

First attempt to characterize *Ribes* genetic resources with SSR markers in Switzerland

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Introduction

The identification of ancient varieties of cultivated berries for a rational conservation scheme has long been problematic due to the lack of unambiguous pomological descriptions. With the development of genotyping techniques such as microsatellite markers (SSR), the situation has improved. Within the frame of the **National Action Plan for the Conservation and Sustainable Use of Plant Genetic Resources for Food and Agriculture (NAP-PGRFA)**, the characterization by SSR of the Swiss collection of ancient accessions of blackcurrants, redcurrants and gooseberries was launched (project 05-NAP-P66 initiated in 2015). The aims of this ongoing project are to identify or confirm potential duplicates and misnamings/mislabeings and to create a genetic profile database for future comparisons.

Material and Methods

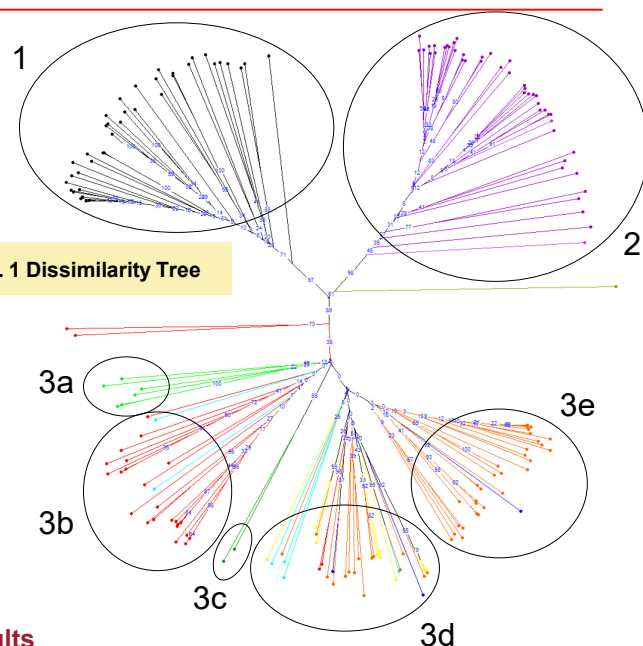
286 *Ribes* accessions from the ProSpecieRara collection. DNA purification: DNeasy® Plant Mini Kit (Qiagen), amplification: TProfessional TRIO Thermocycler® (Biometra), separation: 4300 DNA Analyser (Li-cor). SSR markers: e1-O01^a, e1-O21^a, e3-B02^a, e4-D03^a, g1-A01^a, g1-B02^a, g1-K04^a, g1-M07^a, g2-B20^a, g2-G12^a, g2-H21^a, g2-L17^a, gr2-J05^a, MTT-5^b et RJL-7^c. Construction of unweighted neighbor joining dissimilarity tree: DARwin 6.0.13 software^d (Jaccard's coefficient).

Discussion

The kit of markers allowed to separate the accessions into three main groups and to join onto nearby branches some accessions suspected to have inherited genetic traits from a common species. As expected numerous duplicates were discovered, this far coherent with the first morphological descriptions. The correspondence between genotype and phenotype will be investigated further to make sure the marker kit is performant enough to justify the exclusion of duplicates from the conservation scheme.

References, acknowledgements

- a** <http://www.fruitbreeding.co.uk/RibesGenomicsSSRs.asp>
b Korpelainen H. et al. (2007). *Biotechniques* 42:479-480 484-486
c Brennan R. et al. (2002). *Mol Ecol Notes* 2:327-330.
d Perrier, X., Jacquemoud-Collet, J.P. (2006). *DARwin software* <http://darwin.cirad.fr/>
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Results

The 286 accessions generated 181 different profiles. Among the duplicates, several were intentional (blind controls), most were suspected as identical and several consisted of punctual mutations affecting their phenotype. As expected, the accessions were separated into three main groups: 1 blackcurrants (black), 2 gooseberries (purple) and 3 redcurrants (other colours). Cluster 3a contains *R. multiflorum* (green) and its hybrids except when *R. spicatum* is involved (cluster 3c), most *R. petraeum* and *petraeum*-like (red) are located in cluster 3b, *vulgare* x *spicatum* hybrids (yellow) cluster in 3d whilst *R. vulgare* and hybrids with *petraeum* (orange) are spread within 3d and 3e (Fig. 1). The high heterogeneity of redcurrants is illustrated by the numerous exceptions.

Conclusion and future plan

Several markers were selected for the establishment of the genetic profiles of Swiss *Ribes* accessions. A parallel between genotypic and phenotypic descriptions has been initiated and should confirm the pertinence of the markers selected. Although several duplicates were confirmed, some still need a validation based on morphological studies. The definitive results should allow to optimize the choice of accessions intended for preservation and provide a better description of the ancient varieties collected in Switzerland. Hopefully, the addition of chloroplastic markers will provide some insights on the interspecific crossings and complete the general picture. The verification of official varieties will require exchanges with other European collections.