

## **Analysis of an East Asian *Vitis* species to identify a new resistance to downy mildew**

Nagarjun Malagol, Anna Schwandner, Daniel Zandler, Reinhard Töpfer and Ludger Hausmann

Julius Kühn Institute (JKI) – Federal Research Centre for Cultivated Plants, Institute for Grapevine Breeding Geilweilerhof, Siebeldingen

E-mail of corresponding author: [nagarjun.malagol@julius-kuehn.de](mailto:nagarjun.malagol@julius-kuehn.de)

Almost all European grapevine cultivars (*Vitis vinifera* L.) are susceptible to downy mildew, a serious grapevine disease caused by the biotrophic oomycete *Plasmopara viticola*. Outbreaks of the pathogen are prevented by regular fungicide treatments to avoid serious yield losses. However, synthetic or copper-based fungicides are known to be detrimental to human health and exhibit eco-toxicological effects. Therefore, the cultivation of resistant new grapevine varieties is one of the imperatives for a sustainable and environmental friendly viticulture.

A wide range of American but only a few East Asian *Vitis* species have been utilized as natural resistance donors for breeding of new resistant cultivars. Several QTLs for resistance to *P. viticola* (*Rpv*), mainly from North American species, have been mapped on various chromosomes. One major long term objective of grapevine breeding is to introgress and pyramidize these naturally occurring resistances of wild *Vitis* species into the *V. vinifera* genetic background to finally develop new varieties with a permanent and robust resistance. This procedure is facilitated by the development and application of molecular markers tightly linked to the resistance (marker-assisted selection; MAS).

To identify a new resistance to downy mildew an unexploited segregating bi-parental mapping population based on East Asian *Vitis* species was analyzed. The study follows a typical QTL mapping approach, explaining the statistically significant association between phenotype and uniformly distributed markers located on a genetic map, to identify the genomic regions responsible for resistance. A SSR marker-based initial framework map was generated that consists of 19 linkage groups with an average of 5.2 markers per chromosome. At the same time, artificial inoculation experiments were carried out to investigate the degree of resistance to *P. viticola* among the F1 individuals of the mapping cross. Automated photographic recordings were made of the treated leaf discs, and were manually scored for disease severity based on reversed 452 OIV scale. Since this manual rating is tedious, time consuming and obtained data is very subjective, a high throughput phenotyping system for downy mildew was developed on convolutional neural network (CNN) platform, to automatically evaluate the disease severity. Compared to the manual evaluation, the CNN efficiently identified and determined the percentage of area covered by downy mildew in the mapping population with an accuracy of 97%. The CNN performance was also validated on a second unrelated population. After the QTL mapping, future aims are the characterization of the resistance mechanism and determination of responsible candidate genes associated with the new resistance to downy mildew.