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IDENTIFICATION OF GENOMIC REGIONS INVOLVED IN DUS TRAITS
IN OILSEED RAPE

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Identification of genomic regions involved in DUS traits in Oilseed rape.

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Abstract: Registration and Protection of new varieties of oilseed rape rely upon the description of a limited number of morphological characteristics. As the number of varieties under test and part of the reference collection increases, the assessment of distinctness based on these traits becomes more and more difficult. In this context, molecular markers could assist distinctness, uniformity and stability (DUS) testing of the cultivars. The structural triangular shape between morphological and genetic distances based on molecular markers (Lombard, 2000) makes difficult the direct use of molecular markers for plant registration. The use of molecular markers in genetic linkage disequilibrium with the morphological traits used in DUS tests could improve the correlation between morphological and genetic distances. Then, if a reliable prediction of phenotypic similarity from molecular data could be found, it could be used to help the comparison between candidate and reference cultivars by setting them close to each other in the field. In order to test this hypothesis, we initiated a study to identify molecular markers linked to genetic factors controlling morphological traits used in DUS. Three doubled haploid populations which have been used to build a consensus genetic linkage map of oilseed rape (Lombard and Delourme, 2001) were evaluated for different morphological traits: leaf colour at rosette stage, leaf dentation, leaf number of lobes, flower size and colour. Results indicate that several genomic regions could be associated with morphological traits.

References:

Lombard V., 2000. Estimation de la proximité génétique des variétés de colza sur la base des marqueurs moléculaires: conséquences pour l'inscription et la protection variétale. Thèse INA Paris-Grignon, 136 pp.

Lombard V., Delourme R., 2001. A consensus linkage map for rapeseed (*Brassica napus* L.): construction and integration of three individual maps from DH populations Theoretical and Applied Genetics (in press).

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