

Genotyping, biochemical and yield component analysis of barley lines with anthocyanin grain pigmentation

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In the current study, the effect of genomic regions inherited by barley near-isogenic lines (NILs) by introducing dominant alleles of *Ant1/Ant2* and *HvMyc2* genes responsible for anthocyanin grain pigmentation into local varieties Aley, Tanay and Vorsinsky2 was investigated.

Genotyping-by-sequencing (GBS) was used to search for genomic regions inherited from donors. The GBS data were processed using a pipeline created at ICG SB RAS, which includes alignment of sequenced reads, variants calling, clustering and phylogram building. *Hordeum vulgare* IBSC_v2 (rel. 51) was used as a reference genome. Relatedness analysis showed that NILs formed clusters with the corresponding recurrent variety, demonstrating their genetic similarity, while donors formed an outgroup.

Antioxidant activity, total phenolic and anthocyanin content in grains, as well as yield-related traits were measured to compare NILs to the parent varieties. All investigated traits were changed in barley NILs with anthocyanin-pigmented grain. Further analysis of genomic regions inherited from donors is expected to reveal the genetic basis of the observed differences.

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The main publications of authors on the subject of the abstract:

Кукоева Т.В. и др. Разработка генетико-селекционного подхода для получения новых сортов ячменя с повышенным содержанием антоцианов в зерне // Генофонд и селекция растений: тезисы V международной конференции 327 (2020): 165-168.

Take-home message:

The introduction of genes responsible for anthocyanin pigmentation of grain affects its biochemical properties and yield-related traits of barley near-isogenic lines. Genotyping by sequencing will allow characterizing donor-derived genomic regions.

