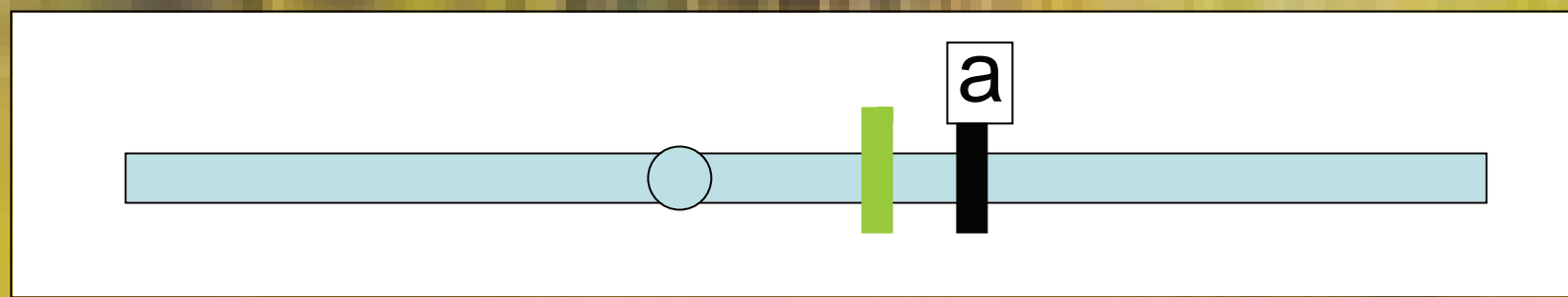
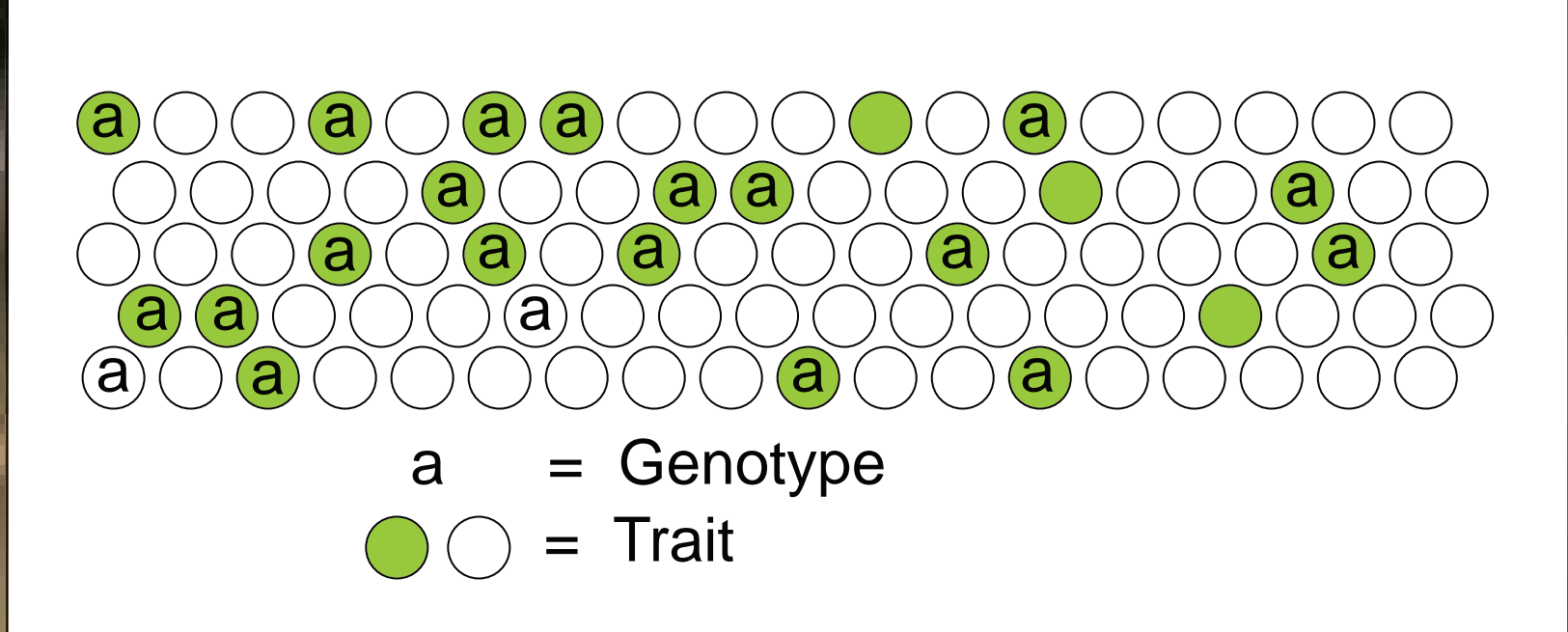


