Boosting the resilience of European shellfish production against climate change-related challenges through genetic selection: ShellFishBoost

The ShellFishBoost consortium

Background:

Bivalve aquaculture is an increasingly **important sector of global blue bioeconomy** however is **threatened by** direct and indirect effects of **climate change**:

- By 2090 suitable areas for bivalve aquaculture will globally decrease by 10% because of climate change;
- **The threat not** deriving **only from average changes** in physiochemical conditions, **but also from extreme events** like heatwaves or extreme droughts, **and**, indirectly, **from increased prevalence to pathogens**.

Aims and scopes:

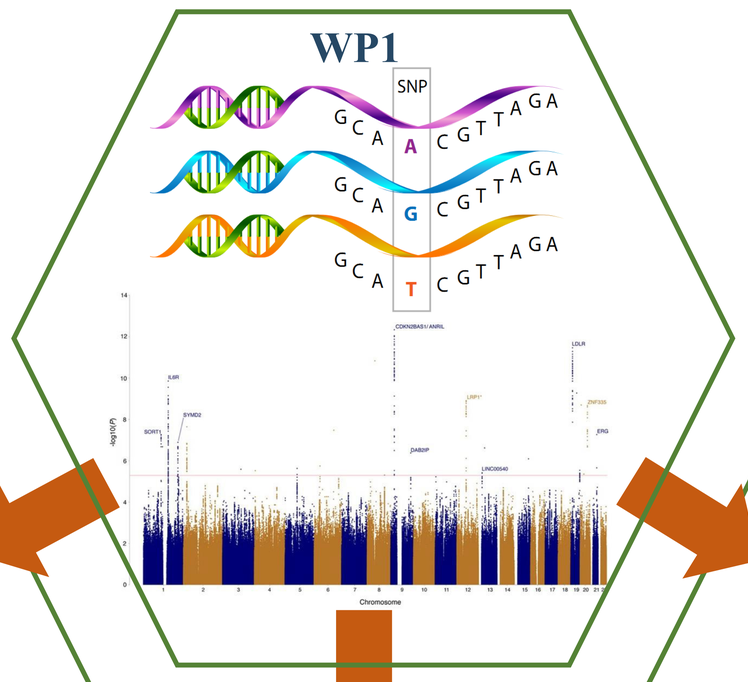
ShellFishBoost aims at **protecting and developing the blue bioeconomic sector of bivalve aquaculture** by addressing key climate-related problems for the main species of bivalves farmed in EU (Fig. 1) **to improve their resilience** through targeted interventions:

✓ The development of **advanced tools for genetic selection** (e.g. optimized breeding schemes);
✓ The **estimate of genetic parameters for key traits** of interest (e.g. growth, disease resistance, resistance to heatwave).
✓ **Co-creating** with key stakeholders **best practices** for **selective breeding** in bivalves

Activities within ShellFishBoost

WP1 – Advance tools for genetics

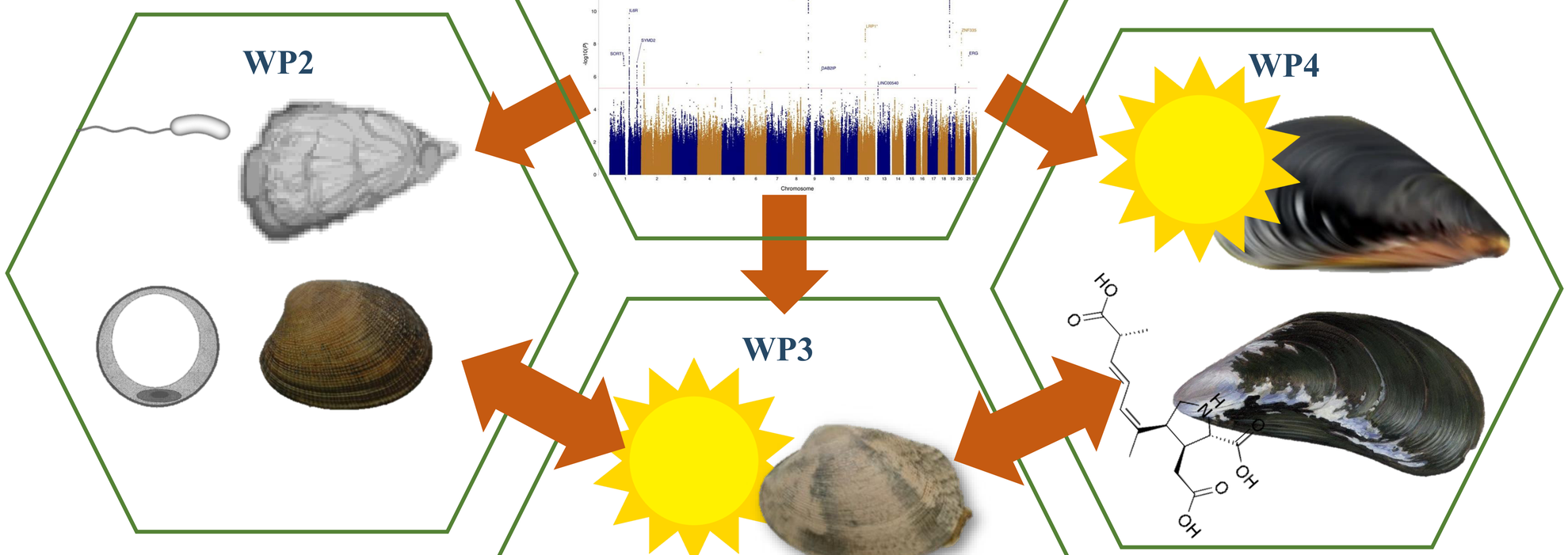
An inventory of all available information on SNPs and existing genotyping tools for all species will be created. SNPs databases will be created from high quality reference genomes. High/medium quality SNP arrays for parentage assignment for all species will be produced.



