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DEVELOPING A STRATEGY TO APPLY SNP MOLECULAR MARKERS IN THE FRAMEWORK OF WINTER OILSEED RAPE DUS TESTING

Document prepared by an expert from France

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In oilseed rape, the expression of phenotypic characters is very sensitive to changes in environmental conditions. To perform valid comparisons, the entire reference collection must be redescribed every year to account for this high inter-annual variability. This represents significant costs and huge technical and logistical challenges in terms of planning and infrastructure (e.g., limited availability of agricultural lands). GEVES (France) and BSA (Germany) carried out a joint project with the objective to develop novel approaches that integrates genetic and phenotypic information to avoid having to redescribe the entire reference collection without compromising the validity of DUS decisions, using single nucleotide polymorphism markers (SNPs) to optimize the management of the reference collection and reduce the number of varieties that need to be included in DUS growing trials. The new model had to be compatible with the different statistical methods used for evaluating distinctness between winter oilseed rape varieties (GAIA or COY).

The objectives of the project were:

- to genotype part of the reference collection and produce a large and consistent molecular dataset for ~2000 winter oilseed rape (WOSR) varieties;
- to use the molecular data to filter and optimise the set of SNP markers;
- to design new models and evaluate different approaches that combine genetic and phenotypic information based on SNP markers and historical field data to optimize DUS testing in WOSR.

We propose a new approach derived from UPOV BMT Model 2 ("Calibration of threshold levels for molecular characteristics against the minimum distance in traditional characteristics") that uses network analysis for defining an "optimal reference collection" which is deduced from the candidates' genotypes. In this model, graph clustering tools are used to identify clusters of related varieties based on their proximity (genetic similarity) within a network representing genetic relationships between candidate and reference varieties; only references from clusters that comprise candidate varieties are included in growing trials. So far, the method as only been tested *in silico*. Depending on the statistical method used for evaluating distinctness (COY-D or GAIA), the model can reduce by 20 to 45% the size of growing trials in the first year with the preliminary thresholds of pairwise genetic distance that we defined. To refine these thresholds, a second follow-up project will be required to test the model in the field, calling all volunteer EOs to participate.

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