

## GENOME WIDE ANALYSIS OF NUTRACEUTICAL USEFUL COMPOUNDS ACCUMULATION IN OAT (*AVENA SATIVA* L.)

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*Avena sativa*, *avenanthramides*, *beta-glucans*, *GWAS*

Oat is an important multi-purpose cereal, cultivated for grain, feed, fodder and straw, alone or in mixture or as dual-purpose crop.

Oat can be considered a healthy food due to the many health-promoting compounds present in its grain. Some of these compounds are represented by proteins, lipids, dietary fiber and include (1-3), (1-4)  $\beta$ -D-glucan ( $\beta$ -glucan), tocopherols, and phenolics. Moreover, oat is characterized by the presence of a unique group of phenol-derived compounds, the avenanthramides, which are not present in other cereals. Avenanthramides consist of an amide conjugate of anthralinic acid and hydroxycinnamic acids. There are about 40 types of avenanthramides, but the most frequent are esters of 5-hydroxyanthranilic acid with *p*-coumaric (2p aka A), and ferulic (2f aka B), and caffeic (2c aka C) acids which occur predominantly in the bran layer of the oat grain.

The aim of this study has been directed to the identification of genetic determinants that influence the AVNs content in oat grains. A genome-wide association study for  $\beta$ -glucan content and the major avenanthramides 2c, 2f, 2p, as well as for their sum has been carried out in a collection of European oats, representing the diversity of a large part of the European oat breeding germplasm.

The content of avenanthramides and  $\beta$ -glucans was then used as a phenotypic

data for a GWAS analysis which made it possible to identify SNPs strongly associated with the phenotypic character (content of avenanthramides and  $\beta$ -glucans).

The marker sequences of the associated regions have been aligned by BLASTn algorithm with the most recent genomes of oats and barley to search for candidate genes acting as genetic determinants for the synthesis or regulation of avenanthramide metabolism.