

Significance of *Aegilops cylindrica* Host. - Jointed Goatgrass in Breeding Programmes

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Date: 17.03.2025 *Issue*: 3/2025



Abstract

Bulgaria is one of the countries on the Balkan Peninsula with a diversity of *Aegilops* species. They are a source of genes for resistance to biotic and abiotic environmental stress factors which, when introduced into the genome of durum and common wheat, can improve their resistance. The interest in these species is also justified by the possibility of using them in breeding to broaden the genetic base of durum and common wheat, and even of barley. The wild relative of wheats, *Aegilops cylindrica* Host., is an annual herbaceous plant known

as **jointed goatgrass**. It is a tetraploid species ($2n = 4x = 28$; CCDD), originating from its ancestors *Aegilops markgrafii* (Greuter) Hammer ($2n = 2x = 14$; CC) and *Aegilops tauschii* Coss ($2n = 2x = 14$; DD). This species is widespread in Bulgaria, which provides grounds for a broader study of the genetic potential of the *Aegilops cylindrica* Host. genotypes distributed in the country and of their traits, for the purposes of wheat and barley breeding.

Distribution countries: Afghanistan, Bulgaria, Czech Republic, Slovakia, Greece, Hungary, Iran, Iraq, Japan, Kazakhstan, Kyrgyzstan, Crimea, Lebanon-Syria, Northern Caucasus, North-western and Southern European Russia, Pakistan, Palestine, Romania, Tajikistan, Turkey, Turkmenistan, Ukraine, Uzbekistan, and the countries of the former Yugoslavia (Slovenia, North Macedonia, Croatia, Serbia, Montenegro, Kosovo and Bosnia).



The species has been introduced into: USA (states – Alabama, Arizona, Arkansas, California, Colorado, Idaho, Illinois, Indiana, Iowa, Kansas, Kentucky, Louisiana, Michigan, Missouri, Montana, Nebraska, Nevada, New Mexico, New York, North Dakota, Ohio, Oklahoma, Oregon, South Dakota, Tennessee, Texas, Utah, Virginia, Washington), Central European Russia, Cyprus, France, Austria, Germany, Great Britain, Italy, Korea, Mexico, Pennsylvania, Poland, and Tunisia, where it is considered an invasive weed.

(<https://www.cabidigitallibrary.org/doi/10.1079/cabicompdiem.108330>), (van Slageren, 1994; Danin and Scholz, 1994).

Botanical description and morphology

Winter annual tufted herbaceous plant, forming from several to many productive tillers. Isolated plants can form more than 100 tillers. At the base, the culms are semi-prostrate, and later become ascending to erect.



Culm length is usually 20–40 cm, but can reach up to 80 cm in height (excluding the awns). The leaves are linear-lanceolate, glabrous or pubescent, 2–5 mm wide and 3–15 cm long. The lowest and the uppermost leaves are shorter than the rest on the culm. Between the leaf sheath and the blade there is a short membranous ligule and pubescent auricles. The inflorescence is a narrow cylindrical spike, slightly tapering towards the tip, 6–12 cm long (excluding the awns) and 3–5 mm thick, consisting of 4–12 (usually 6–8) fertile spikelets arranged compactly and alternately along the main axis of the spike. The spikelets are sessile, 9–10 mm long and about 3 mm wide. The terminal spikelet is conical, shorter and thinner, about 7 mm long and about 2 mm wide. In one spikelet there are 3–5 florets, of which the lower 1–2 are usually fertile, but there may be up to five fertile florets, giving 5 grains per spikelet. The glumes of the lateral spikelets are ovate-elongated, 7–10 mm long, green to purple-green at heading and flowering, with a striated surface and unevenly wide veins (9–13), sunken into the surface, more or less parallel, two-toothed, one of the teeth being short and blunt, and the other forming an awn up to 18 mm long. The lemmas of the fertile florets are 9–10 mm long, narrowly elliptic, boat-shaped and folded lengthwise in the upper part. The lemmas of the terminal (apical) spikelets have a prominent central awn 4–8 cm long, with 2 sharp teeth at the base, and when mature are less branched than the awns of the glumes. The awns of the lemmas of the sterile terminal florets are strongly reduced. The palea is narrowly ovate-elliptic, with 2 sharp, striated keels ending in a sharp tip. The caryopsis is 6–7 mm long, between closely appressed lemmas

and paleas. Usually the uppermost spikelet of the spike has 3–4 awns, shorter than the spike. At fruiting, the spike disarticulates into its constituent spikelets, with the exception of 1–2 tough spikelets at the base.



The fruit is a dorsiventrally flattened grain with a groove along the entire ventral length. The grain colour is red. It reproduces by seed.

Phenology: Flowering (April–August), fruiting (May–August)

Habitats: Uncultivated and heavily disturbed sites, e.g. fallow lands, roadsides, dry, sandy, grassy slopes, pastures. Distributed throughout Bulgaria at altitudes: 0–1750 m.

Ecology: Least affected or threatened species.

