# Host Range and Phylogeny of Cuscuta Campestris Yunck With Newly Added Members From the Poaceae Family in Türkiye

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# Abstract

Field dodder (*Cuscuta campestris* Yunck) is an annual parasitic plant that wraps around the host plant and attaches to haustoria. The dodder attachment occurred rarely in the Poaceae family, and there are limited cases worldwide. During an extensive survey in Thrace, Türkiye, to determine the distribution of *C. campestris* Yunck, the dodder was found attached to monocotyledon plants, including *Setaria viridis* (L.) P. Beauv, *Sorghum halepense* (L.) Pers., *Alopecurus myosuroides* Huds, *Avena fatua* L., *Avena steri*lis L., *Eleusine indica* (L.) Gaertn, *Echinocloa crus-galli* (L.) P. Beauv, *Bromus tectorum* L., *Hordeum murinum* L., *Elymus repens* (L.) Gould, and *Lolium perenne* L. The crop plants attached by dodder include *Secale cereale* L. and *Triticum aestivum* L. The parasite's damage was visible in *Echinocloa crus-galli* (L.) P. Beauv, and *Sorghum halepense* (L.) Pers. For molecular analysis, dodder DNA was extracted by the CTAP method. PCR was performed, and the PCR product was sequenced. The similarity in the sequence was compared with Blast records of other countries, and our local population showed higher similarity with 100 hits. Neighbour-joining was performed on Mega X software, comparing 30 different sequences, and the phylogenetic tree was generated. Compared with *C. campestris* accessions KJ400050 and EU883527 in GENBANK, the Thrace population showed 99% identity.


# Introduction

Angiosperms (flowering plants) are seed-producing plants that constitute 90% of the world's plant kingdom. The number of known and described blooming plants is 295.383, and these plants were divided into two groups: monocotyledons containing 7.273 species and dicotyledons containing 210.008 species (Christenhusz & Byng 2016). Among angiosperms, parasitic plants are one of the most harmful, with 4.200 species from 18 families and 274 genera. The highest number of species are grouped under the genus *Cuscuta*. *Cuscuta* spp. are entirely parasitic weeds in the Cuscutaceae family, but according to some researchers, they are included in the Convolvulaceae family (Yuncker 1932; Emberger 1960; Lawrence 1965; Bailey 1966; Nemli et al. 2015). *Cuscuta* spp. is a plant without or containing a low amount of chlorophyll, which is insufficient for photosynthesis. Therefore, they need host plant invasion for survival.

The genus includes 170 species attacking up to 200 plants (Kadıoğlu 1992; Holm et al. 1997; Garcia et al. 2014). Due to developed vascular bundles for haustoria attachment, dicotyledonous plants are the primary hosts within weeds. Monocotyledon plants are rarely parasitised because of several anatomical restraints, such as vascular bundles or incompatibility of signals necessary for haustorium attachment (Dawson et al. 1994).

The golden dodder *Cuscuta campestris* Yunck is the most widely distributed species of *Cuscuta*ceae worldwide (Kaiser et al. 2015). The golden dodder is reported to be problematic in vegetable plants, causing severe damage (Holm et al., 1997). Yield losses of lucerne, sugar beet, sesame, lentil, chickpea, tomato, alfa, and chilli may reach 100% (Nemli & Öngen 1982; Parker & Riches 1993; Mishra et al. 2005). In fruit tree nurseries, parasite damage delays seedling growth. In addition to causing significant yield

losses in many plant species, it is also extremely important because of vectoring diseases such as viruses to the host plants. The total number of plants invaded by *C. campestris* was reported as 100. These weeds play a significant role in dodder's survival and reproduction, which may start new damages following the growing season (Jones 2018). Following attachment, the parasite can grow and reach 8 cm in length. After maturation, flowers bear and produce seed capsules (Dawson et al., 1984). Germinated seedlings have a short life cycle and need immediate penetration for survival (Nwokocha & Aigbokhan 2013). Only one host plant is sufficient for dodder parasitism and survival. Weeds in the infested areas are good alternate hosts. The dodder can attach to weeds and produce 3000 to 25.000 seeds. Seeds can survive in the soil for 20 years. The seeds remaining in the soil may initiate new invasions in the following growing season (Dawson et al. 1984).

Identifying the species of existing harmful plants is essential to develop proper control strategies and apply them effectively. Accordingly, a study was conducted to determine the monocotyledonous hosts of *C. campestris*, whose host status is often overlooked in these plants. The dodder plant was diagnosed morphologically and then molecularly in the study and was phylogenetically investigated. The article also includes the current host list of *C. campestris* in Türkiye prepared from published research.

# Materials and Methods

### Cuscuta Survey, Sample Collection and Morphologic Identification

Field surveys were conducted in the Thrace Region of Türkiye (Fig. 1). Bordered by Greece and Bulgaria, Thrace is located between the Black and Marmara Seas in the Northwestern part of Türkiye. The region includes Edirne, Kırklareli, Tekirdağ, and European parts of İstanbul and Çanakkale Provinces. The region has 1.385.000 ha of irrigable and non-irrigable agricultural area.

**Figure 1.** Study area map in Türkiye

The research area in the region covered orchards, vineyards, sunflower fields and pasture areas. During the survey, annual precipitation was about 600 mm, and the average temperature was 31°C. Sampled locations were randomly selected. The examined agricultural areas were mostly non-irrigated. Plant species attached by parasitic plants were recorded in fields infested with dodder. Reviewing the morphological structure of existing dodders in the field, samples similar to C. campestris were chosen and collected with the hosts for morphological identification and molecular confirmation of whether the sampled dodder species was *C. campestris*. Herbariums of each host plant were prepared to identify species morphologically. In preparing the herbarium, samples were pressed inside the herbarium board at room temperature and let to dry totally. After drying, they were stuck on cardboard, labelled, and covered with a transparent polyethene cover to prevent external damage.

