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GENETIC DIVERSITY OF RUSSIAN WHITE CABBAGE COLLECTION DETERMINED BY RAPD AND SSR

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The Russian white cabbage germplasm collection keeping at VIR consists of 1080 accessions, including 231 landraces, 249 old cultivars, 347 advanced cultivars and 253 breeding materials.

According to the origin of accessions the collection may be divided into three parts:

1. Foreign material that was involved since 1923 till now.
2. Russian cultivars that were created on the base of the foreign accessions by means of selection and hybridization 50-60 years ago and good adapted to the new local conditions.
3. Russian landraces/old local cultivars and the advanced cultivars created by improvement of Russian endemic material.

As a result of 60-years study of collection in different ecologic-geographical zones of Russia seven eco-geographical groups and 33 cultivar types distinguished on morphological, biological and agronomic characters were described.

The aim of this study was to evaluate genetic diversity of Russian white cabbage (*Brasica oleracea capitata alba*) germplasm collection including variability within populations by RAPD and SSR DNA-fingerprint methods and to reveal the coincidence of previous botanical and molecular classification.

A set of 35 accessions representing 18 European, properly Russian and oriental cultivar types was analyzed using 19 OPA primers for RAPD and 10 primer pairs for SSR analyses.

The different levels of polymorphisms within white cabbage populations with different status was found, e.g. for landraces it may be compared with the polymorphisms between populations. The levels of polymorphisms within European gene pool were large but less than within Russian one: 276 RAPD and 88 SSR descriptors and 308 RAPDs and 90 SSRs were observed respectively. The UPGMA dendrograms of RAPD and SSR analyses showed the concordant position of very distinctive cultivar types, e.g. pointed morphotype, the cultivar types from Netherlands, Dithmarscher Früher type from Germany, and also oriental and properly Russian group of types. The tree generated from SSR data almost completely corresponded to previously reported botanical classification.

In the study the cultivar types are quite conservative taxonomical units with inherent morphological and DNA organization features. However, the bootstrap values for large clusters were usually low and the conclusion about relations between Russian, European and oriental gene pools have not been done.

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