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Fine mapping and marker development of major quantitative trait loci that confers resistance against Hessian fly in Wheat

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Hessian fly (HF) is a major invasive wheat pest in North Africa, southern Europe, North America, and northern Kazakhstan that cause massive economical damage and reduce the grain yield and quality every year. At least 35 different HF-R genes, from H1 to H34 and Hdic, have already been genetically identified. Most of them have been mapped within cluster of NB LLR encoding genes but no HF-R genes have yet been cloned. H34 is a Hessian fly resistance gene, confers high level of resistance against many Hessian fly biotypes. So, it is need of time to develop resistant wheat cultivars adapted to this region to minimize the losses caused by HF.

Methodology and Theoretical Orientation: Previously, it was detected on distal end of short arm of chromosome 6BS using recombinant inbred lines (RILs) from a cross between Ning7840 x Clark. After that, another RIL F5

population was developed from a cross between two of the RILs (RIL118 and RIL 115) to fine map H34. The RIL 118 carries H34 from Clark whereas RIL115 carries the susceptibility allele. Initially, two flanking SNPs were identified at the H34 region using the new RIL population and heterozygous RILs were identified to generate a new F2 population. After screening >3000 F2 plants using the flanking markers, >100 F2 recombinants were selected. Their F3 families were phenotyped to further narrowing the flanking region of H34 to the minimum.

Findings and Conclusion: This study resulted in development of diagnostic markers linked to H34 gene for marker-assisted selection that will lead to the cloning of H34.