The published identification keys, including Yuncker, 1932 were used to identify the hosts and confirm the presence of *C. campestris*. Morphologic identification of the dodder was performed by examining plant morphology at 10-40X magnification with a Leica microscope; images of the anthesis, sepal and petal

were taken with a microscope camera. The attached host plants were photographed with a Nikon Coolpix P900 digital camera.

The prevalence of dodder occurrence was determined based on the incidence of the same parasitic dodder on the same host in different infested locations. The severity of attachment of dodder was rated as low, moderate and high according to Quasem 2008 as follows;

- Low: A single stem or undeveloped dodder surrounds 1–30% of the plant.
- Moderate: 31–60% of the plant is surrounded and attached by a dodder.
- High: 61–100% of the plant was densely surrounded by dodder, producing few flowers.

### Molecular Characterisation of Cuscuta campestris Yunck

Molecular identification of morphologically identified *C. campestris* was carried out, and the DNA of the dodder was isolated from tissue samples. DNA was extracted by the CTAP method (Leford & Douglas, 1999) for molecular analysis. Fresh plant material (100 mg of plant material) ground in liquid nitrogen was transferred to a 1.5 ml polypropylene tube, and 1 ml of DNA extraction buffer [50 mM Tris-HCl pH 8.0, 20 mM EDTA pH 8.0, 0.7 M NaCl, 0.4 M LiCl, 1% w/v CTAB (hexadecyltrimethylammonium bromide), 1% w/v PVP 40, 2% w/v SDS] and ten µl of β-mercaptoethanol (1% final concentration) was added. The mixture was vortexed for 5 seconds and then incubated for 15 min. at 65°C in a water bath. After incubation, 0.5 ml of chloroform/isoamyl alcohol (24:1) was added to the tube and centrifuged for 1 min. to 5 min. in a microfuge at 14 000 rpm. As much as possible, the aqueous phase was transferred to a new 1.5 ml tube and centrifuged for 1 min. at 14.000 rpm, 0.8 ml of the supernatant was transferred to a new tube, and 0.8 ml of isopropanol (cold as an option) was added to the aqueous solution. The tube was mixed gently, and a white DNA precipitate appeared. The tube was then centrifuged for 1 min. at 14.000 rpm, and the supernatant was withdrawn. The DNA pellet was washed with 1 ml of 70% ethanol and centrifuged again for 1 min. at 17. 000 g. Finally, the supernatant was discarded, and the pellets were allowed to dry for 10 min. DNA pellets were resuspended in 50 µl to 100 µl of 10 mM Tris-HCl pH 8.0, 1 mM EDTA.

The DNA concentration in extracted samples (A260/280 A260/230) was measured and amplified with forward and reverse primers (Alsaadi et al. 2016), amplifying the ITS region. All PCR reactions were in a final volume of 20 µl in a 0.2 ml-tube and contained 10 µl 2X PCR Ready Mix (Sigma Aldrich), 1 µl reverse primer, 1 µl forward primer, 2 µl template DNA, 6 µl ddH2O. In PCR reactions using purified DNA as a template, 30 ng DNA was used in each reaction.

Amplification products were separated on a 1.5% agarose gel stained with ethidium bromide. The gel was run for 50 minutes at 80V and visualised under a UV transilluminator. The PCR product was sequenced with an ABI sequencer. The secondary metabolite structure of the sequence was drawn with CLC RNA Workbench Version 23.04.

Phylogenetic analysis was conducted to evaluate the relationships of *C. campestris* with other published *Cuscuta* species. For this purpose, sequence data of *C. campestris* were subjected to GenBank sequence comparison using BLAST. Neighbour-joining was performed on Mega X software comparing 30 different *Cuscuta* sequences (Table I) from NCBI.

**Table I.** Accession retrieved from NCBI and used in phylogenetic studies

| Accessions | | | |
|---|---|---|---|
| AF145453 | AF148273 | | Neyland, 2000 |
| EU883528 | EU883510 | EU883529 | Costa&Stefanovic, 2009 |
| KJ400101 | KJ400102 | KJ400106 | |
| KJ400044 | KJ400048 | KJ400050 | |
| KJ400083 | KJ400080 | KJ400141 | |
| KJ400190 | KJ400192 | KJ400155 | Garcia et al., 2014 |
| KJ400162 | KJ148273 | KJ400133 | |
| KJ400164 | KJ400064 | KJ400171 | |
| KJ400130 | KJ400154 | KJ400150 | |

### Cuscuta campestris Yunck Distribution in Türkiye

*C. campestris* was detected in many weed and crop plants in different locations in Türkiye. The host list and distribution map of *C. campestris* were created by combining the data of studies dating back to the 1925s and our current study's data.

# Results

### Cuscuta campestris Identification, Phylogeny and Monocotyledon Host Plant

In this survey, *C. campestris* Yunck was observed for the first time on eleven Monocoylodenous weed species, including *Setaria viridis* (L.) P. Beauv, *Sorghum halepense* (L.) Pers., *Alopecurus myosuroides* Huds, *Avena fatua* L., *A. sterilis* L., *Eleusine indica* (L.) Gaertn, *Echinocloa crus-galli* (L.) P.Beauv, *Bromus tectorum* L., *Hordeum murinum* L., *Elymus repens* (L.) Gould, *Lolium perenne* L. The other hosts were crop plants, such as wheat (*Triticum aestivum* L.) and rye (*Secale cereale* L.) (Figure II).

