

**DETERMINATION OF APHID RESISTANCE GENES IN LOCAL BREAD  
WHEAT (TRITICUM AESTIVUM L.) VARIETIES OF UZBEKISTAN  
USING DNA MARKERS**

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**Abstract** In this paper, we report the determination of genetic polymorphisms between 30 bread wheat varieties commonly cultivated in Uzbekistan using six SSR markers. All SSR markers were associated with Russian wheat aphid (*Diuraphis noxia*) resistance genes (*Dn*) such as *Dn1*, *Dn2*, *Dn4*, *Dn5*, *Dn6*, *Dn8*, *Dn9*, *Dnx* and *Dn626580*.

**Keywords:** Russian wheat aphid, bread wheat, *Triticum aestivum* L., SSR markers, resistance.

Aphids are major insect pests in wheat that cause yield loss directly (35-40%) by sucking the plant sap and indirectly (20-80%) through viral transmission [1]. Plants activate the signaling system and increase the concentration of such compounds as jasmonic and salicylic acids and ethylene during the pest is sucking plant sap. Phosphoinositol, lipoxygenase, and NADF-oxidase signaling systems were activated when two biotypes of *D.noxia* damaged plants containing the *Dn7* resistance gene. The gene expression was higher in the barley plants infected with the RWA1 biotype of aphid compared with the higher virulent biotype RWA2 [2].

Recently, molecular breeding such as marker-assisted selection (MAS) were carried out to facilitate the genetic pyramiding of several genes/QTL into a single

genotype to achieve resistance to the different biotypes of the same species [3, 4]. This allows replacing the complex phenotypic screening of plant resistance with a rapid and highly efficient methodology [5, 6]. For the implementation of marker-assisted selection for aphid resistance, first, DNA markers or genes associated with resistance traits should be identified. In practice, several types of DNA markers are used to identify QTLs associated with economically important traits in plants. The types of DNA markers can influence the research results.

The genomic DNA was isolated from the young leaf tissues using the CTAB method [7]. The quantity and quality of the genomic DNA were determined by comparison with a standard DNA of lambda phage (50 ng/ $\mu$ l) in a 0.8% agarose gel. The PCR analysis was conducted using six SSR markers such as Xgwm44, Xgwm111, Xgwm337, Xgwm635, Xgwm642, and WMC473 associated with certain aphid resistance genes. The size of PCR amplicons were visualized in a 3% agarose gel under UV light.

Five different alleles were amplified for marker Xgwm44 across all wheat genotypes, of which the 155 bp allele was genetically associated with resistance to aphid pests [8]. This resistance allele (Xgwm44\_155) was identified in nine wheat varieties. Besides, the Xgwm44\_139 allele was associated with yellow rust resistance according to [9], and it was observed in four wheat varieties.

The results will allow breeders for the rapid creation of new wheat varieties through marker-assisted selection for the resistance to aphids.

### References

1. Aslam M, Razaq M, Akhter W, Faheem M, Ahmad F (2005) Effect of sowing date of wheat on aphid (*Schizaphis graminum* RONDANI) population. *Pak Entomol* 27: 79–82.
2. Botha A.-M., Swanevelder Z.H., Lapitan N.L.V. Transcript profiling of wheat genes expressed during feeding by two different biotypes of *diuraphis noxia*.// *Environ. Entomol.*, 2010, 39(4) : - P. 1206-1231.

3. Melchinger, A.E. Use of molecular markers in breeding for oligogenic disease resistance. *Plant Breed.* 1990, 104, 1–19.
4. Mundt, C.C. Pyramiding for resistance durability: Theory and practice. *Phytopathology* 2018, 108, 792–802.
5. Collard, B.C.Y.; Mackill, D.J. Marker-assisted selection: An approach for precision plant breeding in the twenty-first century. *Philos. Trans. R. Soc. B Biol. Sci.* 2008, 363, 557–572.
6. Paux, E.; Faure, S.; Choulet, F.; Roger, D.; Gauthier, V.; Martinant, J.P.; Sourdille, P.; Balfourier, F.; Le Paslier, M.C.; Chauveau, A.; et al. Insertion site-based polymorphism markers open new perspectives for genome saturation and marker-assisted selection in wheat. *Plant Biotechnol. J.* 2010, 8, 196–210.
7. Paterson AH, Brubaker CL, Wendel JF (1993). A rapid method for extraction of Cotton (*Gossypium* spp) genomic DNA suitable for RFLP or PCR analysis. *Plant Mol. Biol. Rep.* 11:122-127.
8. Tocho, E.; Ricci, M.; Tacaliti, M. S.; Giménez, D. O.; Acevedo, A.; Lohwasser, U.; Börner, A.; Castro, A. M. (2012). Mapping resistance genes conferring tolerance to RWA (*Diuraphis noxia*) in barley (*Hordeum vulgare*). *Euphytica*, 188(2), 239–251. doi:10.1007/s10681-012-0710-4
9. Xing LI, Wen-xiang YANG, Ya-ning LI, Da-qun LIU, Hong-fei YAN, Qing-fang MENG, Ting ZHANG. A SSR Marker for Leaf Rust Resistance Gene Lr19 in Wheat. *Agricultural Sciences in China*. Volume 5, Issue 2, 2006. Pages 111-115. [https://doi.org/10.1016/S1671-2927\(06\)60027-8](https://doi.org/10.1016/S1671-2927(06)60027-8).