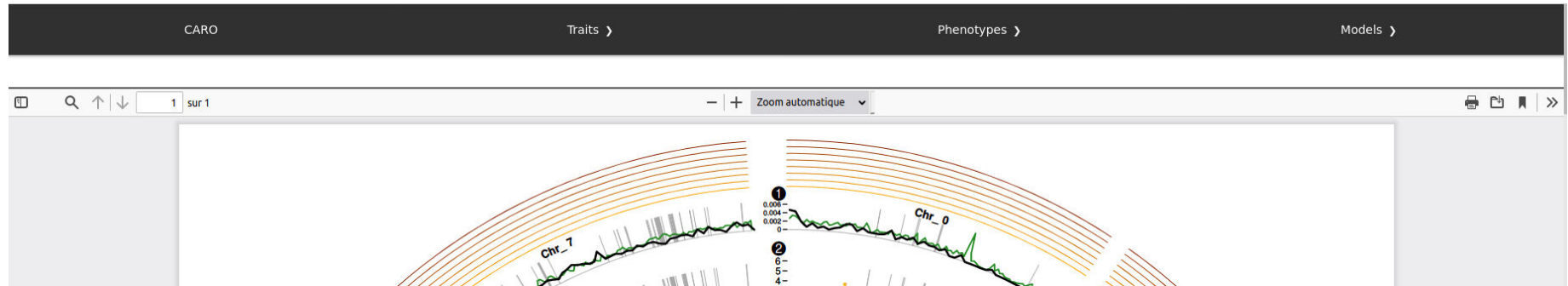


How to browse on this website

1/ First select a trait on the drop-down menu « Traits », e.g. « Black Spot »

2/ Then you will have access to a new drop-down menu « Phenotypes », « Parameters » or similar to more precisely select a phenotype of interest, e.g. « Blackspot - 3 years »



3/ Then a pdf is expected to be loaded. By default, the results shown are those from the general model of GWASpoly. For more information regarding the GWASpoly model, see next slide.

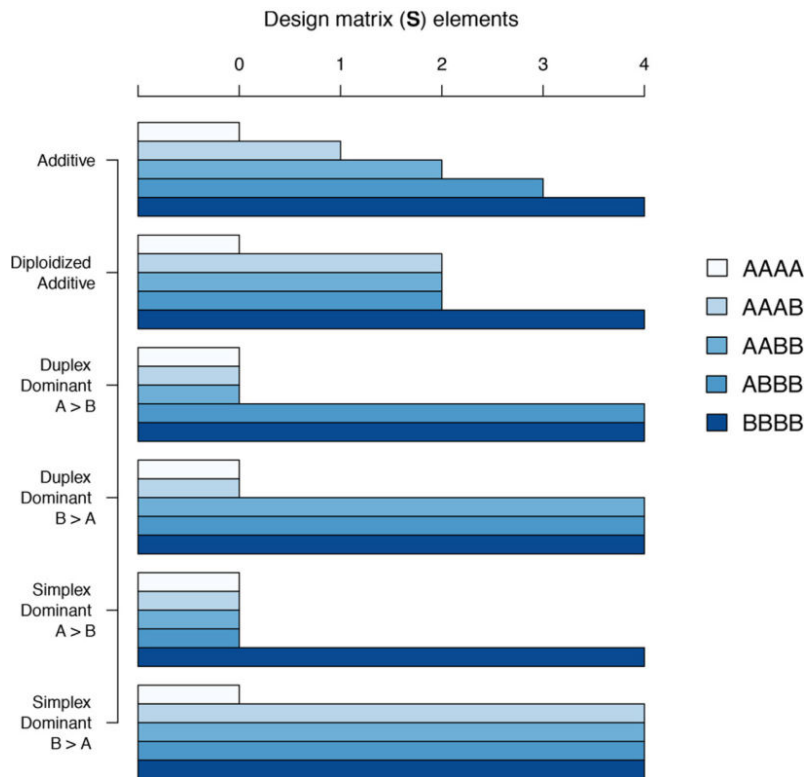
4/ To select any other model than the general model, a new drop-down menu (« Models ») is then available, e.g. select « additive »

Why so many different GWAS models ?

It is important to note that a GWAS on polyploids creates an additional degree of complexity regarding the genetic dominance of a given trait.

Note that even if all our 204 rose genotypes are not tetraploids, all were genotyped as tetraploid (most are still truly tetraploids, the remaining genotypes are mostly diploid). At each SNP, each individual has 5 possible classes of alleles B {0, 1, 2, 3, 4} depending on the observed dosage levels of allele B.

i.e. AAAA, AAAB, AABB, ABBB or BBBB



The general model is a simple model where the SNP effect can be on any of the classes. This model generally shows too many associated SNPs (and can therefore be considered as quite noisy)

The other models are more specific regarding the dominance (see opposite and the GWASpoly paper for details)

How to read the results?

