

Inter-varietal Chromosome Substitution

Bread wheat (*Triticum aestivum*) can tolerate changes in its basic chromosome number due to its allohexaploid constitution ($2n = 42$). Monosomics are the most common form of wheat aneuploids and they can be found at a frequency as high as 2–3% of the seed of commercial wheat varieties. This property was put into use for genetic analysis by the pioneering work of Professor E. Sears, who obtained a complete set of aneuploids including monosomics, nullisomics, tetrasomics and lines with telocentric chromosomes in a spring variety, Chinese Spring. **Chromosome substitutions between wheat (*Triticum aestivum* L.) varieties provide an effective mean of analyzing the genetics of quantitative characters. They are widely used to study the influence of an individual chromosome on quantitative trait loci (QTLs) such as grain yield, bread-making quality, photoperiodic and vernalization response, plant height and disease resistance.** Credit is due to Sears (1953) and Kuspira and Unrau (1957) for the development of the first inter-varietal substitution lines of wheat. **Sears developed the technology, via a backcrossing scheme to monosomics, for substituting individual chromosomes from one variety to another to create single chromosome substitution lines (SLs).** The task is laborious and timeconsuming, requiring the prior creation of monosomic series. The majority of the first sets of chromosome substitutions were developed using Chinese Spring as recipient. However, Chinese Spring does not carry favorable characters, and it is therefore not used widely in agriculture. The production of inter-varietal substitution lines involving donor and recipient varieties with contrasting characters was needed to identify genes of agronomic importance. One set of substitution lines using Spring wheat var. Saratovskaya 29 and Yanetzki's Probat as recipient and donor, respectively, was produced in Novosibirsk, Russia. German var. Yanetzki's Probat (YP) is also a spring variety with contrasting qualities and increased grain protein content. This set of substitutions was efficiently used to estimate the genetic contribution of donor chromosomes.

One disadvantage of using aneuploid techniques for the development of precise genetic stocks was the difficulties in verifying the correctness of substitution lines, although phenotypic, molecular and cytological observations could help.

Example: Two monosomic alien substitution lines (MAS lines, $2n=41=40+5R$) of wheat *Triticum aestivum* L. cv. 'Saratovskaya 29' have inter-varietal substitution lines for chromosomes 5A and 5D. In the MAS lines, chromosomes 5A or 5D of 'Saratovskaya 29' were replaced by homoeologous univalent chromosome 5R of rye *Secale cereale* L. cv. 'Onokhoiskaya,' which bears the *Hp* marker gene coding for hairy peduncle. The donors included 18 spring and winter wheat varieties. The MAS lines were developed by crossing monosomic lines of 'Saratovskaya 29' for chromosomes 5A and 5D (a recent variety) to a wheat-rye substitution line of 'Saratovskaya 29' 5R(5D) (a donor variety) followed by cytological and morphological selection of plants with chromosome configuration $20II + 5RI$ in metaphase I of pollen mother cells from F-1 and F-2 plants with slightly hairy peduncles. Use of MAS lines with the *Hp* marker gene allows acceleration and abbreviation of cytological analysis and elimination of the probability of

‘univalent switch’ in the course of the development of substitution lines. The method was applied to the development of 22 ‘Saratovskaya 29’ lines with inter-varietal substitution for chromosomes 5A and 5D. Fourteen and thirteen microsatellite markers located in chromosomes 5A and 5D, respectively, were used to prove the authenticity of the inter-varietal substitution lines. According to these markers, 21 substitution lines from 22 studied were correct.