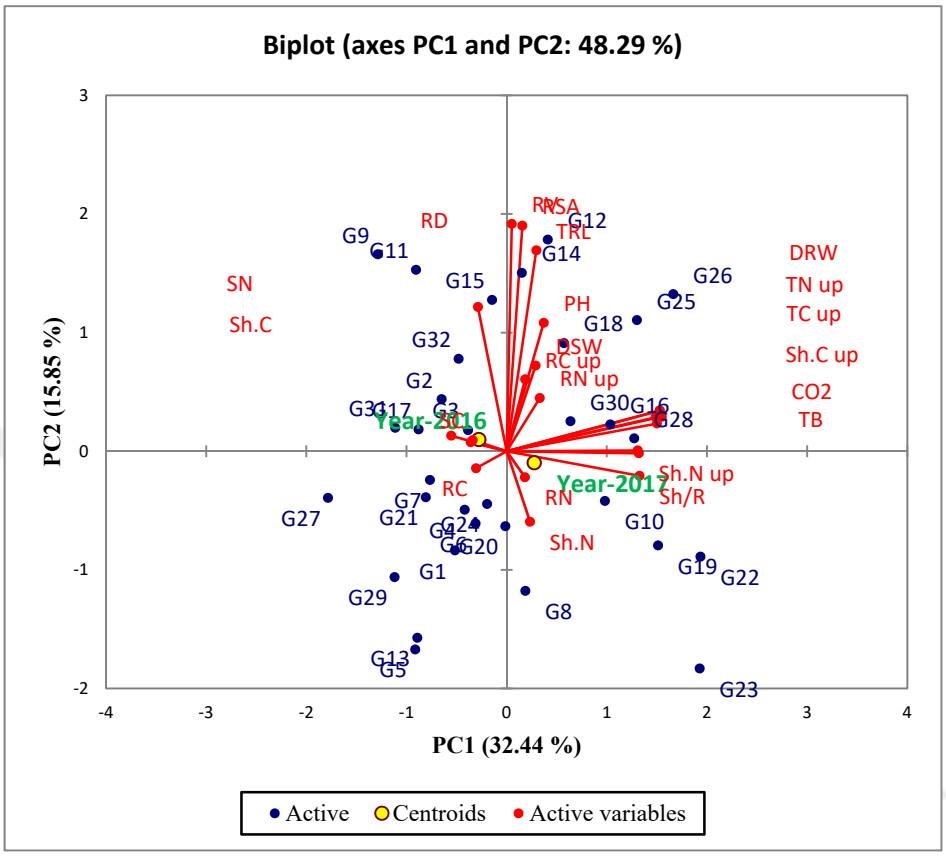

Figure 4.6. Adana location Biplot display the variates, sweet sorghum genotypes numbered from G1 to G16 Year 2016) and from G17 to G32 the year 2017) and the parameters: dry shoot weight (DSW), dry root weight (DRW), total biomass (TB), soil carbon stock (SCS), soil nitrogen stock (SNS), shoot itrogen (Sh.N), shoot carbon (Sh. C), root nitrogen (RN), root carbon (RC), total nitrogen uptake (TN up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA) and root volume (RV).

As can be seen in Figure 4.6. for year 2017, Total biomass, total nitrogen, shoot carbon, total carbon and CO_2 fixation are highly correlated with each other. Since they are representing 32.44 % of variation under PC1 which are very significant parameters.

For the experiment carried out in Adana location in year 2016, four groups were obtained from the hierarchical clustering which can be seen in Figure 4.7 group 1 had Topper 76, UNL hybrid-8, and Gülşeker, group 2 had P1579753, Williams Cowley, Roma, Thesis ad Tracy, group 4 has Grassi, M81-E and Ramada and in Group 4 Neb. Sugarcane, No 5 USDA, Smith and No91 USDA. The genotype that had the least genotypes was P157953 and Williams which is found in group which is less than 2.5 %, the dissimilarity between group 1 and group 2, 3 and 4 is approximately 25%, while between group 2 and group 3 and 4 is above 15% and as for the dissimilarity between group 3 and group 4 the dissimilarity between them is above 10%.

In 2017, the genotypes were classified into three groups, from the left the first group had N091, Grassi, Theis, Topper 76, UNL. hybrid 5 Ramada, and Roma, in group 2 Gülşeker, Nebraska Sugarcane and Smith while group 3 had No5, Cowey, P157955, Tracy and Williams the dissimilarity between group 1 and group 2 and group 3 is above 30% but below 35%, between group 2 and group 3 the percentage dissimilarity between them is above 15% but below 20% (Figure 4.8). Looking at the dendrogram in general the lowest dissimilarity is found between Cowley and P1579753 which is found in group3, in group one the lowest dissimilarity was between Roma and Ramada the dissimilarity in group1 the dissimilarity within the subgroup found within this group was less than 15% and this subgroup are No91 , Grassi, M81-E and Thesis while the other subgroup is Topper 76, UNL hybrids-3, Ramada and Roma, in group two the dissimilarity was found to be between Gülşeker and, Nebraska Sugarcane and Smith , while in group 3 the dissimilarity between the subgroup No5, Cowley and P127953 and Tracy and Williams was approximately 10% (Figure 4.8).

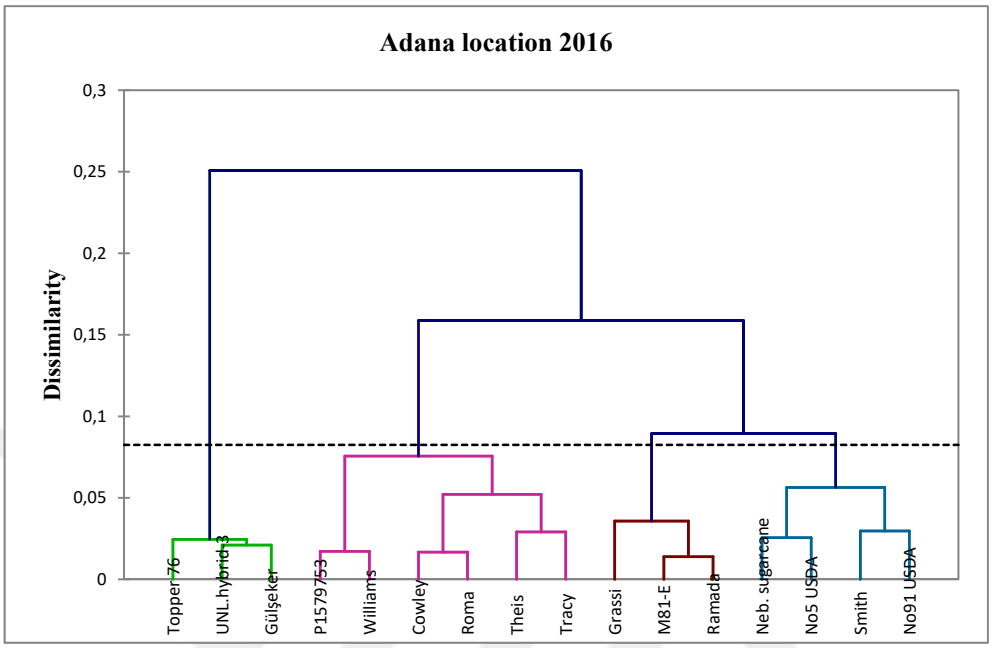

Figure 4.7. Dendrogram of the 16 sweet sorghum genotypes based on 22 parameters: Plant hieght (PH), dry shoot weight (DSW), dry root weight (DRW), total biomass (TB), shoot/root ratio (Sh/R), soil carbon stock (SCS), Soil nitrogen stock (SNS), shoot itrogen (Sh. N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total nitrogen uptake (TN up), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA) and rRoot volume (RV).

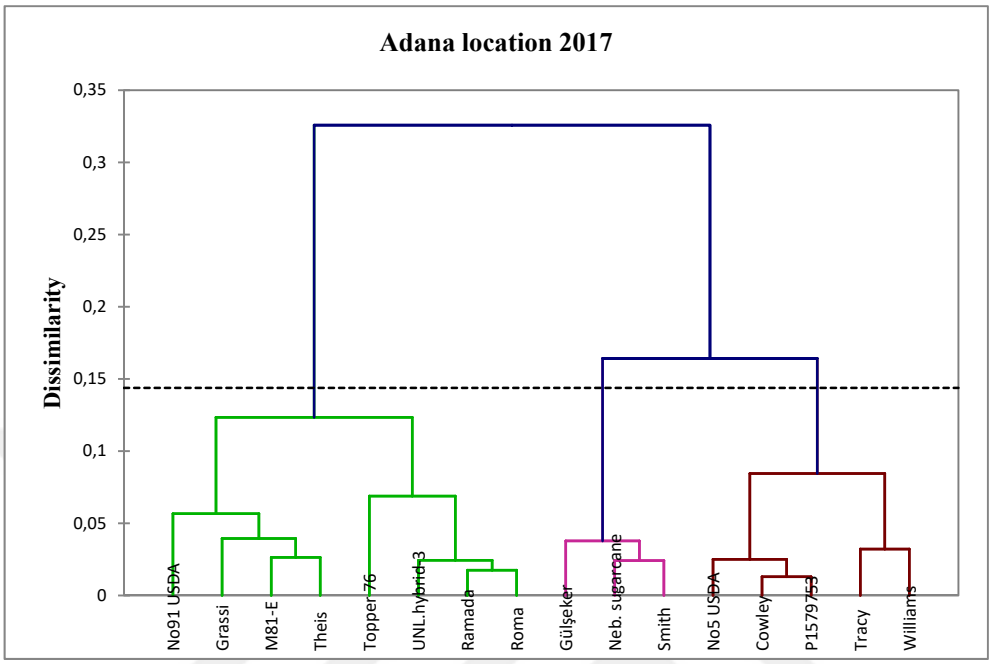

Figure 4.8. Dendrogram of the 16 sweet sorghum genotypes based on 22 parameters: Plant hieght (PH), dry shoot weight (DSW), dry root weight (DRW), total biomass (TB), shoot/root ratio (Sh/R), soil carbon stock (SCS), soil nitrogen stock (SNS), shoot nitrogen (Sh. N), shoot carbon (Sh. C), root nitrogen (RN), root carbon (RC), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total nitrogen uptake (TN up), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA) and root volume (RV).

