



## **ABSTRACT**

*"Combining multiple traits for Genome-wide association mapping"*

**Dr Arthur Korte**

**Gregor Mendel Institute of Molecular Plant Biology  
Vienna  
AUSTRIA**

Genome-wide association studies (GWAS) have become an obvious general approach for studying the genetics of natural variation. Although a plethora of significant associations of SNPs with different traits have been recently described (some of which have already been verified experimentally), these analyses have been focused on the identification of associations within a single trait. When inbred lines are available, it is possible to study many different traits for the same genotype under different experimental conditions. An obvious next step is to derive a GWAS model that enables the joint analysis of different traits, while accounting for population structure. Hence we derived an extended version of the broadly used mixed model and validated our statistical model through simulations. We could verify that our model both increase the power to identify new SNPs and control the false discovery rate. Due to the simultaneous testing of both the gene and the gene-environment effect in the model we can identify both, SNPs that are globally important in both traits (not influenced by the environment) and SNPs important for gene-environment interaction (having different effects in the respective trait(s)). This method opens the possibility to simultaneously analyze related traits and gain insights into their underlying genetic architecture. Applying the model on real data leads to the identification of novel associations, which were not identified by the marginal analysis