EVALUATION, CHARACTERISATION AND UTILISATION OF LATVIAN PEA (Pisum sativum L.) GENETIC RESOURCES

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Increasing emphasis is being placed on the need for northern Europe to become more self-sufficient in the production of protein crops. This necessitates increased utilisation of legumes, including peas. Grey peas are a staple food in Latvia, and have been traditionally grown and used for food. There is still a strong consumer interest in grey peas, particularly at Christmas and New Year celebrations. However, the area under cultivation is quite small, and the vast majority of production is utilised for local consumption. All the varieties grown are Latvian cultivars, developed at the Priekuli Plant Breeding Institute and the Stendze Central Breeding Institute. An application for geographical designation for one of the local cultivars has been made in collaboration with a local farmer and a distributor. The Latvian gene bank holds a total of 63 pea accessions, the majority of which are grey peas. The collection includes 10 varieties, 1 landrace, and 52 accessions which were repatriated from the N.I. Vavilov Research Institute of Plant Industry (VIR) collection. In some cases, the identity of these repatriated accessions can be deduced from the names, but the identity of the majority of them is unknown, and may include landraces, breeding lines and other germplasm. Descriptors for peas have been developed, and all varieties has been characterised. In addition, SSR markers have been utilised to genetically fingerprint the majority of the collection. The SSR data has been analysed in an attempt to identify the genetic relationships of the unknown accessions repatriated from the VIR collection with the accessions known provenance. Genetic diversity within the collection was also assessed.

Evaluation of pea varieties according to plant descriptors

Descriptors for peas have been developed, and all 10 pea varieties in the Latvian genetic resources collection have been characterised using plant morphological descriptors for three years (2007-2009).

SSR fingerprinting

Seeds were germinated and DNA was extracted from fresh leaves. Six individuals from each accession were used. For pea collection fingerprinting, six SSR markers were used: AD270, AC58, AB25, AD61, AA355, AB53 (Lordon et al (2005) Theor Appl Genet 111:1022-1031).

Comparison of agronomic properties of white blossoming pea varieties developed at Priekuli Plant Breeding Institute (2010 – 2012)

The genetic fingerprinting of the Latvian pea collection enabled the genetic diversity and relationships between the accessions to be investigated. The pea varieties and landraces are fairly well characterised, having been described according to the developed descriptors, and some pedigree information is also available. However, little or no information is available about the accessions which were repatriated from the VIR institute beyond seed colour and accession name. The amount of genetic diversity within the varieties is lower than in the VIR accessions coverage allele number 11.2 and 20.7, and observed heterozygosity 0.18 and 0.24 respectively. Analysis of the genetic relationships indicates that there is no separate grouping of the varieties from the VIR accessions. The dendrogram confirms some known relationships, e.g. ‘Retrija’ is a selection from the land race ‘Bruņins Retels’, however not others, e.g. ‘Pioner’ and ‘Rota’ have one common parent, and ‘Rota’ is a parent of ‘Alma’. In other cases, accessions with similar seed colour were grouped together, e.g. ‘Linija066’, ‘Linija062’, ‘Linija91’ and ‘Linija56’ are yellow; ‘Zaiga’ and ‘Perenjūk44-31’ are green.

Analysis of the genotyping results will enable a more targeted assessment of the accessions repatriated from the VIR institute, and can serve as a basis for rational utilisation and conservation of the Latvian pea genetic resource collection, as well as a basis for evaluation of new acquisitions.

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