Table 4.57. Correlation matrix (Pearson): Adana location in year 2016

Variables	PH	DRW	DSW	T.B	Shoot/roo	SC	SN	Sh.C	RC	RN	Sh. N	R N up	Sh.N uo	TN up	RC up	Sh. C up	TC up	CO2	RD	TRL	RSA	RV
PH	**1**																					
DRW	0.311	**1**																				
DSW	0.194	**0.659**	**1**																			
T.B	0.308	**0.996**	**0.723**	**1**																		
Shoot/root	0.274	**0.675**	-0.101	**0.609**	**1**																	
SC	-0.350	-0.255	0.156	-0.217	**-0.504**	**1**																
SN	-0.272	-0.347	0.061	-0.312	**-0.558**	0.237	**1**															
Sh.C	-0.228	-0.092	0.083	-0.075	-0.268	-0.001	0.140	**1**														
RC	-0.293	-0.039	0.271	-0.005	-0.339	0.384	0.123	0.253	**1**													
RN	0.263	0.009	0.264	0.039	-0.284	-0.174	0.209	0.275	-0.320	**1**												
Sh. N	**-0.657**	-0.174	-0.168	-0.179	-0.083	0.227	0.286	-0.150	-0.217	0.008	**1**											
R N up	0.317	0.479	**0.846**	**0.538**	-0.211	0.001	0.164	0.191	-0.003	**0.734**	-0.115	**1**										
Sh.N uo	-0.010	**0.881**	**0.548**	**0.874**	**0.618**	-0.144	-0.212	-0.153	-0.170	0.033	0.306	0.412	**1**									
TN up	0.029	**0.890**	**0.619**	**0.890**	**0.559**	-0.136	-0.181	-0.123	-0.162	0.118	0.276	**0.508**	**0.994**	**1**								
RC up	0.124	**0.611**	**0.984**	**0.676**	-0.154	0.213	0.074	0.124	0.438	0.185	-0.199	**0.788**	0.482	**0.548**	**1**							
Sh. C up	0.288	**0.996**	**0.669**	**0.994**	**0.653**	-0.248	-0.335	-0.005	-0.016	0.029	-0.185	0.495	**0.873**	**0.883**	**0.625**	**1**						
TC up	0.279	**0.990**	**0.737**	**0.996**	**0.580**	-0.201	-0.298	0.010	0.040	0.050	-0.194	**0.552**	**0.860**	**0.879**	**0.698**	**0.995**	**1**					
CO2	0.279	**0.990**	**0.737**	**0.996**	**0.580**	-0.201	-0.298	0.010	0.040	0.050	-0.194	**0.552**	**0.860**	**0.879**	**0.698**	**0.995**	**1.000**	**1**				
RD	0.397	0.203	0.264	0.217	0.049	0.461	-0.114	-0.403	-0.018	-0.118	-0.260	0.129	0.062	0.075	0.247	0.176	0.192	0.192	**1**			
TRL	0.297	0.411	0.339	0.417	0.193	-0.057	0.025	0.005	-0.081	-0.009	-0.230	0.257	0.302	0.316	0.295	0.414	0.417	0.417	0.193	**1**		
RSA	0.381	0.391	0.367	0.402	0.154	0.116	-0.007	-0.138	-0.062	-0.043	-0.271	0.259	0.257	0.274	0.327	0.383	0.392	0.392	0.493	**0.946**	**1**	
RV	0.419	0.348	0.371	0.364	0.105	0.224	-0.029	-0.212	-0.035	-0.058	-0.293	0.252	0.201	0.220	0.337	0.336	0.350	0.350	**0.660**	**0.856**	**0.977**	**1**

Values in bold are different from 0 with a significance level alpha=0.05

16 sweet sorghum genotypes based on 22 parameters: Plant hieght (PH), dry shoot weight (DSW), dry root weight (DRW), total biomass (TB), shoot/root ratio (Sh/R), soil carbon stock (SCS), soil nitrogen stock (SNS), shoot itrogen (Sh.N), shoot carbon (Sh. C), root nitrogen (RN), root carbon (RC), root carbon uptake (RC up), shoot carbon uptake (Sh. C up), total nitrogen uptake (TN up), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA) and root volume (RV).

Table 4.58. Correlation matrix (Pearson): Adana location in year 2017

Variables	PH	DRW	DSW	T.B	Shoot/roo	SC	SN	Sh.C	RC	RN	Sh. N	R N up	Sh.N uo	TN up	RC up	Sh. C up	TC up	CO2	RD	TRL	RSA	RV
PH	**1**																					
DRW	0.390	**1**																				
DSW	0.181	0.233	**1**																			
T.B	0.395	**0.997**	0.306	**1**																		
Shoot/root	0.261	**0.812**	-0.372	**0.766**	**1**																	
SC	-0.136	0.386	-0.154	0.366	0.487	**1**																
SN	-0.341	-0.283	-0.039	-0.280	-0.237	0.159	**1**															
Sh.C	-0.094	0.069	-0.262	0.047	0.207	**0.499**	-0.009	**1**														
RC	-0.184	-0.070	-0.308	-0.093	0.077	-0.016	-0.079	0.303	**1**													
RN	0.262	0.059	-0.182	0.043	0.159	0.190	0.118	-0.059	0.002	**1**												
Sh. N	-0.164	-0.273	-0.064	-0.272	-0.243	-0.306	-0.374	0.059	0.125	-0.278	**1**											
R N up	0.310	0.242	**0.815**	0.300	-0.258	-0.009	0.008	-0.245	-0.278	0.417	-0.195	**1**										
Sh.N uo	0.394	**0.987**	0.241	**0.985**	**0.793**	0.342	-0.362	0.059	-0.061	0.021	-0.122	0.232	**1**									
TN up	0.406	**0.987**	0.282	**0.988**	**0.768**	0.337	-0.356	0.044	-0.075	0.044	-0.131	0.283	**0.999**	**1**								
RC up	0.156	0.236	**0.984**	0.307	-0.367	-0.157	-0.051	-0.217	-0.134	-0.182	-0.055	**0.800**	0.244	0.284	**1**							
Sh. C up	0.382	**0.996**	0.205	**0.991**	**0.825**	0.430	-0.281	0.155	-0.043	0.061	-0.277	0.220	**0.981**	**0.979**	0.212	**1**						
TC up	0.387	**0.995**	0.276	**0.996**	**0.781**	0.410	-0.279	0.136	-0.053	0.046	-0.276	0.277	**0.981**	**0.982**	0.284	**0.997**	**1**					
CO2	0.387	**0.995**	0.276	**0.996**	**0.781**	0.410	-0.279	0.136	-0.053	0.046	-0.276	0.277	**0.981**	**0.982**	0.284	**0.997**	**1.000**	**1**				
RD	0.309	-0.075	0.348	-0.046	-0.329	**-0.613**	0.085	-0.117	-0.038	0.198	0.118	0.428	-0.054	-0.030	0.352	-0.092	-0.063	-0.063	**1**			
TRL	0.179	0.323	**0.755**	0.375	-0.126	-0.070	0.137	0.025	-0.246	-0.120	-0.349	**0.600**	0.272	0.301	**0.744**	0.326	0.377	0.377	0.250	**1**		
RSA	0.242	0.293	**0.773**	0.347	-0.180	-0.202	0.148	-0.006	-0.235	-0.051	-0.303	**0.658**	0.249	0.282	**0.765**	0.291	0.344	0.344	0.479	**0.969**	**1**	
RV	0.282	0.265	**0.754**	0.319	-0.207	-0.298	0.147	-0.034	-0.214	0.005	-0.254	**0.674**	0.230	0.263	**0.748**	0.260	0.312	0.312	**0.636**	**0.903**	**0.981**	**1**

Values in bold are different from 0 with a significance level alpha=0.05

16 sweet sorghum genotypes based on 22 parameters: Plant hieght (PH), Dry shoot weight (DSW), Dry root weight (DRW), Total biomass (TB), Shoot/root ratio (Sh/R), Soil carbon stock (SCS), Soil nitrogen stock (SNS), Shoot itrogen (Sh.N), Shoot carbon (Sh.C), Root nitrogen (RN), Root carbon (RC), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total nitrogen uptake (TN up), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total carbon uptake (TC up), carbon dioxide (CO_2), Plant height, Root diameter (RD), Total root length (TRL), Root surface area (RSA) and Root volume (RV).

Table 4.59 and 4.60 shows that the correlation between factors and variables in Şanlıurfa location for the years 2016 and 2017 from the PC analysis which explained approximately 85.46 of the variation that was extracted and PC1, PC2 PC3 and PC4 has explainable variation of 32.4%, 15.85%, 24.40% and 12.67% respectively. Taking the factor loadings into consideration in PC1, dry root weight (DRW), total biomass (TB), shoot/root ratio (SH/R), shoot nitrogen uptake (Sh. N up), total nitrogen uptake (TN up), shoot nitrogen uptake (Sh. N up), total carbon uptake (TC up) and carbon dioxide (CO_2) showed the highest correlation. In PC2, total root length (TRL), root surface area (RSA) and root volume (RV) showed the highest correlations, in PC3 soil carbon stock (SC), soil nitrogen (SN), shoot carbon % (Sh.C), root carbon % (RC) and shoot nitrogen % (Sh. N) had the highest correlation and PC4 had root nitrogen uptake (RN up) and root carbon uptake (RC up) as the variable with the highest correlation (Figure 4.9).

In relation to the genotype used (G30) No91 USDA genotype in year 2017, (G16) Gülşeker genotype in year 2016, (G10) Topper 76 genotype in year 2016, and (G28) UNL. hybrid-3 genotype in year 2017 are highly affected by the variables found within this PC1, while for PC2 (G14) No91 genotype in year 2016, (G12) UNL. hybrid-3 genotype in year 2016 and (G15) No5 genotype in year 2016 are found to be highly affected by the variables that lies close to PC2 axis (Figure 4.9).

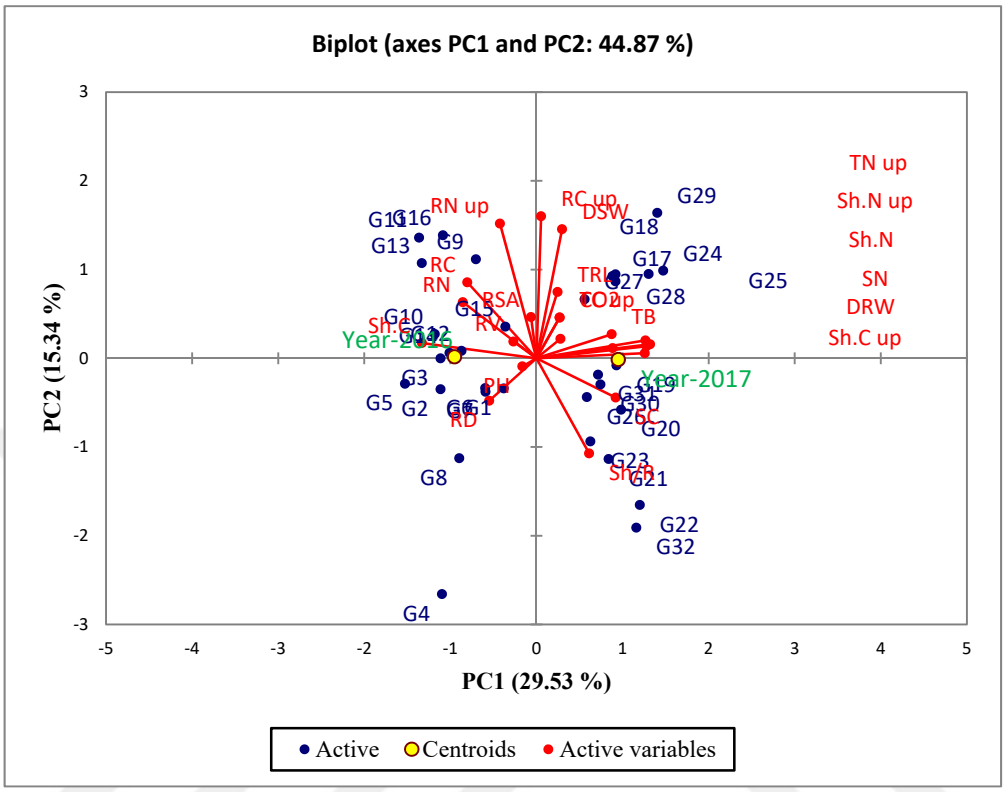

Figure 4.9. Şanlıurfa location Biplot display the variates, sweet sorghum genotypes numbered from G1 to G16 year 2016) and from G17 to G32 the year 2017) and the parameters: dry shoot weight (DSW), dry root weight (DRW), total biomass (TB), soil carbon stock (SCS), soil nitrogen stock (SNS), shoot itrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), total nitrogen uptake (TN up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA) and root volume (RV).