Genomic -assisted Analysis and Exploitation of Barley Diversity (EXBARDIV)



Our objective is to establish an incremental association mapping approach based on different population types for the discovery of new gene alleles in wild and landrace barley, which can be exploited for crop breeding

Association mapping

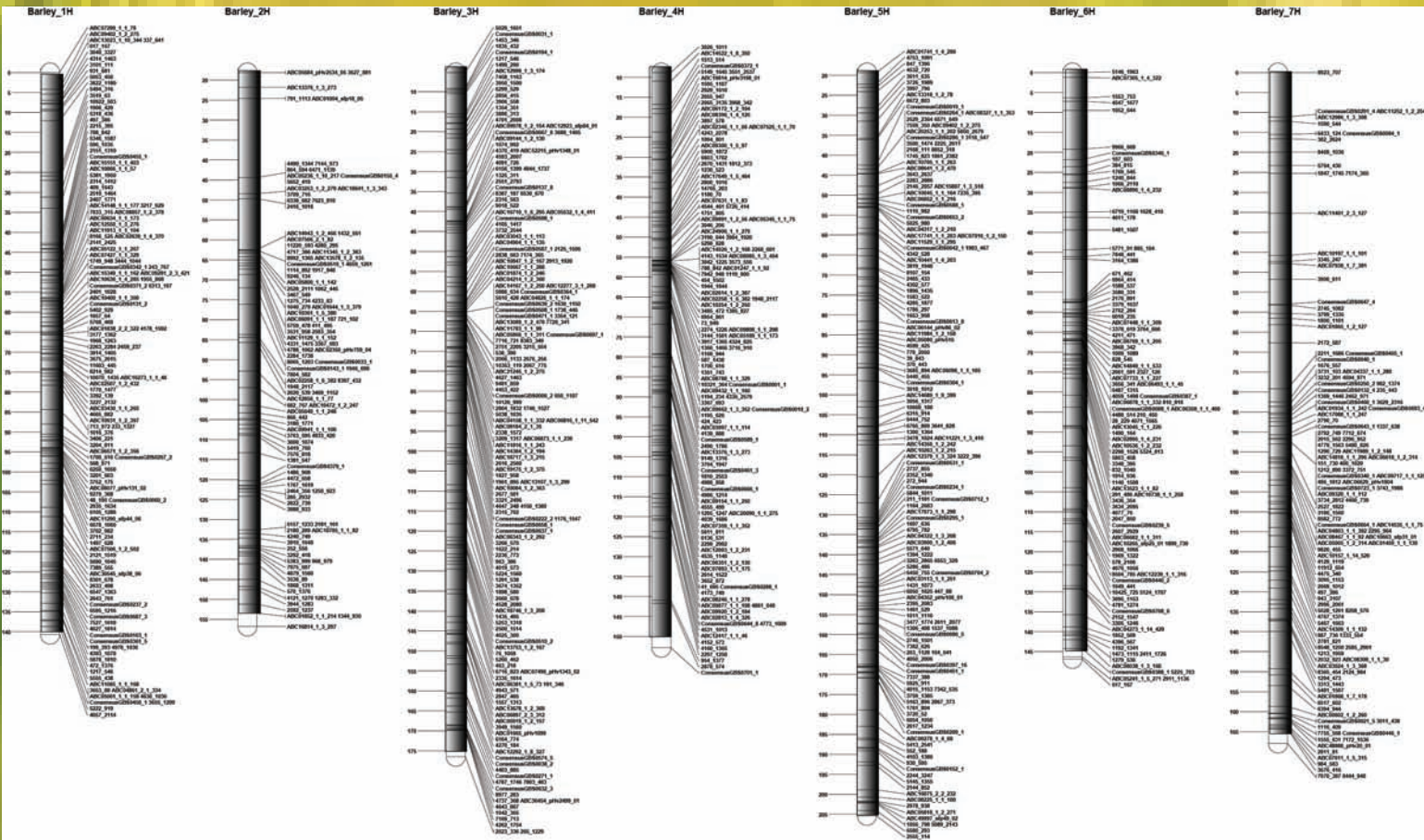


A strong association between a trait and a marker implies a close physical linkage in the genome (IF the population of individuals is unstructured)