The attachment level in plants ranged from low to moderate. The haustorium of the field dodder was observed in the leaf, stem and spikelet (Table II). Partly wilting was observed in some moderately infected plants like *Avena sterilis* L. Yellow to light green colour changes in the leaves of attached plants were visible. *Cuscuta* attachment was prevalent in *Alopecurus myosuroides* Huds and *Sorghum halepense* (L.)

Pers. However, none of the detected plants were highly contaminated, and plant death was not observed due to the intense damage.

**Table II.** The intensity of attachment of *Cuscuta campestris* Yunck on monocotyledonous plants in Tekirdağ, Thrace (Low: 1–30%, Moderate: 31–60%, High 61–100%)

| Host plant | Intensity of attachment | Attached plant part |
|---|---|---|
| *Alopecurus myosuroides* Huds. | Moderate | Leaf and stem |
| *Avena sterilis* L. | Low | Stem |
| *Avena fatua* L. | Low | Stem |
| *Bromus tectorum* L. | Moderate | Spikelet and stem |
| *Eleusine indica* (L.) Gaertn | Moderate | Leaf, stem, spikelet |
| *Echinocloa crus-galli* (L.) P.Beauv. | Moderate | Leaf, stem, spikelet |
| *Elymus repens* (L.) Gould | Moderate | Spikelet and stem |
| *Hordeum murinum* L. | Moderate | Leaf, stem, spikelet |
| *Lolium perenne* L. | Low | Stem |
| *Secale cereale* L. | Moderate | Stem |
| *Sorghum halepense* L., | Moderate | Leaf and stem |
| *Setaria viridis* L., | Moderate | Leaf, stem, spikelet |
| *Triticum aestivum* L. | Moderate | Stem |

**Figure II.** Attachment of *Cuscuta campestris* Yunck on A) *Secale cereale* L. B) *Lolium perenne* L. C) *Avena fatua* L D) *Triticum aestivum* L. E) *Alopecurus myosuroides* L. F) *Sorghum halepense* (L.) Pers., G) *Eleusine indica* (L.) Gaertn H) *Avena sterilis* L. I) *Hordeum murinum* L.

The collected *C. campestris* plant had a distinctive appearance, primarily leafless, with yellow or orange stems and branches. The parasitic plant had white flowers with a bell-shaped corolla and calyx with ovate overlapping lobes, filiform styles, exerted stamens, elliptic anthers, campanulate corolla tube, capitate stigma, capsule-like fruit, and inflorescence with several stalked flowers (Figure III-IV).

**Figure III.** *Cuscuta campestris* Yunck A) Attachment to host stem B) Flower C) Anthesis D) Capsule and seeds E) A plant moderately parasitised by dodder

The PCR amplification of ITS primers of *C. campestris* was approximately 650 bp. The sequence contained 599 bases. When the secondary structure was examined, ten hairpins were observed.

**Figure IV.** A. The amplified products of ITS primers B. Secondary structure of a sequence of *Cuscuta campestris* Yunck

The sequence data of *Cuscuta campestris* collected in this study in Thrace was deposited in NCBI GENBANK with accession number MW251503. The similarity was compared with Blast records of other countries, and our local population showed higher similarity with 125 hits. Compared with *C. campestris* KJ400050 (Garcia et al. 2014) and EU883527 (Costa & Efanovic 2009), our population showed 99% identity (567–576 nucleotide) and 95% coverage. In contrast, *C. campestris* from our study was 86% similar to *C. monogyna* (KJ400133; Garcia et al. 2014)d *approximata* (KJ400040; Garcia et al. 2014) species deposited in GENBANK.

The species were divided into two clusters in the Neighbour-joining tree with 1000 bootstraps. *C. campestris*, from this study, was grouped in the same cluster as *C. campestris, C. gymnocarpa, C. australis var. tinei*, and *C. pentagona.* However, the sequence data obtained in this study were closely grouped with the other field dodder species due to the high similarity.

**Figure IV.** Neighbour-joining phylogenetic tree of *Cuscuta campestris* and some *Cuscuta* species. The tree was prepared with Mega X software.

### Cuscuta campestris Yunck Distribution in Türkiye

There are 16 parasitic plant species from the Cuscutaceae family in the flora of Türkiye, and one of them is *C. campestris*. This species has been detected in many cultivated plants and weeds (İlhan et al. 2018). The number of hosts that *C. campestris* can attach with haustorium increased to 63, together with the 13 plant species determined in this study. Of these, 45 were weeds; the rest were annual or perennial crops. The complete names and families of host species are listed in Table 2. The distribution map is represented in Fig. 5. The parasitic weed was reported in 40 of 81 provinces.

Table 2
Host plant range of *Cuscuta campestris* in Türkiye

| COMMON NAME | HOST PLANT | FAMILY | REFERENCE |
|---|---|---|---|
| Black grass | *Alopecurus myosuroides* Huds. | Poaceae | This study |
| Winter wild oat | *Avena sterilis* L. | | |
| Wild oat | *Avena fatua* L. | | |
| Downy brome | *Bromus tectorum* L. | | |
| Goosegrass | *Eleusine indica* (L.) Gaertn | | |
| Barnyyard grass | *Echinocloa crus-galli* (L.) P.Beauv. | | |
| Couch grass | *Elymus repens* (L.) Gould | | |
| Foxtail barley | *Hordeum murinum* L. | | |
| Perennial ryegrass | *Lolium perenne* L. | | |
| Rye | *Secale cereale* L. | | |
| Johnson grass | *Sorghum halepense* L., | | |
| Green foxtail | *Setaria viridis* L., | | |
| Wheat | *Triticum aestivum* L. | | |
| Pigweed | *Amaranthus retroflexus* L. | Amaranthaceae | Şin et al. 2020 |
| Lambsquarters | *Chenopodium album* L. | | |
| Wild carrot | *Daucus carota* L. | Apiceae | |
| Absint wormwood | *Anthemisia absinthium* L. | Asteraceae | |
| Common coclebur | *Xanthium strumarium* L. | | |
| Field sow thistle | *Sonchus arvensis* L. | | |
| Common cichory | *Cichorium intybus* L. | | |
| Common dandelion | *Taraxacum officinale* F.H.Wigg | Asteraceae | |
| Canadian horseweed | *Conyza canadensis* (L.) Cronq. | | |
| Wild raddish | *Raphanus raphanistrum* L. | Brassicaceae | |
| Pricky lettuce | *Lactuca serriola* L. | | |
| Bindweed | *Convolvulus arvensis* L. | Convolvulaceae | |
| Squirting cucumber | *Ecbalium elaterium* L. | Cucurbitaceae | |
| Black horehound | *Ballota nigra* L. | Lamiaceae | |

