

Genetic Background Selection in Grapevine Breeding exemplified by the Cross 'Blaufraenkisch' x 'Catawba'

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Wild vines originally from North America, like the species *Vitis labrusca*, are an important resistance source in grapevine breeding. But a common problem of interspecific crosses is to meet the wine quality requirements due to possible off-flavor inheritance. In order to face this problem more efficiently, it is proposed to use the marker-assisted selection (MAS) strategy. In this study it is shown how this can be accomplished.

The natural methyl anthranilate (MA) is assumed to contribute to the Labrusca-typical "foxy" flavor and called to account mothball taste. MA does not exist in perceivable concentrations in the high-quality European *Vitis vinifera*. For the localization of the chromosomal region responsible for MA synthesis, MA was quantified in 226 descendants of the cross population 'Blaufraenkisch' x 'Catawba' by gas chromatography.

The triannual studies revealed one main quantitative trait locus (QTL) on the linkage group (LG) 4. In this QTL, a DNA sequence similar to the *aamt1* gene can be found on the *Vinifera* 'Pinot noir PN40024' reference genome. AAMT1 is a key enzyme in the MA synthesis in maize where it is produced in case of leaf damage and therefore is probably involved in plant defense attracting the herbivores' predators.

The second step was to perform ancestry investigations: 'Catawba' is one of the oldest commercialized North American cultivars. In former times it was speculated to originate from *V. vinifera* and a native wild species. Its genetic fingerprint was compared systematically with the data of the Geilweilerhof grapevine repository and revealed *V. vinifera* 'Sémillon' as its ancestor. The genetic map of 'Blaufraenkisch' x 'Catawba' consists of 337 genome-wide SSR markers. Using this marker data it was possible to identify the *Vinifera* alleles of 'Blaufraenkisch' and 'Sémillon' in the progeny for background selection in a marker-assisted backcrossing (MABC) approach. As expected, the *Vinifera* portion was 73.54 % in average with a maximum value of 82.95 % and a minimum of 62.90 % among the offspring. The trait-independent *Vinifera* markers plus the knowledge about the MA QTL can now promote breeding programs with the 'Catawba' progeny: A screening can be done for the genotypes with the highest *Vinifera* portion and having no MA QTL on LG 4 to use them for crossing the next generations. For the breeders, the information about the chromosome where the allele for the undesired quality trait is located is already sufficient without enclosing the region more precisely.