WP4 – Toxin accumulation

Focus of this WP will be **toxin accumulation in mussels**:

- To disentangle genomic architecture of toxin accumulation from harmful algal blooms, Mediterranean mussels (*M. galloprovincialis*) and blue mussels (*M. edulis*) with known levels of toxin in their tissues will be genotyped using SNPs from WP1.
- Genetic parameters (heritability and genetic correlations) will be quantified for production traits and for toxin accumulation.



WP2 – Disease resistance

Focus of this WP will be **disease resistance in oysters and clams**:

- Using the new high-density genotyping tools from WP1, novel Quantitative Trait Loci (QTLs) for disease resistance against *Ostreid Herpes Virus* OsHV-1 and the bacteria *Vibrio aesturianus* will be discovered and existing QTLs will be validated in the Pacific oyster *C. gigas*.
- A similar approach will be carried for the Manila clam *R. philippinarum* challenged against the protozoan parasite *Perkinsus spp.*

WP5 – Co-creating best practices and strengthening the capacities for selective breeding in bivalves

Co-creation groups for defining best practices, creating a short training course on selective breeding

WP3 – Climate change resilience

Focus of this WP will be **climate extremes and traits associated with resilience** to these extremes **in oysters and clams**, in particular heatwaves and sudden salinity drops:

- Using SNP-arrays developed in WP1, novel QTLs linked with these extreme events will be produced in the European oyster *O. edulis*, and in the clams *R. philippinarum* and *R. decussatus*.
- Genetic parameters (heritability and genetic correlations) will be quantified for production traits and for resistance traits.

Bivalve species within ShellFishBoost:

Crassostrea gigas | *Ruditapes philippinarum* | *Ruditapes decussatus* | *Ostrea edulis* | *Mytilus galloprovincialis* | *Mytilus edulis*

Sustainable Blue Economy Partnership

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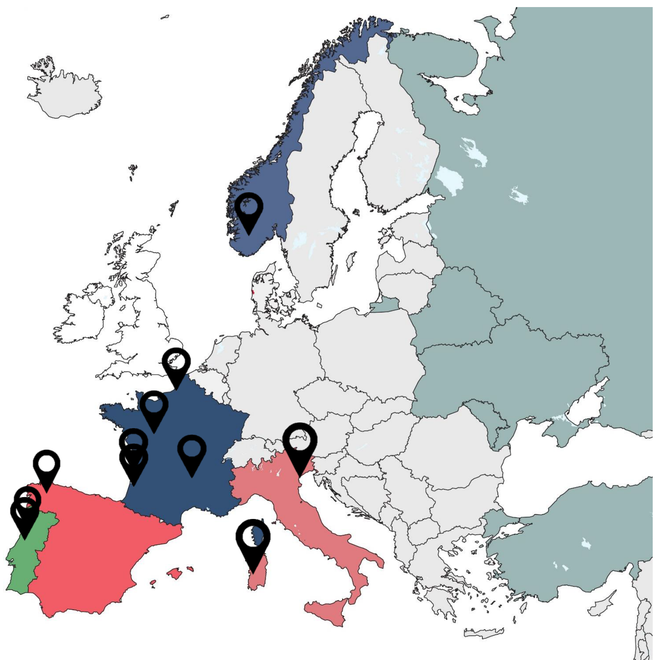

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