According to the dendrogram (Figure 4.10) the genotype were classified into three groups group 1 had Neb. Sugarcane and topper 76, group 2 had Williams, Roma, Thesis, Gülşeker,Cowley, No91, UNL hybrid-3, Tracy, Ramada, Smith, Grassi, P157953 and No5 as group 3, the least dissimilarity was found between Cowley and No91 and Ramada and Smith which was less than %2 while the highest dissimilarity was found to be between Nebraska Sugarcane and Topper

76 which was around 6%, the dissimilarity around group, group 1 and group 2 and 3 is around 14% while the dissimilarity between group 2 and group 3 is 10% (Figure 4.10).

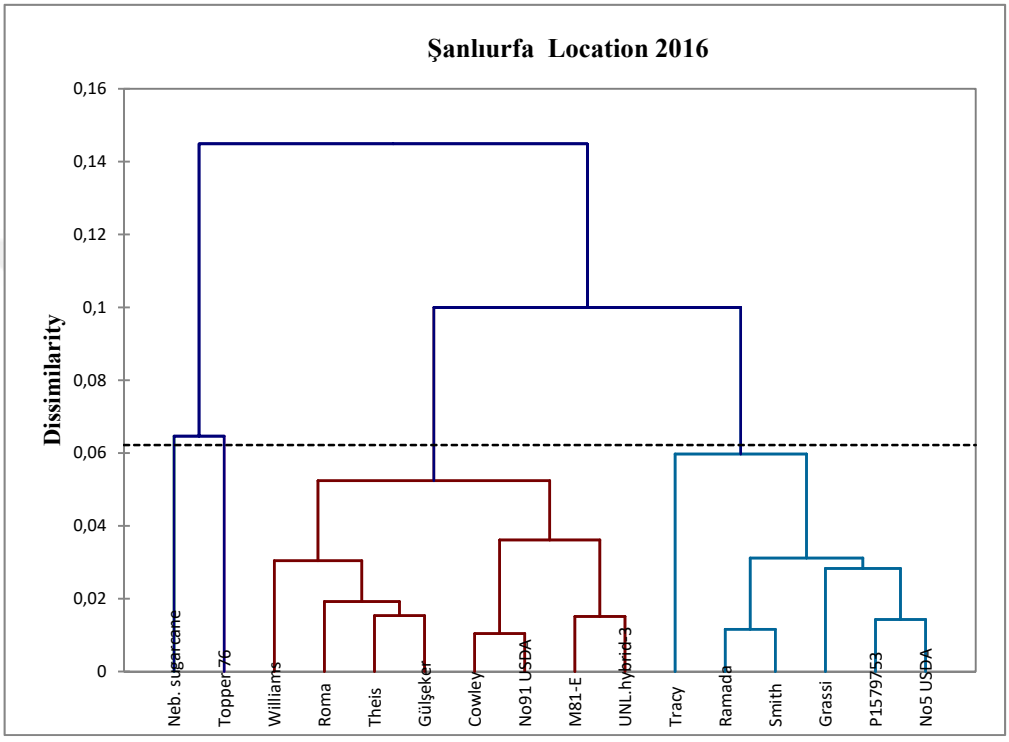

Figure 4.10. Dendrogram of the 16 sweet sorghum genotypes based on 22 parameters: plant hieght (PH), dry shoot weight (DSW), dry root weight (DRW), total biomass (TB), shoot/root ratio (Sh/R), soil carbon stock (SCS), soil nitrogen stock (SNS), shoot itrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total nitrogen uptake (TN up), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA) and root volume (RV).

While in 2017 the genotypes are grouped into 3 groups starting from the left side of the graph group 1 has UNL. Hybrid-3, Smith, Gülşeker, Cowley, M81-E, Nebraska Sugarcane, Grassi, Williams, in Group 2, P1579753 and Ramada and

Group 3 has No91, No5, Tracy, Topper 76, Roma and Thesis. While in 2017 the closest genotype was between M81-E and Nebraska Sugarcane, the dissimilarity between group 1 and group 2 was more than 20% whereas the dissimilarity between group 2 and group 3 was more than 10%. The lowest dissimilarity was found in group 1, while group 2 only two genotypes, which has a dissimilarity less than 5% in group 3 the smallest dissimilarity is between Roma and Thesis which is also below 5% (Figure 4.11).

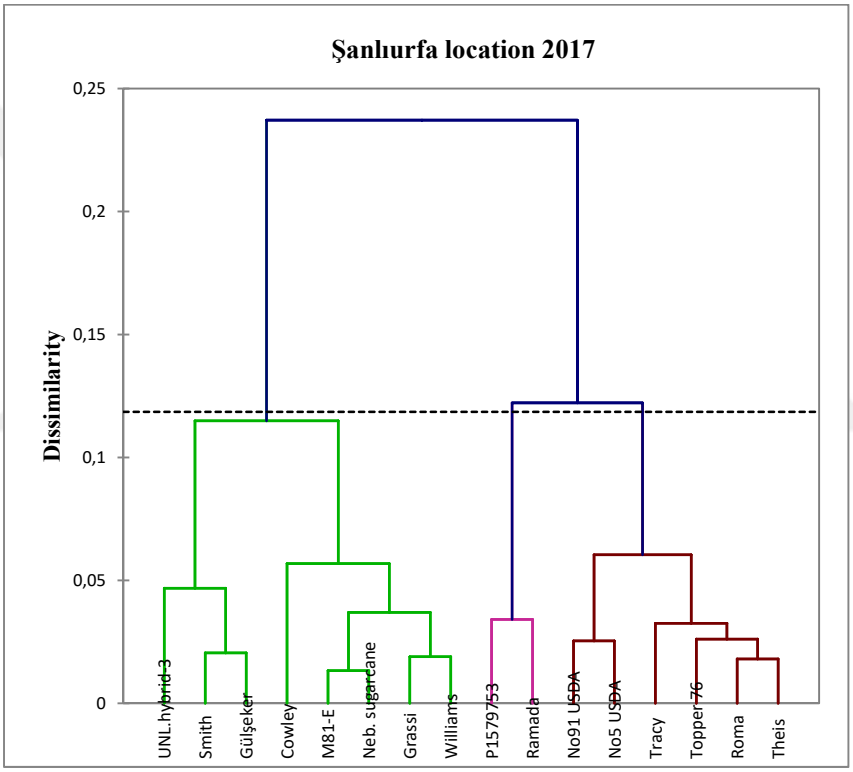

Figure 4.11. Dendrogram of the 16 sweet sorghum genotypes based on 22 parameters: plant hieght (PH), dry shoot weight (DSW), dry root weight (DRW), total biomass (TB), shoot/root ratio (Sh/R), soil carbon stock (SCS), soil nitrogen stock (SNS), shoot itrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total nitrogen uptake (TN up), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA) and root volume (RV).

Table 4.59. Correlation matrix (Pearson): Şanlıurfa location in year 2016

Variables	PH	DRW	DSW	T.B	Shoot/roo	SC	SN	Sh.C	RC	RN	Sh. N	R N up	Sh.N uo	TN up	RC up	Sh. C up	TC up	CO2	RD	TRL	RSA	RV
PH	**1**																					
DRW	-0.218	**1**																				
DSW	0.114	-0.264																				
T.B	-0.203	**0.981**	-0.071	**1**																		
Shoot/root	-0.191	**0.737**	**-0.830**	**0.595**	**1**																	
SC	0.119	0.151	-0.368	0.082	0.326	**1**																
SN	0.392	0.219	0.402	0.308	-0.170	-0.167	**1**															
Sh.C	0.244	-0.367	**0.599**	-0.259	**-0.676**	-0.342	**0.567**	**1**														
RC	0.048	-0.185	-0.061	-0.204	-0.011	-0.253	-0.444	-0.191	**1**													
RN	-0.208	-0.007	0.142	0.022	-0.123	-0.474	-0.130	0.264	0.228	**1**												
Sh. N	-0.288	-0.193	-0.170	-0.234	-0.004	-0.306	-0.353	0.109	-0.021	0.139	**1**											
R N up	-0.084	-0.164	**0.680**	-0.033	**-0.568**	**-0.565**	0.125	**0.533**	0.150	**0.821**	0.002	**1**										
Sh.N uo	-0.361	0.201	-0.293	0.148	0.304	-0.242	-0.273	-0.061	-0.078	0.121	**0.921**	-0.084	**1**									
TN up	-0.373	0.181	-0.212	0.145	0.236	-0.311	-0.258	0.005	-0.061	0.222	**0.924**	0.037	**0.993**	**1**								
RC up	0.123	-0.315	**0.967**	-0.131	**-0.825**	-0.428	0.283	**0.551**	0.194	0.203	-0.170	**0.710**	-0.309	-0.224	**1**							
Sh. C up	-0.166	**0.961**	-0.100	**0.974**	**0.582**	0.066	0.400	-0.097	-0.261	0.074	-0.180	-0.013	0.190	0.189	-0.170	**1**						
TC up	-0.144	**0.911**	0.095	**0.961**	0.423	-0.020	0.464	0.014	-0.225	0.117	-0.217	0.131	0.130	0.146	0.031	**0.980**	**1**					
CO2	-0.144	**0.911**	0.095	**0.961**	0.423	-0.020	0.464	0.014	-0.225	0.117	-0.217	0.131	0.130	0.146	0.031	**0.980**	**1.000**	**1**				
RD	0.398	0.025	0.017	0.029	0.100	0.140	0.113	-0.098	-0.003	-0.069	-0.133	-0.030	-0.103	-0.108	0.006	-0.019	-0.018	-0.018	**1**			
TRL	-0.364	-0.125	**0.648**	0.001	**-0.521**	-0.322	0.287	0.421	-0.273	0.194	0.032	**0.515**	-0.031	0.033	**0.571**	-0.003	0.113	0.113	-0.154	**1**		
RSA	-0.211	-0.140	**0.654**	-0.013	**-0.500**	-0.289	0.307	0.394	-0.258	0.207	-0.020	**0.533**	-0.083	-0.018	**0.578**	-0.034	0.083	0.083	0.232	**0.922**	**1**	
RV	-0.031	-0.141	**0.591**	-0.027	-0.430	-0.228	0.309	0.332	-0.219	0.178	-0.081	0.479	-0.138	-0.080	**0.522**	-0.059	0.047	0.047	**0.539**	**0.739**	**0.942**	**1**

Values in bold are different from 0 with a significance level alpha=0.05

16 sweet sorghum genotypes based on 22 parameters: Plant hieght (PH), dry shoot weight (DSW), dry root weight (DRW), Total biomass (TB), Shoot/root ratio (Sh/R), Soil carbon stock (SCS), Soil nitrogen stock (SNS), Shoot itrogen (Sh.N), Shoot carbon (Sh.C), Root nitrogen (RN), Root carbon (RC), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total nitrogen uptake (TN up), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total carbon uptake (TC up), carbon dioxide (CO_2), Plant height, Root diameter (RD), Total root length (TRL), Root surface area (RSA) and Root volume (RV).

