

At Svalöf Weibull (SW) breeding strategies are increasingly involving the use of molecular markers. In particular microsatellites (SSRs) are attractive because they are abundant, have high level of polymorphism are wide dispersed throughout the genome and co-dominant. The ease of assay by the polymerase chain reaction (PCR) which can be operated through an automated system further makes SSRs ideal for large-scale analysis. Our interest in pea SSRs are for two main purposes: 1) fingerprinting SW cultivars which is becoming increasingly important in order to protect germplasm and 2) linkage to genes of interest for

This poster summarises our first experience with 40 pea SSR markers recently identified as being polymorphic in five model genotypes at Agrogene.

Pea lines used for studying SSR polymorphism in breeders material.

Comments
Important in Canada and Sweden
First semi leafless cultivar from Svalof AB
Stiff straw with leaves
Important in Canada and US, green seed
Green seed, for Finnish peasoup
Green seed, for Granda and US, green seed
Good yield, bad seedcoat, done well in Denmark
New, doing well in Canada
New, doing well in Canada, green seed
Resistant to powder y mildew for Canada
Old, long, weak straw, forage pea
Even older, long weak straw, forage pea
Powder y mildew resistant. Official trials in UK
New cultivar in Sweden, good in US
Official trials in Sweden, gromising
Official trials in Sweden, promising
Official trials in Sweden, Germany, Austria
Resistant to powdery mildew
Good seed quality, highyield
Gardenpea Pea line Rigel x Bohatyr Jl 143 x Birte SW Rigel Fjord x Bornatyi Fjord x Bohatyr JI 113 x Birte Bohatyr x Sv U 51041 9590 x Carneval (9591 x Carneval) x Orb Rigel x Timo Hero x Parvus Hero x Parvus
Monopol x Ambrosia
Highlight x Patriot
Rigel x Bohaty
Majoret x Solara
Loto x Majoret
Bridge x SW 92519
(Carneval x SW 92536) x Exchequer
9592 x Carneval
Breeder CDC
Breeder CDC
Breeder Cebecco SW 94594 SW 955180 SW 955180 SW Nessie SW Universal (95577) SW Celine (965222) SW 975607 SW 975496 CDC 9507 Carrera Kungs Kelvedon Wonder Breeder Hursts Gardenpea

Fig. 1 PCR fragments from Agrogene pea SSR marker PSMSD21 detected in MetaPhor gel ed per pea line. Note that three lines segregated at this locus





Results

Using 22 forage pea lines and one gardenpea cultivar 33 SSRs were polymorphic 6 SSRs were monomorphic and one SSR did not amplify.

2-4 alleles were detected per SSR marker. The average numbers of alleles were 2.6 per locus.

A dendrogram (Fig. 2) was in accordance with the breeding history in a few cases. For example: SW 955180 and Carneval share a common subgroup and SW 955180 was recently extracted as a mildew resistant line from Carneval. The dendrogram did not reflect the breeding background in some cases. For example

Majoret and Karita are sister lines but are genetically distant from each other and from both parents Fjord and Bohatyr. A possible explanation could be polymorphism within pea lines (Fig. 1).

Conclusions

The Agrogene SSRs could be used successfully to detect DNA polymorphism in breeders material.

Pea genotypes could easily be distinguished based on their SSR profiles

Mapping populations can be created from modern lines for identifying SSR markers linked to important genes.

The agarose detection system that we are using did not reveal the full potential of the SSR markers. Our next experience with pea SSR will be using a multiple capillary detection system (SCE9610) for future automated pea microsatellite analysis.

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Fig. 2.

The relative genetic distance between 24 pea lines based on 21 polymorphic loci. The dendrogram based on Nei's genetic distances using UPGMA was drawn using Popgene version 1.31 software.

