1 Introduction

Since the first reported linkage of an agronomically important trait (a quantitative trait locus affecting seed weight) to a simply controlled gene (seed color) in common bean by Sax (1923), it has taken more than 60 years for genetic markers to become a qualified tool for widely optimizing genotype building in plant breeding programs. With the advent of molecular marker technology, the identification of genetic markers displaying linkage to any genetically inherited trait became feasible. However, most types of molecular markers, though nowadays PCR-based, are still too impractical to be used in large-scale marker-assisted selection (MAS) schemes due to the complexity of the assay preventing the appropriate automation, insufficient robustness or inadequate level of detected polymorphism (Koebner and Summers 2003). Due to their high polymorphic information content, sequence-tagged microsatellite sites are presently the most appropriate marker class for MAS. The future development of single nucleotide polymorphism (SNP) markers will provide access to affordable and high-throughput genotype determination assays and automated data analyses that are crucial for breeders’ acceptance of MAS. MAS will then increasingly be applied to obtain improved efficiency and effectiveness in the selection of genotypes with traits that are difficult and expensive to phenotype, for the pyramiding of disease resistance genes in single genotypes, and for the carefully directed choice of parental lines in crossing programs allowing a controlled combination of alleles targeted for selection.

2 Requirements of Markers for Marker-Assisted Selection

Key issues in successful deployment of molecular markers in MAS are as follows:

1. Markers should co-segregate or map as close as possible to the target gene (within 2 cM), in order to have low recombination frequency between the
target gene and the marker. A better estimate of map distance between the
target gene and the marker will be obtained by analysing further mapping
populations which have genotypes in common with those used in the ini-
tial mapping population. Accuracy of MAS will be improved if, rather than
a single marker, two markers flanking the target gene are used (Peng et al.
2000).
2. For unlimited use in MAS, markers should display polymorphism between
genotypes that have and do not have the target gene.
3. Cost-effective, simple PCR markers are required to ensure genotyping
power needed for the rapid screening of large populations.

Microsatellite markers, also termed sequence-tagged microsatellite site
(STMS) or simple sequence repeat (SSR) markers, which use the high muta-
tion rates of repeated short DNA motifs are presently the most complete tool
for MAS. Extensive collections of mapped SSR markers from both the non-
coding and expressed portion of the genome are, or will be available in the
near future for all major crop species. To allow absolute allele recognition
and, consequently, to exploit the full range of marker alleles at a given locus
in a panel of breeding lines, SSRs need to be processed on polyacrylamide gel
or capillary electrophoresis machines. However, these high demands on frag-
ment detection can be compensated by the simultaneous electrophoresis of
different SSR marker samples carrying distinguishable fluorescent dyes in a
single lane/capillary.

Development is moving away from anonymous to functional and candi-
date gene markers as primary MAS tools since linkage relationships which
limit the overall applicability of anonymous markers will no longer exist or
will be reduced to a minimum. ‘Perfect’ markers have already been made
available for the gibberellin-insensitive semi-dwarfing genes \textit{Rht-B1b}
and \textit{Rht-D1b} (Ellis et al. 2002) and the null \textit{Wx-B1} allele of the granule-bound
starch synthase I (McLauchlan et al. 2001) of wheat and may be provided by
forthcoming map-based cloning experiments and genetic association map-
ning studies (Rafalski 2002). Resistance gene analogs (RGAs) are a useful
resource as candidate gene markers for disease resistance genes (Mohler et al.
2002; Madsen et al. 2003) since RGAs showing close genetic linkage to resis-
tance genes often reflect physical proximity (Leister et al. 1999; Wei et al.
1999). Furthermore, a huge number of candidate gene markers for complex
traits will be supplied by investigations directed at the identification of genes
differentially expressed among extreme phenotypes, e.g., for potato late
blight disease (Ronning et al. 2003).

The marker type by which functional alleles are discriminated from their
allelic variants relies on small insertion-deletion (indel) polymorphisms or
single nucleotide polymorphisms (SNPs). SNPs are of particular interest for
their utilization in crop improvement, since they (1) represent the most fre-
quent variations in the genome of any organism, thus, offering the opportu-
nity to find informative markers for a distinct genomic region in any genetic