Table 4.60. Correlation matrix (Pearson): Şanlıurfa location in year 2017

Variables	PH	DRW	DSW	T.B	Shoot/roo	SC	SN	Sh.C	RC	RN	Sh. N	R N up	Sh.N uo	TN up	RC up	Sh. C up	TC up	CO2	RD	TRL	RSA	RV
PH	**1**																					
DRW	0.387	**1**																				
DSW	0.403	**0.652**	**1**																			
T.B	0.403	**0.996**	**0.715**	**1**																		
Shoot/root	0.100	**0.590**	-0.222	**0.518**	**1**																	
SC	-0.042	-0.094	0.072	-0.079	-0.191	**1**																
SN	0.299	**0.524**	**0.604**	**0.552**	0.018	0.188	**1**															
Sh.C	0.154	-0.302	-0.066	-0.285	-0.319	0.157	0.097	**1**														
RC	-0.360	0.037	0.426	0.083	-0.394	-0.003	0.111	-0.122	**1**													
RN	-0.370	**-0.511**	-0.176	-0.491	-0.487	0.265	-0.166	0.488	0.292	**1**												
Sh. N	0.457	0.090	0.096	0.094	0.017	-0.222	0.160	0.049	-0.003	0.107	**1**											
R N up	0.243	0.396	**0.893**	0.467	-0.442	0.216	**0.508**	0.149	**0.534**	0.282	0.143	**1**										
Sh.N uo	**0.531**	**0.885**	**0.601**	**0.884**	**0.500**	-0.191	**0.507**	-0.243	0.051	-0.380	**0.542**	0.408	**1**									
TN up	**0.532**	**0.886**	**0.634**	**0.889**	0.467	-0.175	**0.522**	-0.229	0.078	-0.358	**0.537**	0.450	**0.999**	**1**								
RC up	0.272	**0.572**	**0.976**	**0.639**	-0.296	0.070	**0.562**	-0.083	**0.614**	-0.084	0.089	**0.908**	**0.534**	**0.569**	**1**							
Sh. C up	0.430	**0.983**	**0.663**	**0.982**	**0.559**	-0.081	**0.557**	-0.125	0.021	-0.445	0.095	0.434	**0.872**	**0.875**	**0.578**	**1**						
TC up	0.430	**0.977**	**0.745**	**0.985**	0.465	-0.063	**0.588**	-0.126	0.109	-0.417	0.100	**0.527**	**0.870**	**0.878**	**0.671**	**0.993**	**1**					
CO2	0.430	**0.977**	**0.745**	**0.985**	0.465	-0.063	**0.588**	-0.126	0.109	-0.417	0.100	**0.527**	**0.870**	**0.878**	**0.671**	**0.993**	**1.000**	**1**				
RD	0.453	0.216	0.178	0.220	0.116	-0.106	-0.120	0.213	-0.210	-0.018	0.128	0.159	0.223	0.227	0.107	0.269	0.260	0.260	**1**			
TRL	-0.101	0.329	0.252	0.332	0.168	-0.030	0.415	-0.123	0.167	-0.192	-0.266	0.173	0.170	0.175	0.258	0.331	0.338	0.338	-0.296	**1**		
RSA	0.188	0.457	0.310	0.457	0.291	-0.119	0.270	0.022	-0.001	-0.219	-0.191	0.212	0.300	0.304	0.269	0.495	0.489	0.489	0.390	**0.758**	**1**	
RV	0.318	0.425	0.280	0.424	0.286	-0.154	0.131	0.108	-0.092	-0.173	-0.099	0.198	0.307	0.310	0.222	0.477	0.466	0.466	**0.721**	0.438	**0.918**	**1**

Values in bold are different from 0 with a significance level alpha=0.05

16 sweet sorghum genotypes based on 22 parameters: Plant hieght (PH), dry shoot weight (DSW), Dry root weight (DRW), Total biomass (TB), Shoot/root ratio (Sh/R), Soil carbon stock (SCS), Soil nitrogen stock (SNS), Shoot itrogen (Sh.N), Shoot carbon (Sh.C), Root nitrogen (RN), Root carbon (RC), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total nitrogen uptake (TN up), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total carbon uptake (TC up), carbon dioxide (CO_2), Plant height, Root diameter (RD), Total root length (TRL), Root surface area (RSA) and Root volume (RV).

4.3.1.2. Greenhouse Experiment

Figures 4.12 and 4.13 shows the result of PC analysis carried out on variables collected in soils from Adana location. Generally, the total sum of explainable variation was around 85% as for each PC1, PC2, PC3, PC4 had 54%, 13.7%, 11% and 6.2% respectively however, when each PCs are considered in PC1 dry root weight (DRW), dry shoot weight (DSW) and total biomass (T.B) had an acceptable correlation coefficient which was above 70%, PC2 had mostly negative correlation coefficient which are above 70% and they are total root length (TRL), root surface area (RSA) and root volume (RV). The third component PC3 had positive correlation with the factor which are root carbon% (RC) and root nitrogen % (RN) and as for the last component shoot carbon % (Sh. C), shoot nitrogen % (Sh. N) and total nitrogen uptake (TN up) had positive correlation while root diameter (RD) had a negative correlation.

As can be seen in Figure 4.13, mycorrhizal inoculation significantly affected plant and soil parameters under PC1. The genotypes that are affected by variables that lies close to PC1 are found to be (G16) Gülşeker genotype with mycorrhiza, (G10) Topper 76 genotype with mycorrhiza, (G13) Williams genotype with mycorrhiza, were found to be close to the variables that are highly affected in PC1 while in PC2 (G29) Williams genotype without mycorrhiza, (G17) Cowley genotype without mycorrhiza, (G28) UNL. hybrid-3 genotype without mycorrhiza, (G11) Tracy genotype with mycorrhiza and others were found to be highly affected by the variables that are close to the PC2 axis.

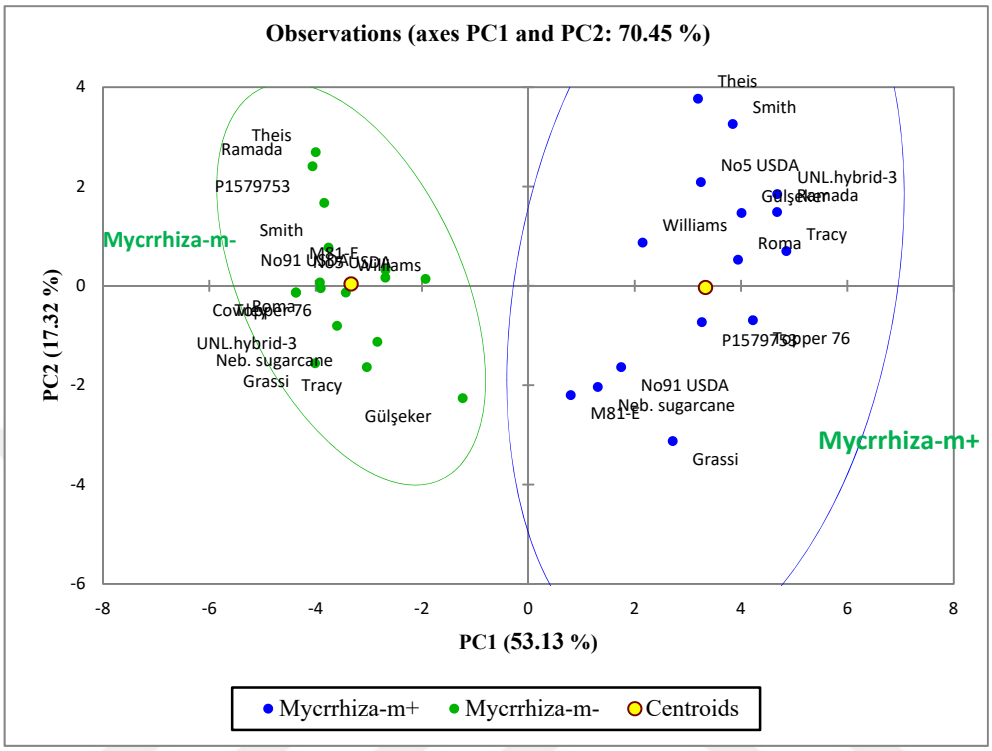

Figure 4.12. Adna Soil Biplot display the variates, sweet sorghum genotypes +M (mycorrhizae) and -M (Non Mycorrhizae) and the parameters: dry shoot weight (DSW), dry root weight (DRW), total Biomass soil carbon stock (SCS), soil nitrogen stock (SNS), shoot nitrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), total nitrogen uptake (TN up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA), root volume (RV) and root colonization (R CL).

The third component PC3 had positive correlation with the factor which are root carbon% (RC) and root nitrogen % (RN) and as for the last component shoot carbon % (Sh. C), shoot nitrogen % (Sh. N) and total nitrogen uptake (TN up) had positive correlation while root diameter (RD) had a negative correlation. In PC1 Shoot nitrogen (Sh. N), plant height (PH), shoot carbon uptake (Sh.C up), total nitrogen uptake (TN up), carbon dioxide (CO_2), total carbon uptake (TC up) and root colonization (R CL) had the highest correlations.