| COMMON NAME | HOST PLANT | FAMILY | REFERENCE |
|---|---|---|---|
| Common mallow | *Malva sylvestris* L. | Malvaceae | |
| Broad-leaved plantain | *Plantago major* L. | Plantaginaceae | |
| Ribwort plantain | *Plantago lanceolata* L. | | |
| Prostrate knotweed | *Polygonum aviculare* L. | Polygonaceae | |
| Curly dock | *Rumex crispus* L. | | |
| Common purslane | *Portulaca oleraceae* L. | Portulacaceae | |
| Stickwilly | *Galium aparine* L. | Rubiaceae | |
| Black nightshade | *Solanum nigrum* L. | Solanaceae | |
| Puncture vine | *Tribulus terrestris* L. | Zygophyllaceae | |

Table 2
continued

| COMMON NAME | SCIENTIFIC NAME | FAMILY | REFERENCE |
|---|---|---|---|
| Sea holy | *Eryngium* sp | Apiaceae | Zare & Dönmez 2020 |
| Rush skeletonweed | *Chondrilla juncea* L. | Asteraceae | |
| Bathurst burr | *Xanthium spinosum* L. | | |
| Barberyy | *Berberis* sp. | Berberidaceae | |
| Restharrow | *Ononis spinose* L. | Fabaceae | |
| Common vetch | *Vicia sativa* L. | | |
| Camelthorn | *Alhagi maurorum* Medik. | | |
| Flax | *Linum usitatissimum* L. (Flax) | Linaceae | |
| - | *Citrus* | Rutaceae | |
| Mullein | *Verbascum* sp. | Scrophulariaceae | |
| Snapdragon | *Antirrhinum majus* L. | Solanaceae | |
| Sugar beet | Beta vulgaris L. | Amaranthaceae | Nemli et al. 2015 |
| Onion | *Allium cepa* L. | Alliaceae | |
| Anise | *Pimpenalla anisum* L. | Apiaceae | |
| Caraway | *Carum carvi L.* | | |
| Melon | *Cucumis melo* L. | Cucurbitaceae | |
| Alfa alfa | *Medicago sativa* L. | Fabaceae | |
| Chickpea | *Cicer arietinum* L. | | |
| Clover | *Trifolium* Tourn. ex L. | | |
| Faba bean | *Vicia faba* L. | | |
| Pepper | *Capsicum annum* L. | Solanaceae | |
| Eggplant | *Solanum melongena L.* | | |
| Potato | *Solanum tuberosum* L. | | |
| Tobacco | *Nicotiana tabacum* L. | | |
| Tomato | *Solanum lycopersicum* L. | | |
| Grapevine | *Vitis vinifera* L. | Vitaceae | |
| Oregano | *Origanum onites* L. | Lamiaceae | Sokat 2019 |

# Discussion

Field dodder (*C. campestris* Yunck) is one of the most common parasitic plants in the world. The weed is considered a harmful parasitic plant due to its broad host range, causing significant plant damage and economic yield loss (Kaiser 2015). In this study in Thrace, 11 weed species were found parasitised by dodder. Likewise, various researchers have done different studies and revealed parasitism in monocotyledons and members of the Poaceae family. *C. campestris* was reported as a parasite to 38 monocotyledonous plants worldwide. These include weeds and crops like *Aegilops* sp., *Avena sterilis* L., *Arundo donax* L., *Bromus* sp., *Echinochloa-crus galli*, *Cynodon dactylon* (L.) Pers, *Lolium temulentum* L., *Triticum durum* Desf, *Setaria glauca*, *Sorghum halepense* (L.) Pers (Qasem 2008; Barath 2021). Its prevalence and host range in monocotyledons are reported to be low due to the low level of enzymes that degrade plant tissues during parasitism of the parasitic plant (Haider et al. 1997). For instance, in a study conducted in Nigeria, mild infection was found in weeds from the Poaceae family. Similarly, the intensity of infection was lower in plants in this study in Thrace. Moderate infection was observed in some hosts, whereas 1–2 clusters of flowers were found on *Bromus tectorum* L. and *Sorghum halepense* L. (Table 1).

In Thrace, the field dodder was found in weeds and crops consumed as food. Plants such as wheat, rye, and weeds like *Hordeum murinum* L. and *Echinocloa crus-galli* (L.) Beauv is used as animal feed. Observing dodder parasitism in consumed plants showed that controlling the parasite is essential, especially in pastures where livestock is grazed. Because the feed prepared with these plants can be poisonous for cattle and horses when it is 50% parasitised by dodder. Affected animals typically suffer from abdominal pain and diarrhoea and may also experience weight loss (Abutarbusch 2013).

