**Combining Association and Selective Signals to Improve Detection of Causal Variants in Adaptive Traits**

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*1.Centre for Research in Agricultural Genomics (CRAG), Autonomous University of Barcelona (UAB), Vall Morontal s/n, Cerdanyola del Valles, Barcelona, 08193, Spain.*

*2. Catalan Institute for Research and Advanced Studies (ICREA), Barcelona, Spain*

*3. Universitat Autònoma de Barcelona (UAB), Bellaterra, 08193, Spain*

The detection of the genetical causes of phenotypic adaptation is a fundamental issue in population and quantitative genetics. The number of causal variants and their selective effects are key factors affecting their identification. Selection leaves a footprint in the patterns of variability, such as an increase of homozygosity and linkage disequilibrium, in the neighborhood of causative variants, which are absent in the non-adaptive traits. Our proposed method combines the association between the phenotype and the genotype and the selective signal. This is performed via an extended genotype homozygosity matrix. This matrix contains the contribution of each individual to genotype homozygosity at each position. It is expected association analyses using this extended matrix will increase power of detecting adaptive loci. Simulated data are generated under different genetic architecture scenarios in order to evaluate the sensibility and the specificity of this methodology for traits having different correlation with fitness.