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Genetic variability of spring rapeseed hybrids based on quantitative traits

Background:

Rapeseed (*Brassica napus* L.) is the most important oilseed crop in Europe and the second in the world. Rapeseed breeders are continuously creating cultivars and hybrids with the main goal to combine high yield, oil content and quality traits. Thus, it is imperative to assess the created germplasm and to distinguish the most promising genotypes.

Objective:

The objective of this study was to determine the genetic variability of 45 spring rapeseed hybrids in order to effectively select those with a combination of high seed and oil yield and other desirable traits, by using multivariate statistical methods.

Methods:

In this study, 45 spring rapeseed hybrids were included. Plant height (PH), number of primary branches per plant (NB), number of pods per plant (NP), pod length (PL), number of seeds per pod (NSP), seed weight per pod (WSP), 1000 seed weight (W1000), seed weight per plant (WSPL) and oil content (O) were determined on 10 randomly selected plants from the middle row of each plot. Based on seed weight per plant and oil content, oil yield per plant (OY) was estimated and days to flowering (DF), flowering duration (FD), ripening duration (RD) and vegetative growth duration (VG) were assessed on a plot basis. The PCA analysis was applied to identify traits with the highest contribution to the total variability of the hybrids, and based on these traits, the dendrogram was constructed.

Results:

The PC analysis identified four PCs with eigen values > 1, which explained 73.9% of the total variation of the hybrids. It classified the germplasm into 7 groups, based on all traits. However, out of 15 analysed traits, only 10 significantly contributed to the PC1 and PC2, and were selected for construction of the dendrogram, by using Ward's distance and UPGMA method. The hybrids were grouped in four clusters. The first one comprised the highest number of hybrids, characterized with high seed and oil yield, and short vegetative growth duration, and can be divided into two subclusters. The hybrids with low values for seed and oil yield and long vegetative growth season were distributed into the third and fourth cluster.

Conclusions:

The conducted analyses were effective for assessing variability of analysed rapeseed hybrids. The PC analysis successfully identified quantitative traits that explained most of the variability of the studied hybrids. It was an effective tool for uncovering traits for which the hybrids expressed the highest variations. As a result, it facilitated the selection of variables to be used for clustering of the germplasm. The hybrids were classified in four groups, each containing different number of subclusters and genotypes with similar performance. Both analyses served as a useful tool for giving clear overview on the variation within the existing germplasm and can successfully assist in deciding based on which traits to select the genotypes, especially at the beginning of a breeding program. The hybrids with the best performance can be recommended for future production and those with desirable characteristics can be included in a breeding program, for improving the existing rapeseed germplasm.