In this study, *C. campestris* Yunck was identified molecularly with specific primers using the ITS region. The BLASTn comparison was conducted with the local dodder sequence from Thrace, and the phylogenetic tree was generated. The higher similarity was observed with other *C. campestris* records like (EU883529 Costa & Efanovic 2009) from New Mexico. Phylogenetic study and morphologic identification strongly confirmed that the dodder in Poaceae is *C. campestris* Yunck.

Molecular identification of dodder in this research allowed reliable identification quickly. The identification of *C. campestris* in Türkiye mainly involves observing morphologic characteristics. Morphologic conditions unsuitable for identification may result in false decisions. Additionally, this method can only be applied by staff with knowledge of diagnostic features. Molecular identification in this research allowed reliable identification quickly, and this method can be carried out even by unqualified staff. Furthermore, molecular methods can be used for DNA isolation and diagnostic processes at every developmental stage of plants. The ITS region, which includes the 16s, 5.8s and 28s areas, is frequently used in molecular studies. This region also is eligible for phylogenetic analyses (Baldwin 1995).

In addition to the *C. campestris* attachment, different dodder species have been reported as parasitic in monocotyledonous plants. For instance, in Poland, *C. lupuliformis* was parasitic to *Elymus repens* and

*Phalaris arundinacea* (Panek-Wójcicka & Piwowarczyk 2020). Again, in Romania, Tanase et al. (2012) stated that different dodder species can be seen in the Poaceae families.

# Conclusions

This article aimed to give information about the current host range of *Cuscuta campestris* identified in Türkiye. During the surveys carried out within the scope of the study in Thrace, the focus was on identifying the hosts from the Poaceae family of C. campestris. The research is essential to support the literature and update the registered host list, especially from monocotyledon plants in the country.

# Declarations

### Ethics Committee Approval:

Since the article does not contain any studies with human or animal subjects, its approval by the ethics committee was not required.

### Data Sharing Statement:

All data are available within the study.

### Authors' Contributions

The authors conducted the study, prepared the manuscript and approved it.

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### Conflict of Interests

The authors declare no conflicts of interest.

# References

1. Abutarbush SM (2013). Alfalfa dodder (*Cuscuta campestris*) toxicity in horses: clinical, haematological and serum biochemical findings. Veterinary Record 173: 95. doi: 10.1136/vr.101635.
2. Alsaadi A, Saif M, Yasser M (2016). Identification of *Cuscuta campestris* Yuncker in UAE: Study of barcode loci-rbcL, matK and trnh-psbA in the Uae and Egyptian cultivars and in the respective host plants basil and jute. International Journal of Research in Science 2(2): 5.
3. Arıtuluk ZC, Ezer N, Akaydın G (2014). Flora of Tefenni district (Burdur/Turkey). *Biological* Diversity and Conservation 7(3): 146-166. Retrieved from

*https://dergipark.org.tr/tr/pub/biodicon/issue/55880/765587*.

4. Bailey HL (1966). Manual of cultivated plants. The Macmillan Company, New York, 1116.
5. Baldwin BG, Sanderson MJ, Porter JM, Wojciechowski MF, Campbell CS, Donoghue MJ (1995). The ITS region of nuclear ribosomal DNA: a valuable source of evidence on angiosperm phylogeny. Annals of the Missouri Botanical Garden 82: 247-277. *https://doi.org/10.2307/2399880.*
6. Baráth K (2021). Effect of species-environment on host preference of *Cuscuta campestris*. Plant Ecology 222: 1023–1032. https://doi.org/10.1007/s11258-021-01158-w
7. Christenhusz M, Byng J (2016). The number of known plant species in the world and its annual increase. Phytotaxa 261: 201-217. *10.11646/phytotaxa.261.3.1.*
8. Ciğer Ü, Kadıoğlu İ, Yanar Y (2013). Tokat ili şeker pancarı ekim alanlarındaki küsküt (*Cuscuta campestris* Yunck.) üzerinde görülen fungal etmenlerin belirlenmesi. Türkiye İstilacı Bitkiler Kataloğu. Ankara: T.C. Gıda, Tarım ve Hayvancılık Bakanlığı Yayını, 532p.
9. Dawson JH (1984). Control of *Cuscuta* in alfalfa. In: Proceedings of the 3rd International Symposium on Parasitic Weeds. pp. 188–199.
10. Dawson JH, Musselman LJ, Wolswinkel P, Dorr I (1994). Biology and control of *Cuscuta*. RevWeed Sci 6: 265–317.
11. Emberger L (1960). Les Vegetaux vasculaire. Massın et Cie editeurs, Paris-VI, 11(2): 1539.
12. Garcia MA, Costea M, Kuzmina M, Stefanović S (2014). Phylogeny, character evolution, and biogeography of *Cuscuta* (dodders; Convolvulaceae) inferred from coding plastid and nuclear sequences. American Journal of Botany 101(4): 670-690. doi: 10.3732/ajb.1300449.
13. Haidar MA, Orr GL, Westra P (1997). Effects of light and mechanical stimulation on coiling and prehaustoria formation in *Cuscuta* spp. Weed Research 37: 219–228. *https://doi.org/10.1046/j.1365-3180.1997.d01-36.x*
14. Holm L, Doll J, Holm E, Pancho J, Herberger J (1997). World weeds: Natural histories and distribution. John Wiley and Sons Inc: 1129 pp.
15. Jones RAC (2018). Plant and insect viruses in managed and natural environments: Novel and neglected transmission pathways. Advances in Virus Research 149–187. doi:10.1016/bs.aivir.2018.02.006
16. Kadıoğlu I (1992). Küsküt (*Cuscuta* spp.) ve mücadelesi [Dodder (*Cuscuta* spp) and its management]. Herboloji Haberleri Ç. Ü., Ziraat Fak., Bitki Koruma Bölümü, 3(5): 1-11.
17. Kaiser B, Vogg G, Furst UB, Albert M (2015). Parasitic plants of the genus *Cuscuta* and their interaction with susceptible and resistant host plants. Frontiers in Plant Science 6: 45. doi: 10.3389/fpls.2015.00045.
18. Kaya İ, Nemli Y, Demir İ (2018). Türkiye'de Tarım ve Tarım Dışı Alanlarda Görülen Küsküt Türlerinin (*Cuscuta* spp.) Taksonomik Özellikleri, Dağılışları ve Konukçuları [Taxonomic characteristics, distributions and hosts of dodder species (*Cuscuta* spp.) seen in agricultural and nonagricultural