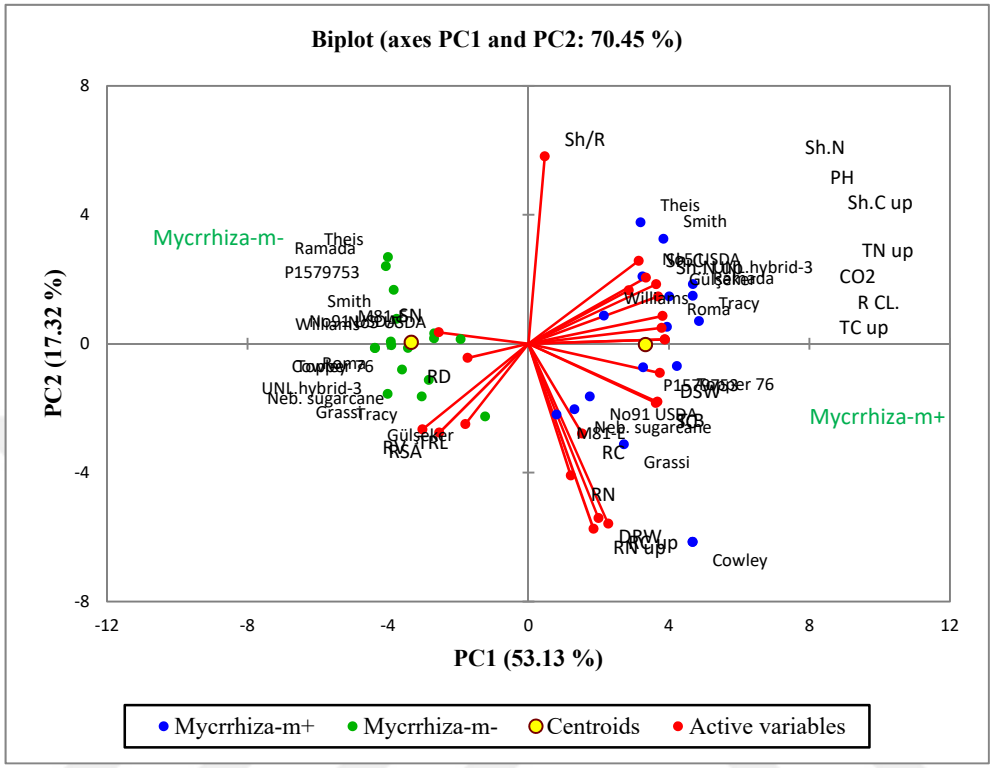

Figure 4.13. Adana soil Biplot display the variates, sweet sorghum genotypes +M (Mycorrhizae) and -M (Non Mycorrhizae) and the parameters: dry shoot weight (DSW), dry root weight (DRW), total Biomass soil carbon stock (SCS), soil nitrogen stock (SNS), shoot nitrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), total nitrogen uptake (TN up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA), root volume (RV) and root colonization (R CL).

As can be seen in Figure 4.12, mycorrhizal inoculation significantly affected plant and soil parameters under PC1. The genotypes that are affected by variables that lies close to PC1 are found to be Gülşeker genotype with mycorrhiza, Topper 76 genotype with mycorrhiza, Williams genotype with mycorrhiza, were found to be close to the variables that are highly affected in PC1 while in PC2 Williams genotype without mycorrhiza, Cowley genotype without mycorrhiza, UNL.hybrid-3 genotype without mycorrhiza, Tracy genotype with

mycorrhiza and others were found to be highly affected by the variables that are close to the PC2 axis.

In the hierarchical clustering carried out on parameters obtained from Adana soil the genotypes were classified into three groups (Figure 4.14). In group one (G29) Williams without mycorrhiza, (G32) Gülşeker without mycorrhiza, (G24) Smith without mycorrhiza, (G4) Nebraska Sugarcane with mycorrhiza, (G3) M81-E with mycorrhiza, (G13) Williams with mycorrhiza, (G16) Gülşeker with mycorrhiza, (G10) Topper 76 with mycorrhiza, (G21) P1579753 without mycorrhiza, (G17) Cowley without mycorrhiza, (G26) Topper 76 without mycorrhiza, (G27) Tracy without mycorrhiza, (G14) No91 with mycorrhiza, (G18) Grassi without mycorrhiza and (G28) UNL. hybrid-3 without mycorrhiza and in group 2 (G11) Tracy with mycorrhiza, (G12) UNL.hybrid-3 with mycorrhiza and (G15) No5 with mycorrhiza and in group 3 (G23) Roma without mycorrhiza, (G31) No5 without mycorrhiza, (G1) Cowley with mycorrhiza, (G8) Smith with mycorrhiza, (G25) Theis without mycorrhiza, (G19) M81-E without mycorrhiza, (G30) No91 without mycorrhiza, (G9) Theis with mycorrhiza, (G20) Neb. Sugarcane without mycorrhiza, (G7) Roma with mycorrhiza, (G2) Grassi with mycorrhiza, (G22) Ramada without mycorrhiza, (G5) P1579753 with mycorrhiza and (G6) Ramada with mycorrhiza, the dissimilarity between group 1, group 2 and group 3 was below 45% with the major dissimilarity appearing within the subgroups of the groups. The percentage dissimilarity between group 2 and group 3 was found to be below %25 Within group 1 the difference between the subgroups G29 and G32 and, G24, G4, G3, G13, G16, G10, G21, G17, G26, G27, G14, G18, G28 was below 25%, within the second groups subgroup the similarity between G11 and, g12 and g15 was found to be below 5%, while within the third group the main difference between G23, G31, G1,G8 and G25 and, G19, G30, G9, G20, G7, G2, G22, G5 and G6 was below 15%

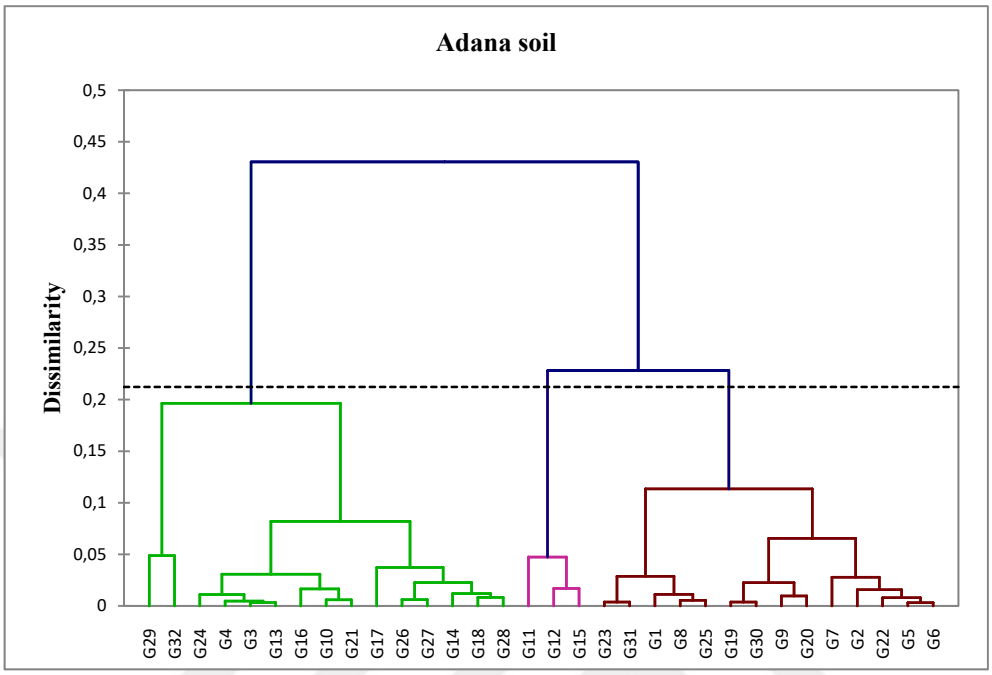

Figure 4.14. Dendrogram of the 16 sweet sorghum genotypes based on 23 parameters: Plant hieght (PH), dry shoot weight (DSW), ry root weight (DRW), total biomass (TB), shoot/root ratio (Sh/R), soil carbon stock (SCS), soil nitrogen stock (SNS), shoot itrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total nitrogen uptake (TN up), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total carbon uptake (TC up), carbon dioxide (CO2), plant height, oot diameter (RD), total root length (TRL), root surface area (RSA), root colonization (R CL) and root volume (RV).

Person correction table 4.61 shown that CO_2 fixation is mainly correlated with plant shoot and root, total dry weight and soil organic carbon and nitrogen.

Table 4.61. Correlation matrix (Pearson): the parameters of sweet sorghum genotypes that grown in (+M and -M) Mycorrhiza in Adana Soil

Variables	DRW	DSW	Sh/R	T.B	SC	SN	Sh.C	RC	RN	Sh.N	RN up	Sh.N up	TN up	RC up	Sh.C up	TC up	CO2	PH	RD	TRL	RSA	RV	R CL.
DRW	**1**																						
DSW	**0.574**	**1**																					
Sh/R	**-0.765**	0.066	**1**																				
T.B	**0.691**	**0.988**	-0.084	**1**																			
SC	**0.599**	**0.883**	-0.048	**0.890**	**1**																		
SN	-0.252	**-0.654**	-0.166	**-0.623**	**-0.686**	**1**																	
Sh.C	0.244	**0.699**	0.229	**0.662**	**0.599**	-0.332	**1**																
RC	0.197	0.277	-0.023	0.280	**0.490**	**-0.361**	0.098	**1**															
RN	**0.369**	0.275	-0.206	0.311	**0.354**	-0.196	-0.056	**0.617**	**1**														
Sh.N	0.086	**0.547**	0.337	**0.498**	**0.565**	**-0.353**	**0.823**	0.183	0.088	**1**													
RN up	**0.822**	**0.497**	**-0.575**	**0.590**	**0.564**	-0.233	0.089	**0.476**	**0.820**	0.098	**1**												
Sh.N up	0.236	**0.734**	0.293	**0.691**	**0.712**	**-0.471**	**0.878**	0.224	0.149	**0.970**	0.222	**1**											
TN up	0.283	**0.753**	0.254	**0.717**	**0.736**	**-0.479**	**0.870**	0.250	0.196	**0.961**	0.280	**0.998**	**1**										
RC up	**0.859**	**0.574**	**-0.587**	**0.666**	**0.710**	**-0.373**	0.218	**0.666**	**0.602**	0.154	**0.876**	0.289	0.338	**1**									
Sh.C up	**0.419**	**0.903**	0.175	**0.875**	**0.780**	**-0.509**	**0.938**	0.182	0.098	**0.757**	0.290	**0.881**	**0.885**	**0.400**	**1**								
TC up	**0.501**	**0.924**	0.094	**0.908**	**0.824**	**-0.526**	**0.913**	0.253	0.165	**0.734**	**0.380**	**0.867**	**0.878**	**0.499**	**0.994**	**1**							
CO2	**0.501**	**0.924**	0.094	**0.908**	**0.824**	**-0.526**	**0.913**	0.253	0.165	**0.734**	**0.380**	**0.867**	**0.878**	**0.499**	**0.994**	**1.000**	**1**						
PH	0.209	**0.599**	0.205	**0.567**	**0.594**	**-0.419**	**0.626**	0.155	0.053	**0.460**	0.139	**0.555**	**0.554**	0.233	**0.674**	**0.666**	**0.666**	**1**					
RD	-0.143	**-0.406**	-0.140	**-0.384**	**-0.466**	**0.384**	**-0.398**	-0.111	0.099	**-0.378**	-0.010	**-0.424**	**-0.419**	-0.170	**-0.436**	**-0.433**	**-0.433**	-0.219	**1**				
TRL	0.046	-0.301	-0.296	-0.257	-0.218	0.191	-0.269	-0.166	-0.211	**-0.372**	-0.097	**-0.389**	**-0.388**	-0.047	-0.318	-0.306	-0.306	**-0.546**	-0.318	**1**			
RSA	-0.021	**-0.483**	**-0.353**	**-0.430**	**-0.403**	0.342	**-0.428**	-0.189	-0.176	**-0.522**	-0.110	**-0.563**	**-0.560**	-0.109	**-0.502**	**-0.488**	**-0.488**	**-0.645**	-0.001	**0.945**	**1**		
RV	-0.092	**-0.614**	**-0.365**	**-0.559**	**-0.557**	**0.456**	**-0.544**	-0.204	-0.131	**-0.614**	-0.119	**-0.675**	**-0.672**	-0.171	**-0.635**	**-0.620**	**-0.620**	**-0.684**	0.315	**0.786**	**0.943**	**1**	
R CL.	**0.378**	**0.835**	0.169	**0.807**	**0.871**	**-0.686**	**0.736**	**0.389**	0.230	**0.763**	0.341	**0.861**	**0.869**	**0.479**	**0.843**	**0.855**	**0.855**	**0.659**	**-0.372**	**-0.452**	**-0.614**	**-0.710**	**1**

Values in bold are different from 0 with a significance level alpha=0.05

16 sweet sorghum genotypes based on 22 parameters: Plant hieght (PH), Dry shoot weight (DSW), Dry root weight (DRW), Total biomass (TB), Shoot/root ratio (Sh/R), Soil carbon stock (SCS), Soil nitrogen stock (SNS), Shoot itrogen (Sh.N), Shoot carbon (Sh.C), Root nitrogen (RN), Root carbon (RC), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total nitrogen uptake (TN up), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total carbon uptake (TC up), carbon dioxide (CO_2), Plant height, Root diameter (RD), Total root length (TRL), Root surface area (RSA) and Root volume (RV).

