

Could a postglacial recolonization route be proposed for German *Vitis vinifera* L. subsp. *sylvestris* (Gmelin) Hegi, based on nuclear microsatellite markers?

Maul, Erika^{1*}; Niederl, Marion²; Griesbacher, Aaron³; Ledesma-Krist, Gloria⁴; Röckel, Franco¹; Töpfer, Reinhard¹

¹Julius Kühn Institute (JKI), Institute for Grapevine Breeding Geilweilerhof, Siebeldingen, Germany

²Karlsruher Institut für Technologie (KIT), Institut für Geographie und Geoökologie, Aueninstitut, Rastatt, Germany

³Nationalpark Donau-Auen GmbH, Schloss Orth, Orth an der Donau, Austria

⁴former researcher at Karlsruher Institut für Technologie (KIT), Institut für Geographie und Geoökologie, Aueninstitut, Rastatt, Germany

*erika.maul@julius-kuehn.de

Abstract

Until the 19th century *Vitis vinifera* L. subsp. *sylvestris* C.C. Gmel., the wild compartment of our cultivated grape, was ubiquitous in many European flood-prone areas between 43° and 49° northern latitude. For the German wild grape, Bronner wrote in 1857 that they grow in thousands in the forests on the banks of the river Rhine. Since then, populations have diminished across Europe. Oberlin criticized the eradication of wild vines by the forest administration in the Rhine Valley in 1881. This happened even before the appearance of Phylloxera in that region. An approximately 100 individuals counting *V. sylvestris* population survived in the hardwood floodplain forest on the Rhine island Ketsch. The question arose: would it be possible to decipher the postglacial recolonization route taken by the ancestors of the Ketsch-population? To answer that question three main refuge areas Iberia, Italy and the Balkans were considered as survival zones. Therefore previously published and own nuclear microsatellite (SSR) data of 599 *V. sylvestris* genotypes were gathered from eight European countries: Austria (81 genotypes), Bosnia-Herzegovina (19), Croatia (70), France (46), Germany (57), Italy (Sicily – 105; mainly from Central and Southern Italy – 109), Slovenia (13), and Spain (99). SSR-marker data for Austrian and German accessions are own data. Eighteen overlapping SSR-markers were selected. They were standardised according to reference varieties and allelic frequency distribution patterns. Statistical analysis revealed that within the wild grapevines considered in the present study a distinct substructure could not be detected. Nevertheless STRUCTURE analysis with 3, 5 and 7 groups led to results indicating increasing discrimination among the different subpopulations. Italian refuge was clearly ruled out as a contributing gene pool. Austrian *V. sylvestris* formed an independent group, only slightly linked to Balkan compartment. Ketsch-population was placed within Western European (France and Northern Spain) *V. sylvestris*.

Keywords: *Vitis sylvestris*, population, postglacial recolonization, microsatellites, diversity