## Workshop Vitis sylvestris

## **Objective:** broad genetic basis of *Vitis vinifera* L. subsp. *sylvestris* (Gmelin) Hegi for deep studies

Maul, Erika<sup>1</sup>\*; Röckel, Franco<sup>1</sup>; and Zdunic, Goran<sup>2</sup> <sup>1</sup>Institute for Adriatic Crops and Karst Reclamation, Split, Croatia <sup>2</sup>Julius Kühn Institute (JKI), Institute for Grapevine Breeding Geilweilerhof, Siebeldingen, Germany \*erika.maul@julius-kuehn.de

## Abstract

*Vitis vinifera* ssp. *sylvestris* is the wild relative of the cultivated grapevine *Vitis vinifera* ssp. *vinifera*. In order to better understand the differences between wild and cultivated compartment of *Vitis vinifera* molecular tools provide excellent diagnostic possibilities. The comparability of different studies would benefit greatly from a methodologically coordinated approach. The aim of the workshop is therefore to discuss a methodological toolkit that allows a broad genetic analysis of *Vitis sylvestris* in its entire distribution area and allows in-depth studies. The workshop will adress the

Identification, preservation, and population genetics of true Vitis sylvestris

- analysis of individuals, which were not genotyped yet
- exclusion of feral types and hybrids
- overall genetic diversity, differentiation etc.
- putative dispersal routes

Marker tools

- Microsatellite-markers
  - agreement and utilization of common reference varieties from cultivated gene pool
  - agreement on a common set of SSR markers
  - gathering of additional non published SSR-data
- SNP-markers
  - discussion on a common genotyping method (WGS, SNP chips, GBS etc.)
  - common data structure with alignment to most recent PN40024 version (at the moment v2; soon v4)
  - plastid genome analysis

Keywords: Vitis sylvestris, genotyping, microsatellites, SNPs