

## Sequencing the *Aegilops tauschii* genome



**Figure 1.**

Spike of *Aegilops tauschii* ssp. *strangulata* accession AL8/78, the accession sequenced in this project, collected by V. Jaaska (Dept. of Botany, Institute of Zoology and Botany, Tartu, Estonia) in Yerevan, Armenia, near the Hrazdan River. The moniliform spikes, a characteristic of *Ae. tauschii* ssp. *strangulata*, are less expressed in Transcaucasia than in eastern Caspian Iran, the center of distribution for *Ae. tauschii* ssp. *strangulata*.

m above sea level; a few populations reach even higher altitudes (VAN SLAGEREN 1994).

*Aegilops tauschii* consists of two phylogenetic lineages, designated as T or L1 and S or L2 broadly affiliated with *Ae. tauschii* ssp. *tauschii* and *Ae. tauschii* ssp. *strangulata*, respectively (DVOŘÁK et al. 1998; MIZUNO et al. 2010; WANG et al. 2013). The L2 lineage includes primarily *Ae. tauschii* ssp. *strangulata* but also the *Ae. tauschii* ssp. *tauschii* var. *meyeri* and some populations of var.

*AEGILOPS TAUSCHII* COSS. is a diploid ( $2n=14$ ), self-pollinating (cleistogamic) goatgrass species in the Triticeae tribe of the grass family. Its natural range is from eastern Turkey to China and Pakistan and a few naturalized populations have been reported in central and northeastern Syria (VAN SLAGEREN 1994). *Aegilops tauschii* encompasses four morphological varieties, of which three, var. *typica*, var. *anathera*, and var. *meyeri*, are grouped taxonomically into *Ae. tauschii* ssp. *tauschii*, while the fourth is the monotypic *Ae. tauschii* ssp. *strangulata* (EIG 1929; KIHARA & TANAKA 1958). *Ae. tauschii* ssp. *tauschii* is found throughout the distribution of the species whereas *Ae. tauschii* ssp. *strangulata* grows in a narrow band along the southern Caspian and

in Transcaucasia. *Aegilops tauschii* is a plastic species growing from about 1800

*typica* (LUBBERS et al. 1991; DVOŘÁK et al. 1998; WANG et al. 2013). The L1 lineage consists of *Ae. tauschii* ssp. *tauschii* var. *anathera* and the remaining populations of *Ae. tauschii* ssp. *tauschii* var. *typica* (DVOŘÁK et al. 1998). The two lineages are genetically strongly differentiated, and there are virtually no intermediate forms between them (WANG et al. 2013). The L2 lineage occupies low altitudes, less than 400 m above sea level, whereas most of the *Ae. tauschii* ssp. *tauschii* occupies altitudes higher than 400 m above sea level (WANG et al. 2013).

The genome of *Ae. tauschii* is designated by the letter D. The estimates of its size range from 4.02 to 4.98 Gbp (REES & WALTERS 1965; ARUMUGANATHAN & EARLE 1991; JIA et al. 2013). As much as 90% of the genome may consist of repeated sequences.

*Aegilops tauschii* donated the third (D) genome of hexaploid wheat (*Triticum aestivum* L., genomes BBAADD) (KIHARA 1944; MCFADDEN & SEARS 1946). It is a widely believed hypothesis that *T. aestivum* originated by hybridization of domesticated tetraploid emmer (*T. turgidum* L. ssp. *dicoccon*) (MCFADDEN & SEARS 1946; JAASKA 1978; PORCEDDU & LAFIANDRA 1986; KIMBER & SEARS 1987) with *Ae. tauschii* ssp. *strangulata* (NISHIKAWA 1973; NISHIKAWA et al. 1980; JAASKA 1980; NAKAI 1979; LUBBERS et al. 1991; LAGUDAH et al. 1991; DVOŘÁK et al. 1998; DVOŘÁK et al. 2012). However, the belief that the tetraploid ancestor of *T. aestivum* was domesticated emmer has been recently questioned (DVOŘÁK et al. 2012) with a suggestion that the tetraploid ancestor was free-threshing. Most *Ae. tauschii* accessions identified by WANG et al. (2013) as being closely related to the wheat D genome were botanically *Ae. tauschii* ssp. *tauschii*. It therefore seems more correct to suggest that the D genome was contributed by the L2 lineage (sublineage L2E as defined by WANG et al. 2013).

*Aegilops tauschii* ssp. *strangulata* accession AL8/78 (Fig. 1) collected in Armenia was chosen in 1989 for the construction of a physical map because an RFLP-based diversity study suggested it was the most closely related to the wheat D-genome (DVOŘÁK et al. 1998). For this reason, it is used here for physical-map-based sequencing of the *Ae. tauschii* genome. In a recent, more extensive SNP-based diversity study, it was shown that AL8/78 belongs to the lineage L2 (sublineage L2W) and *Ae. tauschii* accessions even more closely related to the wheat D genome than AL8/78 were uncovered in sublineage L2E (WANG et al. 2013).

— Summary by Jan Dvořák

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