

Genetic Analysis and Marker-Assisted Selection using KASP Markers of a Double Haploid Bread Wheat Population

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Abstract

Bread Wheat breeding can rely on different methods, the main objective of this study was to combine Marker Assisted Selection with haplodiploidisation to accelerate the breeding process, focusing on the introduction of high yield, rust resistance genes (*Lr34* and *Lr46*) and dwarf gene *Rht1* gene. This approach was designed to be efficient and precise, significantly speeding up the development of wheat lines with desirable traits by reducing the time and effort typically required in conventional breeding methods. In this context, the concept of genetic gain which is the result of the interaction between heritability, phenotypic variation, selection intensity, and cycle length was rigorously applied. The selection was conducted using ANOVA, PCA, MGIDI analysis, and KASP markers. Analysis of variance revealed significant differences among the parental and the DH lines for all agronomic traits, indicating substantial genetic diversity within the DH lines. From the DH lines, 54 DH lines were selected for their optimal combination of agronomic performance, including early maturity

and high yield potential. Additionally, KASP analysis enabled the selection of one DH ideotype carried *Lr34*, *Lr46*, and *Rht1*. 61 DH lines carrying pyramided resistance genes (*Lr34*, *Lr46*) and the dwarfing gene (*Rht1* and or *Rht2*) based on the presence of favourable marker alleles were identified. Among these selections, 13 DH lines were identified as having the ideal combination of rust resistance, dwarfing gene alleles, and high yield potential. These selections represent a significant advancement in terms of earliness and yield, key traits for improving wheat productivity across diverse environments.

Keywords: *Triticum aestivum* L, Double haploid, Agronomic traits, MAS, MGIDI index.

Abbreviations: DH: Doubled haploid

MAS; Marker-Assisted Selection