Marker assisted selection (MAS) as a breeding tool in rapeseed improvement

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There are some basic requirements before marker assisted selection can successfully be applied to the breeding of a crop plant. The main prerequisite is the availability of a molecular marker system providing a large number of well-distributed markers covering all of the genome. In case a whole genome selection is the objective, like in a marker assisted backcrossing program, a genetic map is required to allow the selection of an evenly spaced set of informative markers. For the marker assisted selection of a specific gene, on the other hand, a set of preferably tightly linked markers has to be developed.

In rapeseed, the first molecular marker systems applied to genetic analysis and marker assisted selection have been RFLP and RAPD markers. Based on a cross between two winter rapeseed lines a genetic map with 250 markers covering 1550 cM (Kosambi) of the rapeseed genome has been developed (Uzunova et al. 1995). Later, this map was supplemented by the mapping of an additional 227 AFLP and 136 SSR markers. The combined map has a total length of 1970 cM (Kosambi) and an average marker density of 1 marker every 3.2 cM. The distribution of the different types of markers across this map clearly indicates that all the major marker systems applied today in plant breeding and plant genetics are suitable for marker assisted selection in rapeseed.

Despite the high marker density of the combined map it still contains some marker intervals of more than 30 cM in length. In addition, the combined map has 21 linkage groups instead of only 19 as one would expect in rapeseed. The most likely explanation for these observations is that there are regions in the rapeseed genome with very high recombination frequencies, expanding these regions on the genetic map. This can pose a problem for the development of tightly linked markers for a marker assisted selection of specific genes as has been encountered during the development of selection markers for a high oleic acid mutation. Using 64 primer combinations a total of about 500 polymorphic AFLP markers were screened for linkage to this mutation in bulked segregant analyses in two segregating populations. Only three loosely linked markers were found (Schierholt et al. 2000). On the integrated map these markers were located to one side of a large marker interval of more than 30 cM, indicating that the target gene may reside in one of the regions with a high recombination frequency, making it difficult to find closely linked selection markers.

Schierholt A, Becker HC, Ecke W (2000) Mapping a high oleic acid mutation in winter oilseed rape (*Brassica napus* L.). Theor Appl Genet 101:897-901

Uzunova M, Ecke W, Weißleder K, and Röbbelen G (1995) Mapping the genome of rapeseed (*Brassica napus* L.). I. Construction of an RFLP linkage map and localization of QTLs for seed glucosinolate content. Theor Appl Genet 90:194–204