

SSR genotyping of old potato varieties to identify mislabelling and synonyms for AEGIS

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The identity (cultivar name) of potato clones in different collections is not always clear or correct. This is hampering the selection of the Most Appropriate Accessions (MAA's) for the AEGIS* collection.

In particular for old cultivars the clone can be mislabelled (H. Campbell in [1]). This was also observed during work for CPVO on the EU Variety Catalogue [3]. Some variety names have been used more than once (e.g. Gloria 1921, 1937, 1972) and it is not always known to the curator what the true identity of a clone is.

The classical differentiation of cultivars based on morphological characteristics is a highly skilled and time-consuming task. To assist in granting Plant Breeders' Rights for potato varieties, a standard fingerprinting method has been developed [2, 3]. The method uses nine microsatellite (SSR) markers. The set was expanded to twelve to increase the level of discrimination. Obviously, somaclonal variants and mutants cannot be separated from the original clone.

For the AEGIS project "*The identification of 500 old potato clones having unreliable variety name by means of fingerprinting using 12 microsatellite (SSR) markers to assist in setting up the AEGIS collection for potato cultivars*", SASA genotyped 379 clones from eight European potato collections. Additionally, the UK and Ireland donated 24 and 30 fingerprints of heritage varieties. The 433 accessions show 397 different profiles. The 27 duplication groups contain two till six accessions. The largest group consists of blue coloured varieties. In the case of the duplicate group Fortuna / Morgane_1985, it is unclear which one has been mislabelled. If available in SASA's (not public) database, profiles of crossing parents and/or offspring might resolve this. However, the Potato pedigree database [6] indicates for the name Fortuna four different varieties. In general, a preferably public database containing as many profiles as possible would be helpful. However, the results from different labs have to be harmonized to allow the data to be compatible, which can be a drawn out and potentially expensive process. The harmonization should be endorsed by CPVO.

The results of the genotyping project have been made public at its website [5]. The curators can use them to improve their selection for AEGIS.

* *AEGIS [4] is a European Genebank Integrated System, to establish a European plant genetic resources collection, which would be a virtual European Genebank, maintained with agreed quality standards, and freely available in accordance with the International Treaty on Plant Genetic Resources for Food and Agriculture.*

References:

- [1] Frese, L. and R. Hoekstra (2009) Report on a Network Coordinating Group on Sugar, Starch and Fibre Crops. Third Meeting, 8-9 October 2009, Quedlinburg, Germany
www.ecpqr.cgiar.org/archive_phase_viii/sugar_starch_fibre_crops/network_meeting_quedlinburg_2009.html
- [2] Reid, A., L. Hof, D. Esselink and B. Vosman (2009) Potato cultivar genome analysis. In: Methods in molecular biology, plant pathology, vol.508, ed. R. Burns, 295–308. New York: Springer.
- [3] Reid, A., L. Hof, G. Felix, B. Rücker, S. Tams, E. Milczynska, D. Esselink, G. Uenk, B. Vosman and A. Weitz (2011) Construction of an integrated microsatellite and key morphological characteristic database of potato varieties on the EU Common Catalogue. Euphytica 182: 239-249.
- [4] www.aegis.cgiar.org
- [5] <http://documents.plant.wur.nl/cgn/pgar/AEGISpotato>
- [6] www.plantbreeding.wur.nl/potatopedigree