Taxonomy of the species:

Royal Botanic Gardens (<https://powo.science.kew.org/taxon/urn:lsid:ipni.org:names:384583-1>)

The species *Aegilops cylindrica* Host. belongs to division *Magnoliophyta* Cronquist, Takht. & W. Zimm. ex Reveal (Angiosperms), class *Liliopsida* Batsch (Monocotyledons), order *Poales* Small, family *Poaceae* Barnhart (Grasses), genus *Aegilops* L. (Wild wheat).

Synonyms: *Aegilops caudata subsp. cylindrica* (Host) Hegi; *Aegilops caudata var. cylindrica* Fiori; *Aegilops caudata var. hirsuta* Hegi; *Aegilops cylindrica f. brunnea* (Popova) K. Hammer; *Aegilops cylindrica f. brunusica* van Slageren & Eldarov; *Aegilops cylindrica f. ferruginea* (Popova) K. Hammer; *Aegilops cylindrica f. fuliginosa* (Popova) K. Hammer; *Aegilops cylindrica f. gahvayii* Aminov & Eldarov; *Aegilops cylindrica f. garamtil* Aminov & Eldarov; *Aegilops cylindrica f. prokhanovii* (Tzvelev) K. Hammer; *Aegilops cylindrica f. pullusica* van Slageren & Eldarov; *Aegilops cylindrica f. rubiginosa* (Popova) K. Hammer; *Aegilops cylindrica subsp. aristulata* Zhuk.; *Aegilops cylindrica subsp. pauciaristata* (Eig) Chennav.; *Aegilops cylindrica unr. pubescens* Kloos; *Aegilops cylindrica var. albescens* Popova; *Aegilops cylindrica var. aristulata* (Zhuk.) Tzvelev; *Aegilops cylindrica var. brunnea* Popova; *Aegilops cylindrica var. ferruginea* Popova; *Aegilops cylindrica var. flavescens* Popova; *Aegilops cylindrica var. fuliginosa* Popova; *Aegilops cylindrica var. gobustanica* van Slageren & Eldarov; *Aegilops cylindrica var. hirsuta* (Hegi) Hegi; *Aegilops cylindrica var. kastorianum* Karat.; *Aegilops cylindrica var. khizii* Aminov & Eldarov; *Aegilops nova* Winterl ex Borbás; *Aegilops cylindrica var. longiaristata* Lange; *Aegilops cylindrica var. multiaristata* Jansen & Wacht.; *Aegilops cylindrica var. pauciaristata* Eig; *Aegilops cylindrica var. prokhanovii* Tzvelev; *Aegilops cylindrica var. pubescens* Jansen; *Aegilops cylindrica var. rubiginosa* Popova; *Aegilops cylindrica var. rumelica* Velen.; *Aegilops cylindrica var. typica* Eig.; *Aegilops squarrosa var. cylindrica* (Host) Mutel; *Cylindropyrum cylindricum* (Host) Á.Löve; *Cylindropyrum cylindricum subsp. pauciaristatum* (Eig) Á.Löve; *Triticum caudatum subsp. cylindricum* (Host) Asch. & Graebn.; *Triticum cylindricum* (Host) Ces., Pass. & Gibelli; *Triticum cylindricum var. rumelicum* (Velen.) Stoj. & Stef.; *Cylindropyrum cylindricum subsp. cylindricum*; *Triticum cylindricum* Cesati, Pass. & Gib.

Significance of the species *Aegilops cylindrica* Host.

Aegilops cylindrica Host. is a valuable source of genes associated with salt tolerance. It has been established that the D genome in *Ae. cylindrica* Host. possesses genes such as *AecHKT1;5*, *AecSOS1*, *AecNHX1* and *AecVP1*, responsible for preventing the transport of Na ions into the tissues of the roots and coleoptiles of the plant (Kiani et al., 2015). Two genotypes have been identified – USL26, which is tolerant to salinity, and genotype K44, which is sensitive (Arabbeigi et al., 2014). This species is the subject of various studies by scientists and breeders, and although it is not the most sought after in breeding materials involving interspecific wheat hybridizations, breeding programmes are looking for new sources for improving not only resistance. Studies show that the species has the ability to absorb from the soil essential minerals such as Mn, Fe, Ca, Mg, K, Na, Cr, Ni, Co, and to store them in the grain (Mohammad et al., 2015). Prins et al. (2016), in a study of the diversity of enzymes in the Calvin cycle among genera and species of the tribe *Triticeae*, indicate *Aegilops cylindrica* Host. as an enzyme system with higher assimilation parameters, which makes it a potential donor of genes related to the improvement of photosynthesis. Genes associated with the presence of subunits of high molecular weight storage proteins have also been isolated in *Ae. cylindrica*, which could replace the well-characterized similar genes from bread wheat, leading to the use of a wider range of high molecular weight subunits exhibiting greater diversity (Wan et al., 2002; Kan et al., 2006; Sun et al., 2006; Farkhari et al., 2007; Zhang et al. 2008).