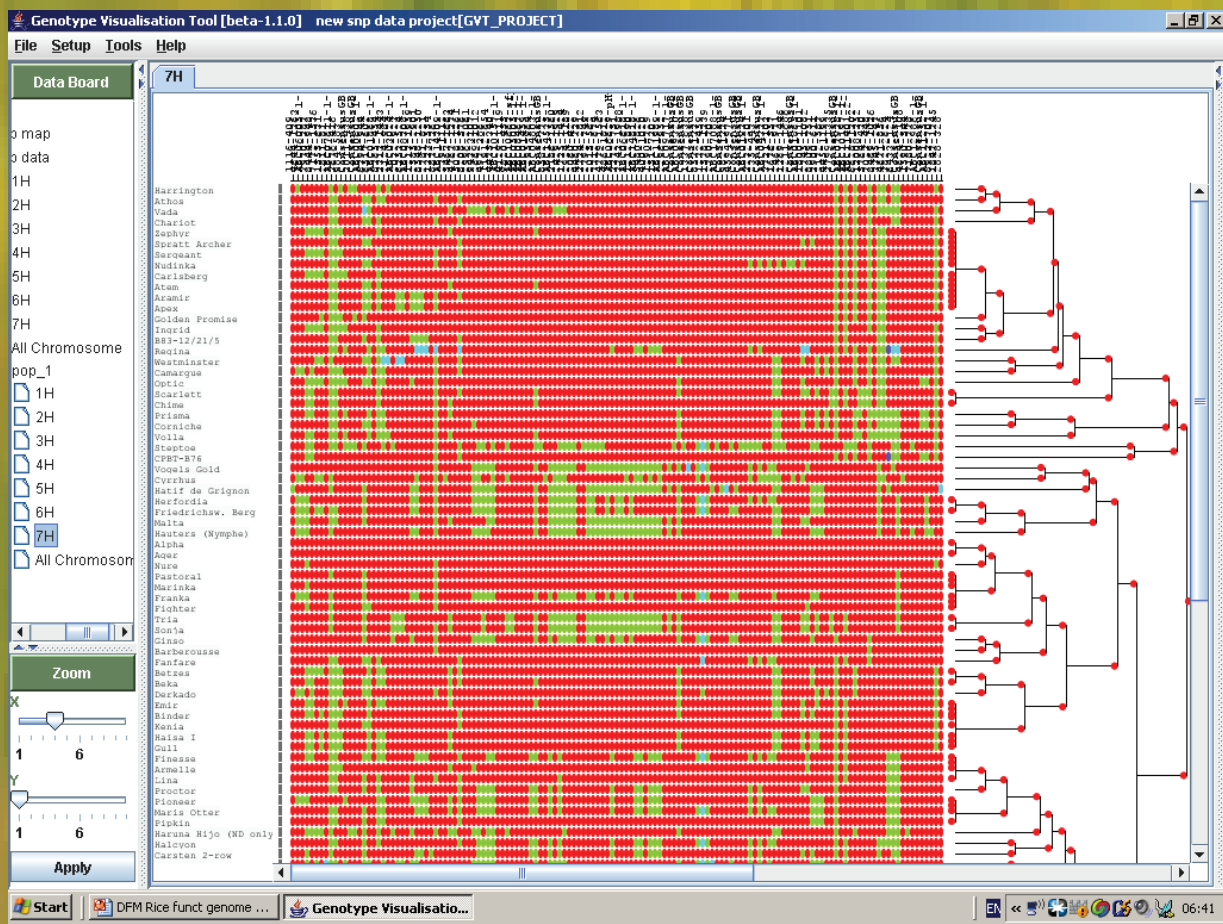
Andy Flavell, University of Dundee at SCRI
Klaus Pillen, Max Plack Institute, Koln
Alan Schulman, MTT Agrifood Helsinki
Andreas Graner, IPK Gatersleben
Luigi Cattivelli, CRA Fiorenzuola d'Arda
Søren Rasmussen, Copenhagen University
Joanne Russell, Scottish Crop Research Inst.