Figures 4.15 and 4.16 shows the total explainable variation after PC analysis was carried out on observations collected in a greenhouse experiment Şanlıurfa soil. The total explainable variation was around 81% and PC1, PC2, PC3 and PC4 accounts for 48%, 13.1%,8.7% and 6.1% variation respectively according to each PC's in PC1 dry shoot weight (DSW), total biomass (T.B), Sh. carbon uptake (Sh. C up up), root carbon uptake (RC up), total carbon uptake (TC up) and carbon dioxide (CO_2) had the highest correlations, in PC2 total root length (TRL), root surface area (RSA) and root volume (RV) showed the highest correlation coefficients with the factor.

The genotypes that are highly affected by the variables that lies closes to the PC1 axis are Theis genotype with mycorrhiza, M81-E genotype with mycorrhiza, No5 USDA genotype with mycorrhiza and No91 genotype, others like Grassi genotype with mycorrhiza, UNL. hybrid-3 genotype with mycorrhiza, Williams genotype with mycorrhiza and Gülşeker genotype with mycorrhiza are moderately affected, based on the closeness of this genotype to the PC1 axis and to the variables, while No5 without mycorrhiza, Williams genotype without mycorrhiza were also highly affected by the variables that lies close to the PC2 axis.

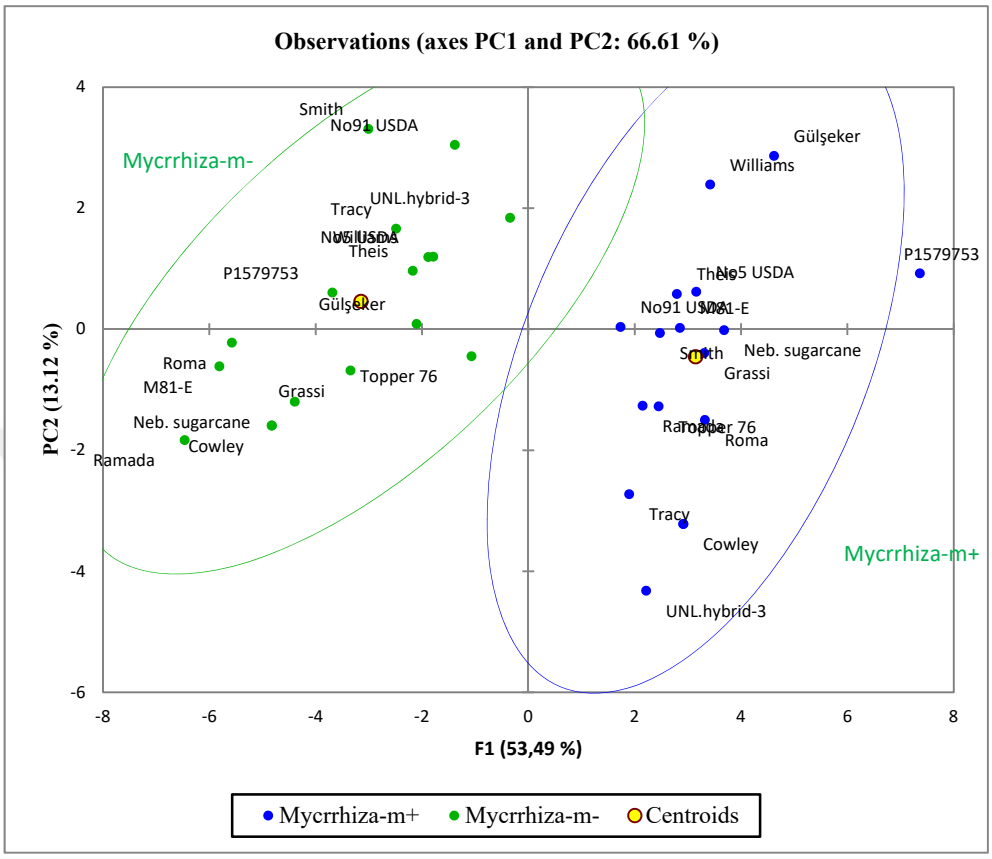

Figure 4.15. Şanlıurfa Soil Biplot display the variates, sweet sorghum genotypes +M (Mycorrhizae) and -M (Non Mycorrhizae) and the parameters: dry shoot weight (DSW), dry root weight (DRW), total Biomass soil carbon stock (SCS), soil nitrogen stock (SNS), shoot nitrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), total nitrogen uptake (TN up), total carbon uptake (TC up), carbon dioxide (CO_2), Pplant height, root diameter (RD), total root length (TRL), root surface area (RSA), Root volume (RV) and root colonization (R CL).

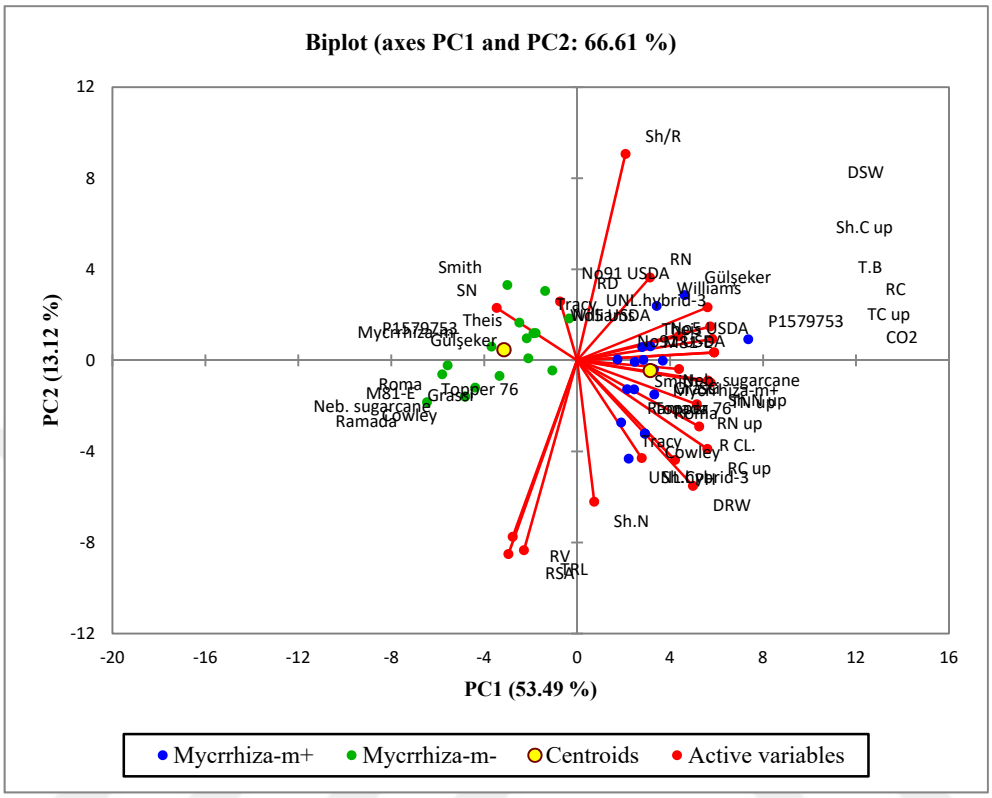

Figure 4.16. Şanlıurfa Soil Biplot display the variates, sweet sorghum genotypes +M (Mycorrhizae) and -M (Non Mycorrhizae) and the parameters: dry shoot weight (DSW), dry root weight (DRW), total biomass soil carbon stock (SCS), soil nitrogen stock (SNS), shoot nitrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), total nitrogen uptake (TN up), total carbon uptake (TC up), carbon dioxide (CO_2), Plant height, root diameter (RD), total root length (TRL), root surface area (RSA), root volume (RV) and root colonization (R CL).

The hierarchical clustering that was done on Sanliurfa soil and presentation is given in (Figure 4.17). The genotypes are classified into three main groups (G6) Ramada with mycorrhiza, (G10) Topper 76 with mycorrhiza, (G26) Topper 76 without mycorrhiza, (G20) Nebraska Sugarcane without mycorrhiza, (G18) Grassi without mycorrhiza, (G23) Roma without mycorrhiza, (G29) Williams without mycorrhiza, (G12) UNL. hybrid-3 with mycorrhiza, (G22) Ramada without

mycorrhiza, (G11) Tracy with mycorrhiza, (G7) Roma with mycorrhiza, (G17) Cowley without mycorrhiza, and (G19) M81-E without mycorrhiza, group 2 has (G14) No91 USDA with mycorrhiza, (G24) Smith without mycorrhiza, (G3) M81-E with mycorrhiza, (G28) UNL.hybrid-3 without mycorrhiza, (G1) Cowley with mycorrhiza, (G5) P1579753 with mycorrhiza, (G25) Theis without mycorrhiza, (G21) P1579753 without mycorrhiza, (G2) Grassi with mycorrhiza, and (G13) Williams with mycorrhiza and group 3 has (G15) No5 with mycorrhiza, (G16) Gülşeker with mycorrhiza, (G8) Smith with mycorrhiza, (G9) Theis with mycorrhiza, (G27) Tracy without mycorrhiza and (G30) No91 without mycorrhiza. The dissimilarity between group 1 and group 2 and group 3 is found to be below 45 % as for the difference between group 2 and group 3 was found to be below 30% the least dissimilarity amongst genotypes was to be in the groups within group 1's subgroup it was found to be (G10) Topper 76 with mycorrhiza , (G26) Topper 76 without mycorrhiza, (G23) Roma without mycorrhiza and (G29) Williams without mycorrhiza, while in group 3 it was (G8) Smith with mycorrhiza and (G9) Theis with mycorrhiza (Figure 4.17).