areas in Turkey]. Turkish Journal of Weed Science 21(1): 1-7. Retrieved from *https://dergipark.org.tr/tr/pub/tjws/issue/42558/512833*

19. Lawrence HM (1965). Taxonomy of vascular plants. The Mamillan Company, Newyork, p. 823.
20. Lefort F, Douglas GC (1999). An efficient micro-method of DNA isolation from mature leaves of four hardwood tree species *Acer, Fraxinus, Prunus* and *Quercus*. Annals of Forest Science 56 (3): 259-263. ffhal-00883270f
21. Mishra JS, Moorthy BTS, Manish B (2005). Efficacy of herbicides against field dodder (*Cuscuta campestris*) in lentil, chickpea and linseed. Indian Journal of Weed Science 37(3/4): 220-224.
22. Mumcu Ü, Korkmaz H (2018). Ethnobotanical uses of alien and native plant species of Yeşilırmak Delta. Acta Biologica Turcica 31 (3): 102-113. Retrieved from *https://dergipark.org.tr/en/pub/actabiotr/issue/38849/452908*
23. Nemli Y, Kaya İ, Tamer ŞR (2015). *Cuscuta campestris*. Türkiye İstilacı Bitkiler Kataloğu 271-282, Ankara Türkiye.
24. Neyland R (2001). A phylogeny inferred from large ribosomal subunit (26S) rDNA sequences suggests that *Cuscuta* is a derived member of Convolvulaceae. Brittonia 53: 108-115. *https://doi.org/10.1007/BF02805402*.
25. Nwokocha MI, Aigbokhan EI (2013). Host range and preference of *Cuscuta campestris* (Yunck.) among common weeds in Benin City, Nigeria. Nigerian Journal of Botany 26: 183-205.
26. Panek-Wójcicka M, Piwowarczyk R (2020). Host preferences of *Cuscuta lupuliformis* (Convolvulaceae) in Sandomierz. Fragmenta Floristica et Geobotanica Polonica XXVII(2): 696-702. *https://doi.org/10.35535/ffgp-2020-0050*
27. Parker C, Riches CR (1993). Parasitic weeds of the world: Biology and control. CAB International, Wallingford. 332pp.
28. Qasem JR (2008). Dodder (*Cuscuta* spp.) occurrence and natural hosts in Jordan. *Korean* Journal of Weed Science 28(4): 343-359.
29. Satıl F, Tümen G, Selvi S (2017). Ethnobotanical features of parasitic plants distributed in Balıkesir/Turkey. Biyolojik Çeşitlilik ve Koruma 10(3): 7-11. Retrieved from *https://dergipark.org.tr/tr/pub/biodicon/issue/55729/762124*.
30. Sırrı M, Özaslan C, Fidan M (2020). Parasitic weed species and their hosts in Siirt province of Turkey. ISPEC Journal of Agricultural Sciences 4(4): 808–822. *https://doi.org/10.46291/ISPECJASvol4iss4pp806-820*.
31. Şin B, Öztürk L, Sivri N, Avcı GG, Kadıoğlu İ (2020). Weed hosts of field dodder (*Cuscuta campestris* Yunck.) in Northwestern Marmara Region of Turkey. Anadolu Ege Tarımsal Araştırma Enstitüsü Dergisi 30 (1): 80-86. DOI: 10.18615/anadolu.727224.
32. Sokat Y (2019). Denizli ve Manisa illeri kekik (*Origanum onites*) fideliklerinde bulunan yabancı ot türleri, yoğunlukları ve rastlanma sıklıkları [Weed Species and Their Frequency and Density in Nursery Bed Thyme (*Origanum onites*) in Denizli and Manisa Provinces of Turkey]. Türk Tarım ve Doğa Bilimleri Dergisi 6 (4): 808-813. DOI: 10.30910/turkjans.633605

33. Söker A, Koyuncu O, Yaylacı Ö, Tokur S (2012). Eskişehir ve çevresindeki bazı tarım alanlarındaki tarla yabancı otlarının florası [Weed Flora in Some Agricultural Fields of Eskisehir and Environs]. Artvin Çoruh Üniversitesi Orman Fakültesi Dergisi 13(1): 109-127.
34. Tănase MA, Sand C, Gheorghe M, Moise CS, Stanciu M, Antonie I (2012). Research on the spreading of *Cuscuta* in South-East Transylvania - Romania. Journal of Horticulture, Forestry and Biotechnology 16: 216-219.
35. Türkmen N, Düzenli A (1998). The flora of Dörtyol and Erzin district of Hatay province in Turkey. Turkish Journal of Botany Vol. 22: No. 2, Article 7. Available at: *https://journals.tubitak.gov.tr/botany/vol22/iss2/7*.
36. Yuncker TG (1932). The genus *Cuscuta*. Memoirs of the Torrey Botanical Club 18: 113-331.

