

## Evolution of the S-genome in *Triticum* and *Aegilops*

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Five diploid *Aegilops* species of the *Sitopsis* section: *Ae. speltoides*, *Ae. longissima*, *Ae. sharonensis*, *Ae. searsii*, and *Ae. bicornis*, two tetraploid species *Ae. peregrina* and *Ae. kotschy* (*Aegilops* section) and hexaploid *Ae. vavilovii* (*Vertebrata* section) carry different variants of the S-genome. The B- and G-genomes of polyploid wheats are also the derivatives of the S-genome. Evolution of the S-genome species was studied using C-banding and fluorescence in situ hybridization (FISH) with DNA probes representing 5S and 18S-5.8S-26S rRNA gene families and tandem repeats pSc119.2, pAesp\_SAT86, Spelt-1, Spelt-52, pAs1, pTa-535, and pTa-s53. To align the C- and FISH patterns we used the microsatellites (CTT)<sub>10</sub> and (GTT)<sub>9</sub>, which are major components of the C-heterochromatin in cereals. According to the results obtained, diploid species split into two groups corresponding to *Emarginata* and *Truncata* sub-sections, which differ in the C-banding patterns, distribution of rDNAs and other repeats. The B- and G-genomes of polyploid wheat are shown to be most similar to the S-genome of *Ae. speltoides*. The genomes of allopolyploid wheat evolved as a result of different species-specific chromosome translocations, sequence amplification, elimination and re-patterning of repetitive DNA sequences, which occurred independently in polyploid wheat and in *Ae. speltoides*. The 5S rDNA locus on chromosome 1S was probably lost in ancient *Ae. speltoides* prior to formation of Timopheevii wheat, but after the emergence of ancient emmer. Evolution of *Emarginata* species was associated with an increase of C-banding and (CTT)<sub>10</sub>-positive heterochromatin, amplification of Spelt-52, re-patterning of the pAesp\_SAT86, and a gradual elimination of all D-genome-specific repeats. The emergence of *Ae. variabilis* and *Ae. kotschy* did not lead to significant changes of the parental S\*-genomes. However, partial elimination of 45S rDNA repeats from 5S\* and 6S\* chromosomes and alterations of C-banding and FISH-patterns were detected in both tetraploid species. Similarity of the S<sup>v</sup>-genome of *Ae. vavilovii* with the S<sup>s</sup> genome of diploid *Ae. searsii* confirmed the origin of this hexaploid. A model of the S-genome evolution is suggested.