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Short Communication

'SELECTION 212' — A NEW RUST RESISTANCE SOURCE FROM RYE (*Secale cereale*)

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The search for new genes from secondary and tertiary genepool and incorporating them into cultivar helps in genetic diversification. Rye (*Secale cereale*, RR, 2n = 14) is known for several valuable traits namely, resistance to diseases and pests, hardiness, high photosynthetic activity. With permutation and combination, in BC1F7 generation, cytologically stable plants were identified. Studies revealed identification of a line "Selection 212" which was found resistant to both leaf and stem rust diseases.

Key words: Wheat, *Triticum aestivum, Secale cereale*, resistance, stem rust, leaf rust

Building multiple disease resistance into high yielding varieties is one of the main strategies for improving productivity and yield stability as well as restrict the use of chemicals in controlling diseases. The search for new genes, so called gene hunting, in wild-species and incorporating them into present day cultivars helps in genetic diversification. For enhancing the genetic potential of cultivated wheats, the secondary and tertiary gene pool of wheat was considered important (Mujeeb- kazi, 1995). Rye (*Secale cereale*, RR, 2n = 14), a species of tertiary gene pool is known for several valuable traits like resistance to diseases and pests, hardiness, high protein, high photosynthetic activity, high spikelet number and plant vigour (Rajaram *et al.*, 1983).

In an endeavour to tap the genetic potential of rye, attempts were made by exploiting recombination between homoeologous chromosomes. In this approach, a monosomic line (2n = 41) of cultivar Chinese Spring deficient for chromosomes 5B was crossed with rust resistant, self compatible, amber seeded strain of diploid (2n = 14) rye obtained through gamma - radiation from a red seeded self-incompatible rye, accession number PI366498, procured from USDA. A wheat-rye F_1 hybrid with 27 chromosomes which lacked chromosome 5B of *Triticum aestivum* exhibited extensive chromosome pairing of homoeologous chromosomes (Table 1). This F_1 hybrid was backcrossed to a hexaploid wheat cultivar Sonalika, BC_1F_2 families of (CS mono 5B × rye) F_1 × Sonalika produced a spectrum of aneuploids. Segregating populations were grown at Wellington (South India), a hot spot for rust diseases and only rust resistant derivatives were selected. In BC_1F_7 generation cytologically stable ($2n = 42 = 21^{II}$) plants were identified. A line found resistant to leaf rust (*Puccinia recondita* f.sp. *tritici*) and stem rust (*Puccinia graminis* f.sp. *tritici*) was designated 'Selection 212' (Singh, 1991).

'Sel. 212' has features like aestivum wheat. It is 110 cm tall having amber, long, bold, lustrous seeds. The 1000 kernel weight ranges from 40-44 gms. The days to flowering and

Table 1. Meiotic chromosome pairing in the F_1 hybrids involving monosomic 5B of Chinese Spring and amber rye strains

No. of Chromosome	No. of cells analysed	Univalents	bivalents	trivalents	tetravalents	Chaismata
28	1032	24.27 ± 0.07	1.86 ± 0.04	0.02 ± 0.004	-	1.9 ± 0.04
27	231	10.18 ± 0.17	6.51 ± 0.12	1.14 ± 0.07	0.09 ± 0.02	12.34 +–.0.17

maturity are slightly more than Sonalika i.e. 84 days and 126 days respectively. Sel. 212 is semi-erect in early growth stages having good straw strength but shy tillering. leaves are slightly waxy. Spikes are medium long and medium dense with pseudo black chaff. Auricles have purple pigmentation. Sharma (1997) generated the information regarding effectiveness of this stock to leaf and stem rust pathotypes and inheritance and chromosome location of rust resistance genes in this wheat-rye recombinant.

Seedling tests against 25 pathotypes of leaf rust and 20 pathotypes of stem rust suggested that Sel. 212 is resistant to all the pathotypes. Adult plant tests with most virulent pathotype 77-5 and 40A of leaf and stem rust pathogen respectively also showed high level of field resistance.

Inheritance studies in seedlings against highly virulent pathotypes (77-1, 77-3, 77-4 and 77-5 revealed that a recessive undesignated gene is providing resistance to leaf rust. Inheritance studies at adult plant stage in field with most virulent pathotype 77-5 suggested the presence of an additional adult plant resistance gene, which is likely to be *Lr34* probably derived from Chinese Spring, a parental line of Sel. 212. When inheritance was studies against two selected stem rust pathotypes 122 and 40, it showed that an unknown resistance gene is providing resistance to stem rust. Adult plant inheritance studies for stem rust resistance against pathotype 40A suggested the presence of an adult plant resistance gene *Sr2* in the stock which may have derived from Sonalika, the parent of Sel. 212. Test of allelism detected the presence of stem rust resistance gene *Sr11*, may also be derived from Sonalika.

Linkage analysis established the close linkage between undescribed leaf and stem rust resistance genes. Chromosome location studies using monosomic analysis located these linked leaf and stem rust resistance genes in chromosome 2B of Sel. 212. Cytological analysis of F_1 hybrids of Sel. 212 and parental rye indicated the presence of rye chromatin in Sel. 212.

These undescribed linked leaf and stem rust resistance genes are tentatively named Lr Sel. 2121 and Sr Sel. 2121 respectively. These leaf and stem rust resistance genes effective to all existing leaf and stem rust pathotypes respectively are expected to be of immense value in diversifying the genetic base of rust resistance in the country. The transfer of these linked leaf and stem rust resistance genes would facilitate the breeders in incorporating these novel resistances to both the pathogens.

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