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Cytogenetics and genetics characterization of *Aegilops markgrafii* derived leaf rust resistance in wheat

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Wheat leaf rust caused by the fungus *Puccinia triticina* Eriks is one of the most devastating fungal diseases which has the potential to cause up to 65% yield losses in susceptible cultivars. Genetic resistance is the most economical method of minimizing rust losses. *Aegilops markgrafii* a diploid (2n=2x=14, genome CC) wild relative of wheat is a promising source of genes for resistance to leaf rust. A number of *Ae. markgrafii* Introgression lines (ILs) carrying leaf rust resistance were developed at Indian Agricultural Research Research Institute, New Delhi. One such Introgression Line ER-9-3-700 carrying leaf rust resistance showed wide spectrum resistance against 15 *Puccinia triticina* pathotypes (*Pt*). Cytological analysis revealed normal meiosis with 21 bivalents and, therefore, ER-9-3-700 was selected for genetic analysis of leaf rust resistance. ER-9-3-700 was crossed with susceptible cultivar Agra Local (AL). All the F_1 plants showed resistance against pathotype 77-5 showing dominant nature of leaf rust resistance. F_2 population derived from the cross ER-9-3-700 x AL was screened against pathotype 77-5 at seedling stage in glasshouse. Out of 323 plants screened 249 were resistant and 74 were susceptible showing Mendelian segregation 3 resistant: 1 susceptible (p-value of 0.686 at $\chi^2_{3:1}$= 0.752, 5% level of significance). Results were validated in $F_{2:3}$ families which segregated into expected ratio of 1(resistant family): 2 (segregating family): 1(susceptible family) with p-value of 0.173 at $\chi^2_{1:2:1=}$ 3.50. The results of genetic analysis showed that leaf rust resistance in IL ER-9-3-700 is controlled by a single dominant gene.

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