In other studies on proteins and the respective responsible genes, new genetic resources for gluten have been identified. Different types of low molecular weight subunits have been found in examined accessions of *Ae. cylindrica* in the glutenins, which represent 60% of the storage proteins in the endosperm of wheats and play an important role in dough quality (Wan et al., 2002; Liu et al., 2003; Khabiri et al., 2012; Xin et al., 2015).

In a study of variation in susceptibility to wheat dwarf virus in wild and cultivated wheats (*Triticum* sp. and *Aegilops* sp.) it was found that plants of *Ae. cylindrica* Host. inoculated with wheat dwarf virus are initially severely affected, but subsequently show increased tillering and leafiness, and therefore could be useful genetic resources for improving resistance to wheat dwarf virus (Nygren et al., 2015).

Breeding lines between wheat and *Ae. cylindrica* Host. are of interest to breeders worldwide, also in relation to reducing plant height as well as earliness (Yuhai et al., 2017). One of these donors is line TA001, which is the result of a hybridization between the common bread wheat cultivar “Yannong 15” and the amphiploid SDAU18, which in turn is the result of a cross between the species *Aegilops ventricosa* × *Aegilops cylindrica*. In the study of this line, at least 30 genes responsible for plant dwarfing were identified, including the genes *Rht1*, *Rht3*, *Rht1s*, *RhtKrasnodari1*, *RhtT.aeth*, *RhtHighburg*, *Rht2*, *Rht10*, *RhtAibian1*, *Rht4*, *Rht5*, *Rht6*, *Rht7*, *Rht8*, *Rht9*, *Rht11*, *Rht12*, *Rht13*, *Rht14*, *Rht15*, *Rht16*, *Rht17*, *Rht18*, *Rht19*, *Rht20*, *Rht21*, *Rht22*, *Rht_R107*, *Rht-dp*,

Rht23, and Rht-NM9. Only a few genes, such as Rht1, Rht2, Rht8, and Rht9 have been used more widely in breeding for wheat dwarfing.

Aegilops cylindrica Host. also participates in breeding not only in wheat, but also in barley. One such example is barley breeding lines based on a 7H deletion, which have originated with the involvement of chromosome 2C of *Aegilops cylindrica* Host. (Shi *et al.*, 2000; Nasuda *et al.* 2005; Molnár *et al.*, 2016). It has been established that the same chromosome 2C from *Ae. cylindrica* Host., also has the ability to induce chromosome breakage in common wheat (*Triticum aestivum* L.). This trait is used by breeders in the development of hybridization lines in breeding for resistance to Fusarium head blight. An example of this is line T3AS-Lr7S, created through chromosome translocation and complex involvement of other species (McCain *et al.*, 1990; Farr and Rossman, 2015). Natural interspecific hybridizations and backcrosses between *Aegilops cylindrica* Host. and *Triticum aestivum* L. can lead to gene introgression (Kozub *et al.*, 2004). It has been established that such hybrids may possess herbicide resistance (Hegde and Waines 2004), as well as resistance to fungal diseases and increased tolerance to insect pests (Schoenenberger *et al.*, 2006).



Assoc. Prof. Gergana Desheva, PhD and Chief Assistant Prof. Bozhidar Kyosev, PhD during an expedition for collecting Aegilops accessions in 2024 in Bulgaria.

The increased interest in the species *Aegilops cylindrica* Host. as a potential donor of genes for improving wheat and barley is a prerequisite for many gene banks to set as a main priority in their activities the “*in situ*” and “*ex situ*” conservation of crop wild relatives, including the above-mentioned species. In Bulgaria, a collection of *Aegilops* species is maintained under long-term “*ex situ*” storage conditions in the National Gene Bank at the Institute of Plant Genetic Resources in Sadovo. The diversity in the *Aegilops* collection is represented by 14 plant species. The total number of *Aegilops* accessions amounts to 438, originating from 19 countries, of which 365 accessions are of Bulgarian origin. The species *Aegilops cylindrica* Host. includes 63 accessions, 59 of which represent populations collected from different regions of our country.

In 2023, project BG-175467353-2023-13-0018, KP-06 H76/3 “Study of the genetic diversity of *Aegilops* species in the flora of Bulgaria” was approved for funding by the Bulgarian National Science Fund, one of the specific objectives of which is the collection and conservation (*ex situ*) of *Aegilops* species from the flora of Bulgaria. Enrichment with new genetic plasma of *Aegilops* species, and their in-depth study and provision of free access to them through their inclusion in the exchange collection, will lead to a higher scientific and societal impact, in line with the function of the gene bank to serve a large number of users at regional, national and international level – scientists, breeders, NGOs, environmental organizations, students and pupils in the field of agricultural and biological sciences.

Acknowledgements:

The study is financially supported by the Bulgarian National Science Fund, Ministry of Education and Science, under project KP-06-H76/3 “Study of the genetic diversity of *Aegilops* species in the flora of Bulgaria”.

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