# Figures


**Figure 1**

Study area map in Türkiye


## Figure 2

Attachment of *Cuscuta campestris* Yunck on A) *Secale cereale* L. B) *Lolium perenne*L. C) *Avena fatua* L D) *Triticum aestivum* L. E) *Alopecurus myosuroides* L. F) *Sorghum halepense* (L.) Pers., G) *Eleusine indica* (L.) Gaertn H) *Avena sterilis* L. I) *Hordeum murinum* L.

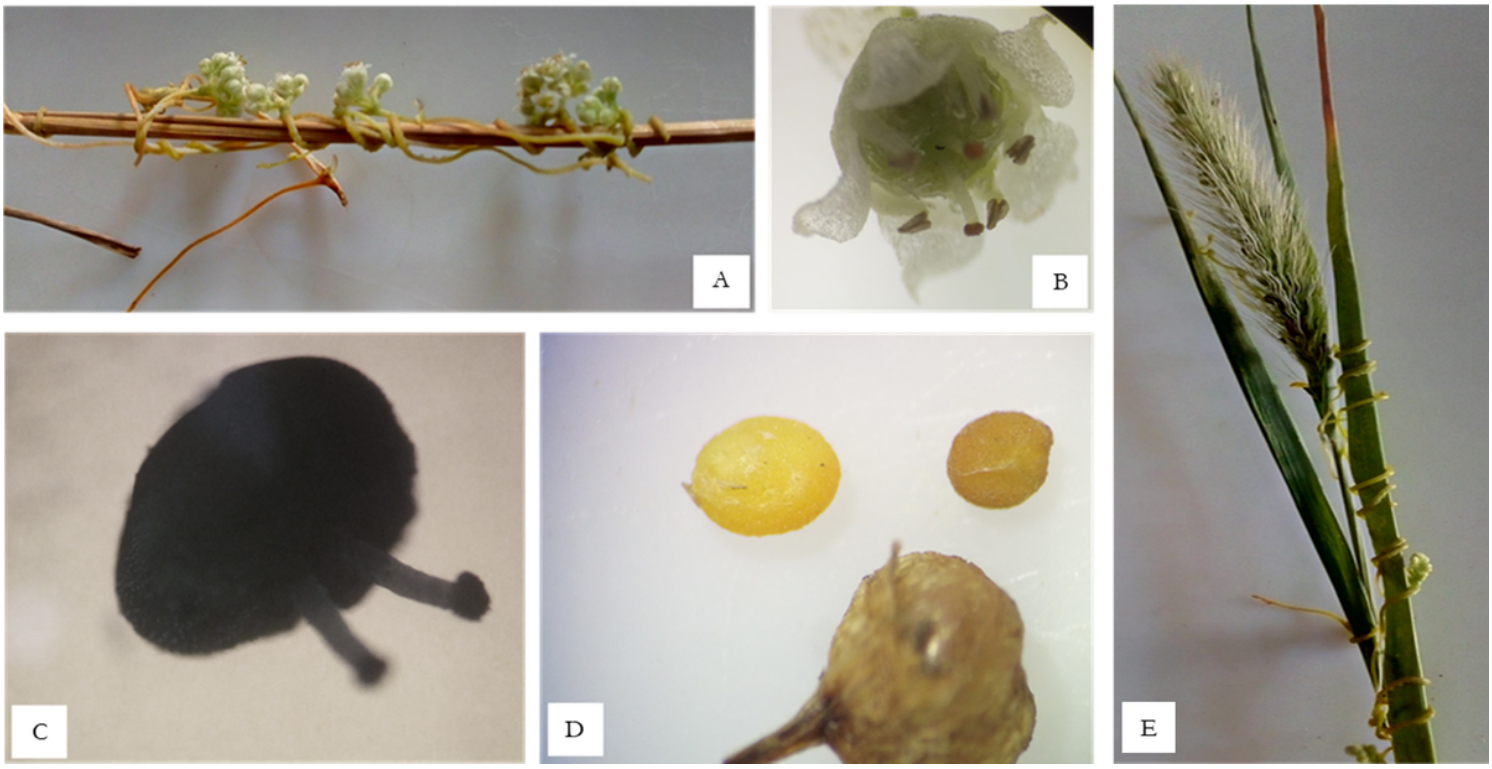



**Figure 3**

*Cuscuta campestris* Yunck A) Attachment to host stem B) Flower C) Anthesis D) Capsule and seeds E) A plant moderately parasitised by dodder