Essential tools

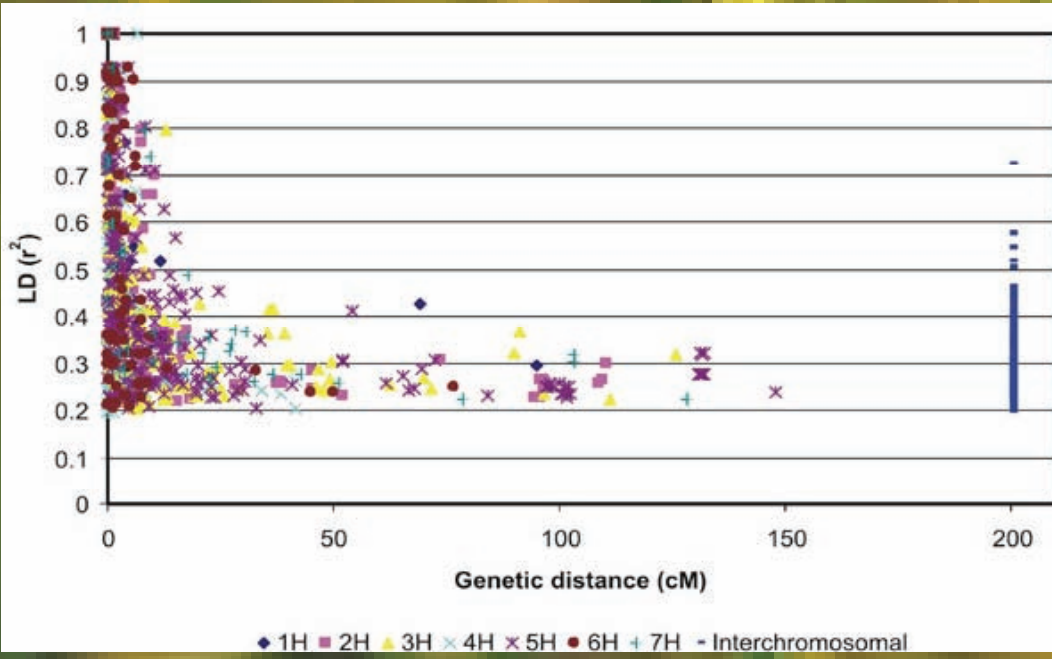


3000 High throughput SNP markers, most with known map locations

The Problem

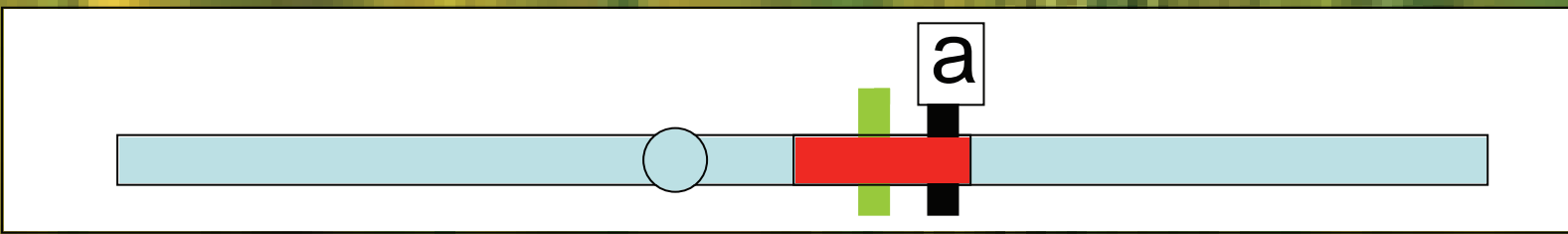


Association mapping has very low resolution in cultivars

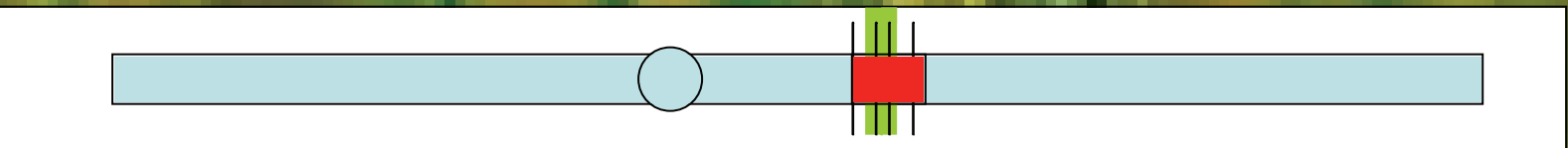


Linkage extends up to ~ 30cM in collections of cultivated barley chromosomes, because they are so highly inbred

The Solution (we hope!)



Identify broad associations in a collection of cultivars



Screen a less inbred collection (with lower *linkage disequilibrium*) at a subset of genes across the region for association with the trait



Repeat at higher resolution (~ saturation gene level) in a wild barley collection

The less inbred the collection screened, the closer the association becomes

The Plan

