**Abstract**

The high yielding potential associated with IRS.IBL translocation involving the short arm of rye chromosome 1R and the long arm of wheat chromosome 1B were well exploited world over for developing disease resistant and high yielding wheat varieties. This was due to the translocation of the effective disease resistance linked genes *Sr*31 for resistance to stem rust (*P. graminis* f. sp. *tritici*), *Lr*26 for resistance to leaf rust (caused by *Puccinia triticinia*), *Yr*9 for resistance to stripe rust (*P. striiformis* f. sp. *tritici*), *Pm*8 for resistance against powdery mildew (caused by *Erisiphe graminis* f. sp. *tritici*) along with useful agronomic traits. However now virulent pathotypes have been reported which has overcome these rust resistance genes. The *Sr31* gene complex has close linkage with the genes controlling secalins (Sec-1). Thus *Sec-1* acts as a marker for the identification of *Sr*31*, Lr*26*, Yr*9 and *Pm*8 genes. SDS - PAGE was used to examine the presence of 1BL.1RS translocation in six Indian wheat genotypes *viz.,* HP 1205, HD 2329, HD 2285, WH 147, Lok-1 and J 24 introgressed with *Sr31+* gene complex with the aim to eliminate the lines carrying these genes, since it is tightly linked to poor baking quality. The SDS - PAGE results showed that all the lines carry *Sec-l* band and are therefore likely to carry the IBL.IRS translocation and the linked genes *Sr*31, *Lr*26, *Yr9* and *Pm*8. This technique could be well exploited to detect the presence of linked genes *Sr*31, *Lr*26, *Yr*9 and *Pm*8 in wheat cultivars as it is an easy, efficient, faster and economical tool to eliminate the lines with 1BL.1RS translocation and developing wheat varieties for better end use quality and reducing the risk to Ug99 stem rust race threat (**Keywords:** *Triticum aestivum*, *Puccinia* sp.*,* protein marker, Ug99).

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