

## Grapevine QTL Browser

We defined a series of **Working Groups**, with the respective WG leader, on the following topics of interest:

- a **Vitis Ontology-dedicated Team**: the abbreviation for pathogen/disease should be homogenized, the E-L and BBCH scale should be included; an intermediate field (a potential Literature sub-folder) between Trait class and Trait name with abbreviation of 3 meaningful letters that we want to use in the QTL name (verify if in the OLS is accepted a new field). The Variable name and the Method name should be verified (now the Method name is not always included in the Variable name). A shared file could be created where the QTL information curators collect the missing traits to be included in the Vitis-Ontology.

Team: Duchêne, Vezzulli, Costantini, Moretto

- a **SSR-dedicated Team**: add the SSR name (and info) missing as well as the SSR sequences to the SSR table. Find SSR primer sequences and SSR sequence (if originally published) for VVCS, SC8, PSCgt, and other series with no information...

Team: Vezzulli, Doligez, Hausmann

- a **SNP-dedicated Team**: add the SNP name (and info) missing, including SNaPshot, SNPlex, GBS if available.

Team: Tello, Costantini, Bettinelli, Holtgräwe

- **Trait class-dedicated Teams**: per each significant Trait class/es define a working team for QTL data annotation: additional curators are suggested between brackets (confirmation is needed)

### **Abiotic stress Team:**

Chedid, Doligez, de Miguel Vega, Marguerit

### **Agronomical Team:**

Roeckel, Tello, Vezzulli, Chedid, Costantini

### **Biochemical Team:**

Costantini, Reshef, Bellin, Duchêne, Vezzulli, (Doligez), (+ helpers needed)

### **Biotic stress Team:**

Bettinelli, Hausmann, Vezzulli, Chedid

### **Morphological Team:**

Carbonell-Bejerano, Hausmann, Costantini, Bettinelli, Vezzulli, (Doligez)

### **Phenological Team:**

Bellin, Costantini, Roeckel, Vezzulli, Bettinelli, (Holtgräwe)

### **Technological Team:**

Reshef, Duchêne, Bellin

- **Marker-dedicated Team**: the aim is to update the literature about studied/developed MMs underlying QTLs, at different levels: i) physical mapping, ii) post fine mapping, and iii) post

genome sequencing. The proposal is to link this information to the QTL genomic/physical interval (see Grapevine Molecular Marker Catalogue, to be developed)

Team: **Hausmann, Vezzulli, Bettinelli**

- **Gene-dedicated Team:** the aim is to update the literature about studied CGs underlying QTLs, at different levels: i) physical mapping only, ii) expression-profiling, and iii) functional validation. The proposal is to link this information to the QTL genomic/physical interval (see Grapevine Gene Catalogue, ongoing). See also the following proposed Workflow on QTL genomic interval inspection. Level of validation from INTEGRAPE.

Team: **Fasoli, Holtgräwe, Bettinelli, Carbonell-Bejerano, Costantini**