



III International Symposium on Molecular Markers in Horticulture



Riva del Garda (Trento)

Italy,



Under the Auspices of the
Autonomous Province of Trento

POSTER - Genetic diversity of bilberry populations of Northern Europe determined by ISSR markers

Authors: zoratti.laura@gmail.com

Name	Surname	Institution	Address	Country
Laura	Zoratti	University of Oulu - Department of Biology	PO Box 3000 - FI90014 Oulu	Finland
Luisa	Palmieri	Fondazione Edmund Mach - Research and Innovation Centre-Food Quality and Nutrition Department-Biotechnology of Natural Products	Via E. Mach 1 38010 San Michele all'Adige (TN)	Italy
Laura	Jaakola	University of Tromsø, Department of Arctic and Marine Biology	NO-9019 Tromsø	Norway
Lara	Giongo	Fondazione Edmund Mach, Research and Innovation Centre –Applied Rosaceous Genomics Group	Via E. Mach 1 38010 San Michele all'Adige (TN)	Italy
Hely	Häggman	University of Oulu - Department of Biology	PO Box 3000 - FI90014 Oulu	Finland

Abstract: Bilberry (*Vaccinium myrtillus*) is one of the most important wild crops growing in the forest in the North European countries. Nevertheless, it is still poorly exploited from a commercial point of view, as only 5-8% of the Scandinavian's forest production is picked up every year. To overcome this problem, it has been enlighten the need to develop improved forest management systems, where good yields of high quality bilberries are produced with manageable cost. One of the major tools to achieve this goal is to develop methods to assess the level of genetic variability between the populations under study.

In this work, DNA was extracted from 32 clones derived from 11 natural populations collected from different locations of Iceland (IS1, IS2), Norway (N2, N4, N7), Sweden (R), Finland (Sodankylä, Parkano, Muhos, Lapinjärvi) and Germany (Kiel).

Genetic variation and population structure of this species were investigated by using inter simple sequence repeats (ISSRs) and data was analysed with different software packages (GenAlex, Structure, NTSYS). The patterns of variation appeared to be consistent for this marker system, and they can be used for management of genetic structure, *in situ* germplasm protection and conservation. Moreover, this genetic knowledge, together with the biochemical and phenotypic information, will be the know-how for the future work addressed to *ex situ* germplasm management and breeding.

Keywords: bilberry, germplasm, ISSR, genetic population

Type of presentation: [Poster](#)

Topics: [Germplasm collections and molecular characterisation](#)