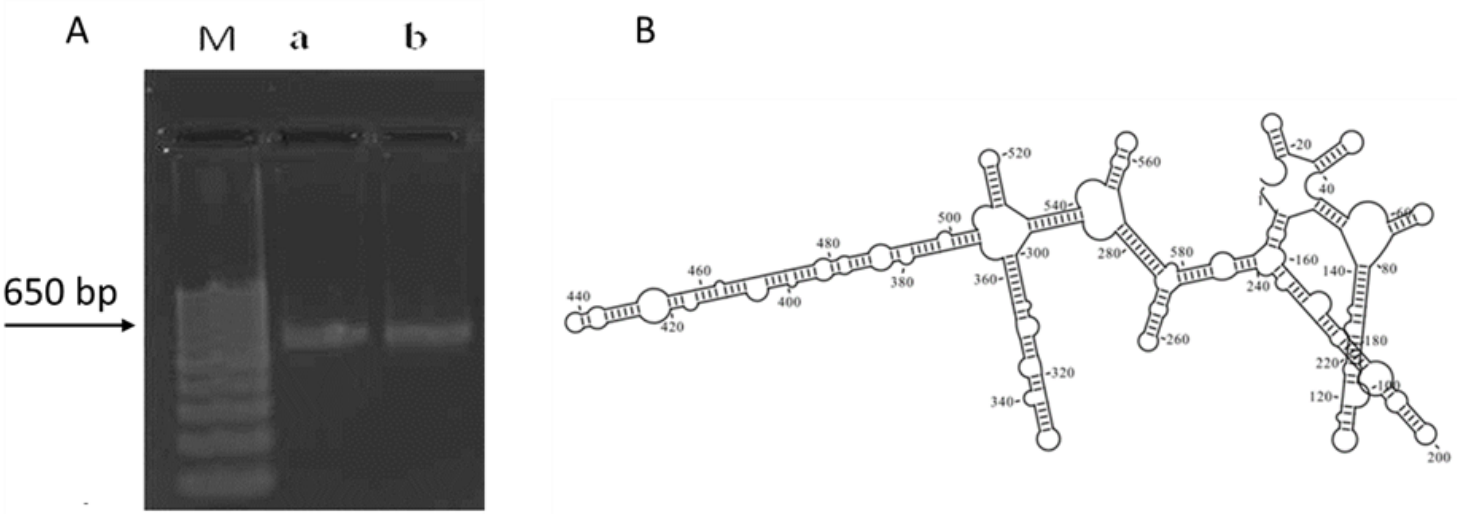
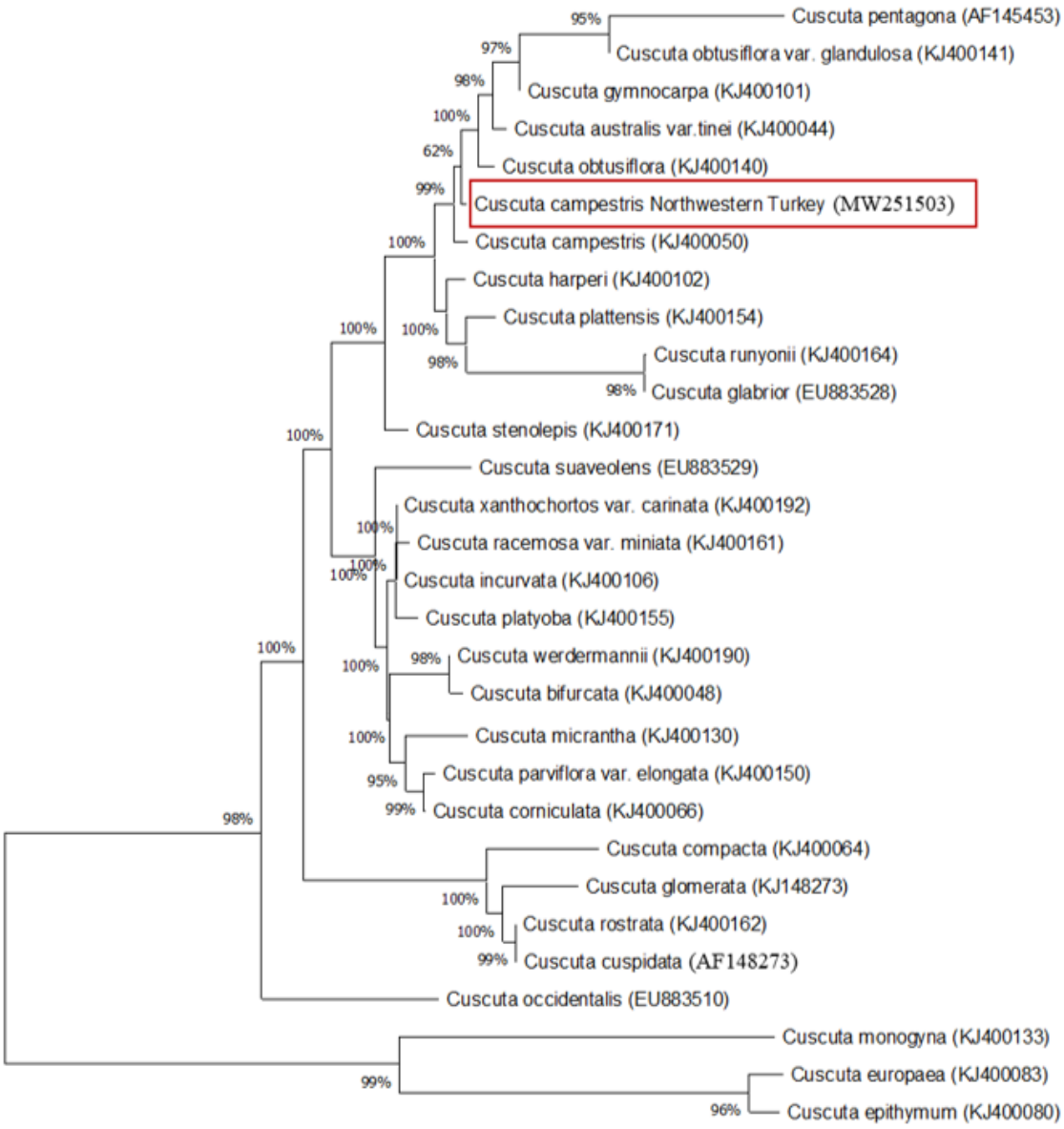



**Figure 4**

A. The amplified products of ITS primers B. Secondary structure of a sequence of *Cuscuta campestris* Yunck




## Figure 5

**Figure IV.** Neighbour-joining phylogenetic tree of *Cuscuta campestris* and some *Cuscuta* species. The tree was prepared with Mega X software.

## Figure 6

**Figure 5.** Distribution map of *Cuscuta campestris*Yunck in Türkiye (Türkmen, 1998; Söker et al. 2012; Ciğer et al. 2013; Arıtuluk et al. 2014; Satıl et al. 2017; Mumcu & Korkmaz 2018; Kaya et al. 2018; Sokat 2019; Sırrı et al. 2020;