All founding data, in both locations' soils, shown that indigenous mycorrhiza inoculation have significant effects on plant growth and plant nitrogen and carbon uptake. Also, CO_2 fixation. This is very important for future challenge with climate change in term of mitigate more atmospheric carbon dioxide into organic carbon.

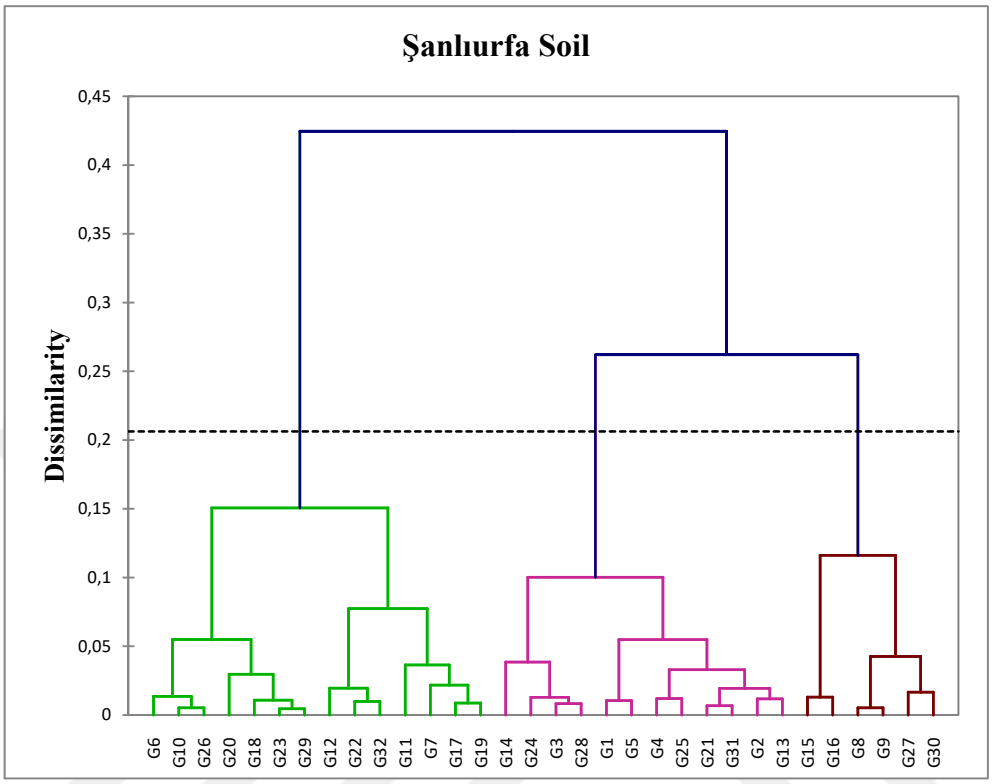

Figure 4.17. Dendrogram of the 16 sweet sorghum genotypes based on 23 parameters: Plant hieght (PH), dry shoot weight (DSW), dry root weight (DRW), total biomass (TB), shoot/root ratio (Sh/R), soil carbon stock (SCS), soil nitrogen stock (SNS), shoot itrogen (Sh.N), shoot carbon (Sh.C), root nitrogen (RN), root carbon (RC), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total nitrogen uptake (TN up), root carbon uptake (RC up), shoot carbon uptake (Sh.C up), total carbon uptake (TC up), carbon dioxide (CO_2), plant height, root diameter (RD), total root length (TRL), root surface area (RSA), root volume (RV) and root colonization (RCL).

Table 4.62. Correlation matrix (Pearson): the parameters of sweet sorghum genotypes that grown in (+M and -M) mycorrhiza in Şanlıurfa soil.

Variables	DRW	DSW	Sh/R	T.B	SC	SN	Sh.C	RC	RN	Sh.N	RN up	Sh.N up	TN up	RC up	Sh.C up	TC up	CO2	PH	RD	TRL	RSA	RV	R CL.
DRW	**1**																						
DSW	**0.671**	**1**																					
Sh/R	-0.193	**0.590**	**1**																				
T.B	**0.733**	**0.996**	**0.518**	**1**																			
SC	**0.584**	**0.665**	0.253	**0.679**	**1**																		
SN	**-0.536**	**-0.485**	-0.096	**-0.508**	**-0.483**	**1**																	
Sh.C	**0.450**	0.224	-0.151	0.258	0.138	-0.261	**1**																
RC	**0.391**	**0.649**	**0.448**	**0.641**	**0.532**	-0.283	**0.372**	**1**															
RN	0.268	**0.393**	0.281	**0.392**	0.225	**-0.427**	0.321	**0.451**	**1**														
Sh.N	0.233	-0.122	**-0.406**	-0.085	0.129	0.084	0.318	0.118	-0.117	**1**													
RN up	**0.847**	**0.668**	-0.008	**0.713**	**0.531**	**-0.605**	**0.488**	**0.497**	**0.732**	0.101	**1**												
Sh.N up	**0.744**	**0.874**	**0.352**	**0.889**	**0.684**	**-0.426**	**0.357**	**0.686**	0.323	**0.369**	**0.682**	**1**											
TN up	**0.773**	**0.880**	0.331	**0.899**	**0.689**	**-0.458**	**0.380**	**0.689**	**0.373**	**0.351**	**0.731**	**0.998**	**1**										
RC up	**0.924**	**0.779**	0.032	**0.823**	**0.662**	**-0.522**	**0.503**	**0.708**	**0.372**	0.238	**0.844**	**0.855**	**0.877**	**1**									
Sh.C up	**0.727**	**0.969**	**0.496**	**0.975**	**0.643**	**-0.508**	**0.455**	**0.689**	**0.433**	-0.031	**0.731**	**0.889**	**0.900**	**0.841**	**1**								
TC up	**0.765**	**0.962**	**0.447**	**0.973**	**0.657**	**-0.519**	**0.469**	**0.704**	**0.433**	0.002	**0.758**	**0.900**	**0.913**	**0.876**	**0.998**	**1**							
CO2	**0.765**	**0.962**	**0.447**	**0.973**	**0.657**	**-0.519**	**0.469**	**0.704**	**0.433**	0.002	**0.758**	**0.900**	**0.913**	**0.876**	**0.998**	**1.000**	**1**						
PH	**0.764**	**0.475**	-0.183	**0.525**	**0.455**	**-0.453**	**0.454**	**0.419**	0.302	0.301	**0.704**	**0.608**	**0.632**	**0.758**	**0.548**	**0.584**	**0.584**	**1**					
RD	-0.127	-0.155	-0.076	-0.158	-0.223	0.201	0.132	-0.077	0.082	-0.105	-0.061	-0.195	-0.185	-0.142	-0.115	-0.121	-0.121	0.003	**1**				
TRL	-0.095	-0.340	-0.347	-0.323	-0.163	0.038	-0.128	-0.193	**-0.478**	0.132	-0.327	-0.250	-0.266	-0.146	-0.331	-0.313	-0.313	-0.181	**-0.512**	**1**			
RSA	-0.156	**-0.442**	**-0.425**	**-0.423**	-0.303	0.070	-0.065	-0.312	**-0.476**	0.035	**-0.379**	**-0.394**	**-0.404**	-0.243	**-0.410**	**-0.396**	**-0.396**	-0.255	-0.185	**0.880**	**1**		
RV	-0.128	**-0.436**	**-0.454**	**-0.415**	**-0.379**	0.092	0.051	-0.312	**-0.360**	0.023	-0.305	**-0.397**	**-0.399**	-0.227	**-0.379**	**-0.367**	**-0.367**	-0.216	0.223	**0.638**	**0.896**	**1**	
R CL.	**0.884**	**0.711**	-0.028	**0.756**	**0.605**	**-0.497**	**0.477**	**0.504**	0.306	0.219	**0.793**	**0.777**	**0.800**	**0.887**	**0.770**	**0.799**	**0.799**	**0.741**	-0.003	-0.320	**-0.369**	-0.293	**1**

Values in bold are different from 0 with a significance level alpha=0,05

16 sweet sorghum genotypes based on 22 parameters: Plant hieght (PH), Dry shoot weight (DSW), Dry root weight (DRW), Total biomass (TB), Shoot/root ratio (Sh/R), Soil carbon stock (SCS), Soil nitrogen stock (SNS), Shoot itrogen (Sh.N), Shoot carbon (Sh.C), Root nitrogen (RN), Root carbon (RC), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total nitrogen uptake (TN up), Root carbon uptake (RC up), Shoot carbon uptake (Sh.C up), Total carbon uptake (TC up), carbon dioxide (CO_2), Plant height, Root diameter (RD), Total root length (TRL), Root surface area (RSA) and Root volume (RV).

5. CONCLUSION

Since climate change is directly related with atmospheric CO_2 concentration, it is better to reduce/mitigate atmospheric carbon dioxide. However, the research question is in which way and how atmospheric CO_2 can be fixed more. Sorghum genotypes are very efficiently grown under less fertile and deficit water conditions. It is better to select efficient genotypes under semi-arid climate conditions for future food security and mitigation of CO_2 caused climate change.

The study was conducted under filed and greenhouse conditions. Under field and greenhouse conditions 16 sweet sorghum genotypes were cultivated during the years 2016 and 2017.

The main hypothesis of project was the sweet sorghum genotypes accumulate/fixed atmospheric C and can leaked carbon into soil through root growth.

In this context, three different sub-hypotheses were determined to be tested:

Hypothesis 1: Different sweet sorghum genotypes have different carbon binding potential under different ecological zone conditions.

Hypothesis 2: Different sweet sorghum genotypes have different mycorrhizal root infection level which develop plant growth and nutrient uptake.

Hypothesis 3: The differences in root systems of sweet sorghum genotypes affect the plant's carbon-holding potential.

The specific objective was to examine the genotypic variability within collected sweet sorghum in terms of dry weight, nutrient uptake, soil carbon sequestration and sweet sorghum genotypes plant tissue carbon store in two divers soil and climate conditions existed locations South of Turkey. In another explanation, the aims of this work were to characterize and compare root biomass and root traits of sixteen sweet sorghum genotypes at field and greenhouse conditions and to estimate their C input and transferred into soil.

The results shown that sweet sorghum genotypes plant biomass and root characteristics are widely varying in both ecological zones of Adana and Şanlıurfa locations in Turkey. Root carbon input rate was dependent on sweet sorghum genotype. In Adana location 4.11 C Mg ha^{-1} taken by UNL-hybrid-3 genotype). Sixteen sweet sorghum genotypes offer to increase soil C under different climatic conditions in Adana and Şanlıurfa in Turkey through increased root biomass inputs and rooting depth. Findings also indicated that sıxteen sweet sorghum cultivations enhance C content in shoot, root and C stock in soils. These results also indicated an enhanced soil carbon sequestration by sweet sorghum. Thus, sweet sorghum has the capacity to sequester C in soil. This study supports the establishment of annual sweet sorghum genotypes cultivation to enhance C and N stock in soil. However, there is a need for long term studies to establish soil C balance under different climatic conditions.

