

Contributions of DNA Molecular Marker Technologies to the Genetics and Breeding of Wheat and Barley*

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- I. INTRODUCTION
- II. MOLECULAR MARKERS IN GENETIC DIVERSITY STUDIES IN WHEAT AND BARLEY
 - A. First and Second Generation DNA Marker Systems
 - B. Application of Markers to Genetic Diversity Assessment
- III. MOLECULAR MARKERS FOR CULTIVAR IDENTIFICATION
 - A. Statutory Testing
 - B. Essential Derivation

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- IV. MARKER ASSISTED SELECTION
 - V. MARKER-BASED GENOTYPING IN CROP BREEDING AND GENETICS
 - A. The Bottleneck of DNA Extraction
 - B. Current Developments in Rapid High Volume Marker Systems
 - C. Third Generation Marker Technologies
 - 1. Single Nucleotide Polymorphisms (SNPs)
 - 2. SNP Recognition within a PCR Product
 - TaqMan and Molecular Beacon*
 - Oligonucleotide Ligation Assay*
 - Oligonucleotide Microarrays*
 - Dynamic Allele-Specific Hybridization*
 - 3. SNP Recognition at the 5' End of the PCR Product
 - 4. Invasive Cleavage by Oligonucleotide Probes
 - VI. THE FUTURE OF MOLECULAR GENOTYPING IN CROP BREEDING AND GENETICS
- LITERATURE CITED

I. INTRODUCTION

Two decades ago, Botstein et al. (1980) described the first DNA profiling technique, restriction fragment length polymorphisms (RFLP), and soon drew attention to the “implications of a virtually unlimited source of genetic polymorphisms for breeding practice” (Soller and Beckmann 1983). The “three major areas of potential marker utilization” were defined as: “(1) varietal and parentage identification, (2) identification of genetic loci affecting quantitative economic traits; and (3) genetic improvement programs, including screening and evaluation of germ-plasm resources, introgression, improvement of commercial hybrids and within population selection.” Molecular markers, at the start of the new millennium, not only have met these expectations, but are opening new horizons unthinkable at the time. Extensive RFLP mapping in wheat (*Triticum aestivum*) and barley (*Hordeum vulgare*) has been carried out throughout the 1990s (Chao et al. 1989; Liu and Tsunewaki 1991; Graner et al. 1991; Heun et al. 1991; Anderson et al. 1992; Devos et al. 1992; Wang et al. 1992; Devos and Gale 1993a; Devos and Gale 1993b; Devos et al. 1993; Xie et al. 1993; Chen et al. 1994; Hohman et al. 1994; Gale et al. 1995; Nelson et al. 1995a,b,c; Van Deynze et al. 1995; Gill et al. 1996; Jia et al. 1996; Marino et al. 1996; Blanco et al. 1998), providing the framework for subsequent genetic analyses relying on polymerase chain reaction (PCR)-based markers.

The advent of PCR (Saiki et al. 1988) and the resulting exponential increase of marker systems suitable for genetic analyses (Table 5.1) has