

Genetic analysis of barley productivity traits in Siberian collection

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Barley (*Hordeum vulgare* L.) is one of the most commonly cultivated cereals worldwide.

Its local varieties may represent a valuable source of unique genetic variants useful for crop improvement. The aim of the present study is to identify the loci associated with grain productivity traits using GWAS and assess the influence of genes that control spike row-type in the studied phenotypes.

In present study, such traits “spike length”, “grain number per main spike”, “1000 grain weight”, “grain weight of main spike” were investigated. These traits are economically important as they are primary determinants of barley yield.

Take-home message:

A genome-wide association analysis using a panel of 94 barley varieties was performed. It turns out that all markers identified by GWAS will be correlated with genes that affect row-type.