Root trait measurements demonstrated a greater diversity of root traits on the sweet sorghum genotypes in term of plant biomass C inputs into soil. However, compared to the sweet sorghum genotypes, their lower C input to soil needs to be recognized to ensure a balanced C budget.

Genotypes UNL. hybrid-3, No91, Gülşeker, Grassi, Theis, Topper 76 and No91 can be suggested to grown in Adana location Figure 4.13, Williams, Tracy, Smith, Theis, UNL. hybrid-3, Cowley and Grassi genotypes can be suggested in Şanlıurfa location (Figure 4.16).

Under greenhouse conditions the results showed that sweet sorghum genotypes plant biomass was higher in indigenous mycorrhizae inoculated soil than non-mycorrhizae inoculated soil. Root colonization and mycorrhizal dependency of sweet sorghum genotypes varied due to addition of indigenous mycorrhizae. The results also demonstrated the effect of indigenous mycorrhizae on growth response, changes in shoot and root, C and N concentration and uptake, root colonization and mycorrhizal dependency of the sweet sorghum genotypes. In contrast, shoot C and N content was higher in non-mycorrhizae inoculated soil than mycorrhizae

inoculated soil. Keeping the importance of indigenous mycorrhizae as bio-fertilizers, present investigations were carried to find out the feasibility of inoculation of some sweet sorghum genotypes with indigenous AM fungi. Result also demonstrated that indigenous mycorrhizae can help to increase soil C sequestration through sweet sorghum genotypes. This study concluded that indigenous mycorrhizae are potential C sink than non-mycorrhizae because they remove CO_2 from the atmosphere and store it into sweet sorghum-soil system.

This study demonstrated that indigenous mycorrhizae enhance N uptake by sweet sorghum genotypes. This result showed less total N availability in mycorrhizae inoculated bulk soil than non-mycorrhizae inoculated bulk soil. Also, shoot and root dry weight was higher in mycorrhizae inoculated pot than non-mycorrhizae inoculated pot. This study also evaluated the potential of indigenous mycorrhizae for C capture from sweet sorghum-soil system. Bulk soil C was highly significant in mycorrhizae inoculated pot compared to non-mycorrhizae inoculated pot. Sweet sorghum can also substantially contribute to environmental cleaning by capturing a significant amount of CO_2.This means that indigenous mycorrhizae have tendency to decrease atmosphericCO_2 affected by C sequestration in soil. This study clearly indicated the potential of using indigenous AM fungi as bio-fertilizer in the sorghum genotypes hence increased significant carbon fixation which is very important for mitigation of CO_2 which is very important for reduction of intensity of climate change.

In Adana soil the highest fix carbon dioxide are Tracy, Roma and Gülşeker, while in Şanlıurfa soil found the highest fix carbon dioxide No5, Theis, Gülşeker, P1579753 and Williams genotypes (Figure 4.14).

Finally, this study concluded that using a variety of sweet sorghum genotypes can be a good source of soil carbon binding under different climate and soil conditions. Both field and greenhouse experiment result are showed that sorghum genotypes growth is directly related with root growth and mycorrhizal colonization. And there is strong relationship in between CO_2 fixation and plant

growth. Genotypes are given divers effect under soil and climate conditions. Results are supporting our hypothesis.

In Adan location for both years of 2016 and 2027, Topper 76 genotypes produced 57.2, 72.9 Mg ha^{-1} biomass produced. In 2017 more biomass was obtained than in 2016. In year 2016 Gülşeker genotype produced 55.3 Mg ha^{-1}, UNL. hybrid-3 produced 67.1 Mg ha^{-1}. For Şanlıurfa location, in 2016 Topper 76 genotype produced 49.0 Mg ha^{-1} and in year 2017 Gülşeker genotype produced 60.7 Mg ha^{-1}.

In 2016, Adana soil UNL. hybrid-3 genotype has highest root length 92.5 km ha^{-1} and root surface 17959 m^2 ha^{-1}. In 2017, Topper 76 genotype have 92 km ha^{-1} root length and have 17081 m^2 ha^{-1} root surface.

In Şanlıurfa location, in the year of 2016 Tracy genotype have high root length 77.2 km ha^{-1} and root surface 15956 m ha^{-2}. In the 2017 Theis genotype have high root length and Gülşeker have the highest surface area 15823 m^2 ha^{-1}, Topper 76 genotype have second highest root surface 14379 m ha^{-2} and have largest root volume 0.026 m ha^{-3}.

In 2016 in Adana location Topper 76 genotype fixed highest carbon dioxide more than the other genotypes. In root, fixed 4.0 Mg ha^{-1} C, in shoot, 24.0 Mg ha^{-1} C, and totally 28.0 Mg ha^{-1} C, and totally 102.9 Mg ha^{-1} CO_2 were fixed. On the other hand, the lowest C fixation was done by Williams genotype in which 2.7 Mg ha^{-1} C, 14.1 Mg ha^{-1} C, and 16.9 Mg ha^{-1} C and totally 62.0 Mg ha^{-1} CO_2 were fixed respectively. It is Topper 76 genotype fixed twice more CO_2 than Williams genotype. This is very important for mitigate atmospheric CO_2. Similarly, 2017 Topper 76 genotypes have fixed highest root, shoot and total C fixation.

In Şanlıurfa, in 2016 Topper 76 genotype produced 2.9 Mg ha^{-1} C, in root, 22.3 Mg ha^{-1} C, in shoot and 25.2 Mg ha^{-1} C, in total biomass. Also, totally 92.6 Mg ha^{-1} CO_2 were fixed. In 2017, in Şanlıurfa soil Smith genotype fixed highest carbon dioxide than the other genotypes. Totally 96.5 Mg ha^{-1} CO_2 were fixed. In same soil Gülşeker genotype fixed 96.1 Mg ha^{-1} CO_2

In both soils, indigenous mycorrhiza inoculation significantly increase plant growth and shoot/root ratio is higher in inoculated plants than non-inoculated genotypes. In both soil PI 575753 genotype is highest mycorrhiza dependent. Also, Gülşeker genotype is highly mycorrhiza dependency. PI 575753, No5, Gülşeker, Roma Topper 76 genotypes have high mycorrhizal colonization in both soils. These genotypes also have significant effects on plant growth and carbon fixation.

Under greenhouse experiment conditions, in Adana location's soil, mycorrhiza inoculated Cowley 72.5 g pot^{-1}, Gülşeker genotype 67.5 g pot^{-1} DSW produced. In non-inoculated Gülşeker genotype produce biomass 64.3 g pot^{-1}.

In Şanlıurfa soil conditions, mycorrhiza inoculated PI 575753 genotype produced mean biomass of 100.6 g pot^{-1}, however non-inoculated Gülşeker genotype produce biomass 65.7 g pot^{-1}.

In Adana location mycorrhiza inoculated and non-inoculated Gülşeker genotypes produce 20.1 Mg C ha^{-1} and 17.2 Mg C ha^{-1} and in totally, 73.9 Mg CO_2 ha^{-1} and 63.1 Mg CO_2 ha^{-1} fixed respectively.

In Şanlıurfa location, mycorrhiza inoculate PI 575753 genotype produced 26.3 Mg ha^{-1} C and totally 96.5 Mg CO_2 ha^{-1} fixed respectively. In non mycorrhizal inoculated soil, Gülşeker genotype produced 16.2 Mg ha^{-1} C, and totally 59.5 Mg CO_2 ha^{-1} fixed.

5.1. Recommendation

This study concluded that the sweet sorghum genotypes can be a good source of soil C sequestration under different climatic conditions of Turkey.

Under filed conditions, for both location of Adana and Şanlıurfa, plant growth and carbon and nitrogen uptake differed in between genotypes. Genotypes UNL.hybrid-3, No91 USDA, Gülşeker, Grassi, Theis, Topper 76 and No91 can be suggested to grown in Adana location. For Şanlıurfa location, Williams, Tracy, Smith, Theis, UNL. hybrid-3, Cowley and Grassi genotypes can be suggested.

For both location indigenous mycorrhizae can be used to fix more atmospheric carbon dioxide. In Adana soil, the highest CO_2 fixed by Tracy, Roma and Gülşeker genotypes. For Şanlıurfa location No5, Theis, Gülşeker, P1579753 and Williams genotypes, fixed the highest CO_2.

For better understand and recommendation, there is a need for long term studies to establish soil C balance under different climatic conditions.

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- 21st World Congress of Soil Science (WCSS) in Rio de Janeiro, Brazil. 12-17 August 2018.
- 18thInternational plant Nutrition Colloquium (IPNC) in Copenhagen, Denmark. 19-24 August 2017.
- 5th EUROSOIL International Soil Science Congress, Istanbul, Turkey 16-21 July, 2016.

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List of Publications

This thesis is based on a number of articles have been published in peer-reviewed Journals and some international Scientific Conferences.

I. **Ahmed I.A.M**, Ortaş I, Yucel C., Oktem A, Yucel D, Md Toufiq Iqbal. 2020. Root traits and carbon input by sweet sorghum genotypes differs in two climatic conditions. Australian Journal of Crop Science 14(1): 51-63.

II. **Ahmed I.A.M**, Ortaş I, Yucel C, Oktem A, Yucel D., Iqbal Md. 2018. Dry weight and nutrient uptake of twenty-one sweet sorghum genotypes grown in two separate locations of Turkey. Australian Journal of Crop Science (AJCS) 12 (07):1191-1199 (2018).

III. **Ahmed I.A.M**, Ortaş I and Yucel C. (2018). Indigenous mycorrhizae enhance carbon and nitrogen uptake by sweet sorghum genotypes grown under two divers soil ecological zones. 21st World Congress of Soil Science (WCSS) in Rio de Janeiro, Brazil. August 12-17. Submitted abstract ID 534 (**Poster Presentation).**

IV. Yucel D., Yucel C., **Ahmed I.A.M**, Ortaş I. 2018. Potential of Sweet Sorghum Genotypes on Carbon and Nitrogen Dynamic under Semi-Arid Climatic Condition in Turkey.*7th International Conference on Clean and Green Energy (ICCGE)*, Paris, France, February 7-9, 2018 **(Poster Presentation).**

V. **Ahmed I.A.M**., Yucel C, Yucel D, Öktem A, Ortaş İ. 2017. Dry weight and Nutrient uptake of Some Sweet Sorghum Genotypes under Different Climatic Conditions of Turkey. 18th International Plant Nutrition Colloquium, 21 - 24 Aug 2017. Copenhagen, Denmark **(Poster Presentation), pp.523-524.**

VI. **Ahmed I. A. M**., Yucel C., Yucel D, Öktem A, Ortaş I. 2017. Root Traits and Carbon Input by Sweet Sorghum Genotype under Different Climatic Conditions in Turkey. 18th International Plant Nutrition Colloquium, 21-24 Aug 2017. Copenhagen, Denmark **(Poster Presentation), pp.871-872, http://www.ipnc2017.org/.**