

**CURRENT STATUS OF STUDYING THE SWEET CHERRY
(*PRUNUS AVIUM* (L.) L.) GENOME**

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Qualitative improvement and a significant acceleration of breeding sweet cherry possible under using marker assisted selection. The genetics research of agronomically-important traits in sweet cherry was actively continues in the last decade. Many molecular studies are still ongoing, but already known genes that determine self-compatibility, self-incompatibility and fruit size in sweet cherry.

Keywords: *S-locus, quantitative trait loci, marker assisted selection, the fruit size, cherry.*

Sweet cherry is an important industrial fruit crop in Ukraine. Over the past decade, Ukrainian breeders create a large number of sweet cherry varieties promising for industrial growing and competitive in the global market. The aim of our study was to search in the literature markers of economically important traits that can be used in marker-assisted selection (MAS) of sweet cherry. According to the Food and Agriculture Organization (FAO) in the world has seen steady increase of the area of cultivation of fruit trees and growing of sweet cherry. Due to the increasing demand for fruit cherries in the world market is the actual need for purposeful assortment improvement in the short term.

The development of molecular markers greatly facilitated the study of genetics of quantitative traits through analysis of quantitative traits loci (QTL) and identification of areas of the genome that control important traits and determine their genetic effect. Molecular markers can be used in practice through a marker-assisted selection, where selection is based on the DNA sequence and not on phenotype.

Worldwide cherries selection is carried on the most important characteristics - both qualitative and quantitative. Qualitative (mono- or oligogenic) are: self-

compatibility / self-incompatibility, color of flesh, juice and exocarp, albinism, dwarfing habit, resistance to powdery mildew. However, most traits are quantitative (polygenic): the growth vigour, early-maturing, date of flowering and ripening (early and late), fruit size, yield, pedicel-fruit retention force, resistance to fruit cracking, bacterial cancer and others.

The main goals of the research morphological and physiological characteristics are reducing the size of the tree, self-compatibility, improve fruit quality and yield.

In the representatives of Rosaceae, Solanaceae and Plantaginaceae families' pollination are under control of gametophytic self-incompatibility system (GSI). This system is a genetically determined by one poliallelic locus (*S*) with two genes that encode specific determinants of self-incompatibility response. In stone fruit crops (tribe Amygdaleae) two coupled *S*-locus genes involved in the response to recognition of incompatibility - *S*-RNase genes and SLF / SFB. According to recent data of Szikriszt, is known 37 *S*-alleles and 45 cross-incompatible groups (CIG). The Ukrainian sweet cherry varieties has already partially investigated in allelic state of *S*-locus, self-compatible cultivars are unknown. There is known method of differentiating varieties of cherries mutant allele *S*₄'.

Among the characteristics of the fruit, main attention paid on size, appearance, color, taste and shelf life.

Diameter of sweet cherry fruit is an important factor in the choice of the consumer and the main component for the formation of the selling and market prices. The size of sweet cherry fruit is considered to be a quantitative basis and as a result it is difficult to analyze using classical genetic methods. In the sweet cherry identified two CNR-genes that located in previously discovered QTL in the second and sixth pairs of chromosomes and are called *PavCNR12* and *PavCNR20*, respectively. Variations in gene *PavCNR12* of sweet cherry can be used to search for homozygotes over allele *PavCNR12-1*. These genotypes show on 9-16% greater weight of the fruit.

The color of exocarp and the fruit varies in the sweet cherry in red and yellow shades. Inheritance of color the sweet cherry fruits in populations studied for a long time. At present three genetic factors is known. The factor of flesh color (*F*) and the

main factor of skin color (*A/a*) are key determinants of fruit color when red color shows incomplete dominance over yellow. The third is a minor factor of skin color (*B/b*), which may give it blush, but is epistatically masked by a dominant allele *A*. Wunsch et al. discovered that differential expression *PavMYB10* in white and red varieties of sweet cherry affects on the level of anthocyanins.

Phenology, especially of reproductive system is critical for fruit trees, because the yield and fruit quality are directly dependent on the proper development of the flower. Dirlewanger et al. analyzed the long-term population data $R \times L$, in Regina and Lapins was discovered stable QTL of flowering date. Totally QTL of flowering date found in the first-seven chromosomes of sweet cherry. The duration of season of ripening period and therefore their realization is the primary advantage for the sweet cherry. In Lapins found one QTL, which partly explains the variation in the terms of ripening.

The signs of resistance to abiotic and biotic factors are economically important. There are underway investigations of genetics of resistance and tolerance to cracking in the sweet cherry fruit. Research of resistance against powdery mildew (*Podosphaera clandestina* (Wallr Fr) Lév) contributed to identify the gene *Pmr1*. Currently, varieties-donor *Pmr1* actively implemented in breeding programs.

According to recent studies, marker-assisted selection of sweet cherry can be carried out only by some commercially valuable traits - possible to determine the allelic status of the gene *PavCNR12*, associated with the fruit size and *S*-locus, identification of germ plasma with defective locus of self-fertility S_4' . We have developed and planned to introduction a new method for identification of allelic variants *PavCNR12* using CAPS-markers. Probably soon it will be possible to determine the color of sweet cherry fruit through the identification of alleles gene *PavMYB10*. Whole genome sequencing is ongoing and active introduction of SNP-markers accelerate the identification genes of important economically valuable traits and marker-assisted selection of sweet cherry.

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