



Pre-breeding strategies for obtaining new resilient and added value berries

Open Call fiche

*Open Call#2: Genomic selection in strawberry (*F. xananassa*)*



Open Call#2: Genomic selection for strawberry (*F. xananassa*)

Genomic selection is used to select breeding material for further hybridization and/or for entering advanced cultivar trials based on their genomic breeding values rather than on phenotypic values. This approach shows better performance than traditional methods such as phenotype-based selection, pedigree-based selection, and marker assisted selection, particularly for polygenically inherited traits.

The objective of this Open Call is to employ state-of-the-art methodology on breeders' material and implement the technology to the breeders. This can help the breeders to do selection in early stages of their breeding program, accelerating the generation cycles by identifying superior parents, and increasing likelihood of identifying good candidates for advanced trialing.

In this Open Call, we will fund **2 projects à 20,000€**.

Who are we looking for?

We are looking for applied strawberry breeders with phenotype data available (or with ability to obtain such within the call's time frame) for a high number of cultivars and/or breeding lines of strawberry (*F. xananassa*). The breeder must also be able to provide extracted DNA and have an interest to develop and apply genomic selection on own breeding material.

For a complete description of the specific requirements you should fulfil for this Open Call, please consult the Guide for Applicants.

Your benefits

If you are selected for this Open Call, you will

- ✓ Learn the methodology for genomic selection through direct support and seminars.
- ✓ Obtain prediction models that are developed on, and amenable to, your own breeding material.

Eligibility criteria

You are qualified to apply for this Open Call if you fulfil the following criteria:

- ✓ You are an [SME according to the definition of the European Commission](#) (<250 employees, <€50m annual turnover);
- ✓ You have to be legally registered in [member states of the European Union or in Horizon 2020 associated countries](#);
- ✓ The application has to be submitted before the deadline of the Open Call;
- ✓ The application has to be in the English language;
- ✓ The application has to be complete (including all required signatures);
- ✓ The application has to address one of the four topics of the Open Calls within BreedingValue;
- ✓ Absence of conflict of interest: You may not have an actual and/or potential conflict of interest during the application process and project implementation (see Declaration of Honour). Accordingly, members currently involved in the BreedingValue project as beneficiaries, subcontracts, linked (third) parties and advisors are not eligible to apply. Should any conflict of interest arise, this will be assessed on a case-by-case basis.

Evaluation criteria

The projects will be selected based on the following criteria:

- ✓ You have an advanced running strawberry breeding program.
- ✓ You (or your sub-contractor) are able to extract high-quality DNA from 768 lines of strawberry (*F. xananassa*). This implies: 1) Sampling, labelling, and immediate flash-freezing of juvenile leaves in 96-well plates (DNeasy 96 Plant Kit, QIAGEN). 2) Storage of leaf samples (at least -20°C) until DNA extraction in-house or shipment to extraction sub-contractor in frozen condition. 3) Extract/provide DNA of a quality grade required by the genotyping assay. 4) Shipment of DNA in frozen condition to genotyping facility.

- ✓ You are able provide phenotype data on the 768 lines: The phenotyping to be performed shall include the susceptibility to powdery mildew. The phenotype retrieval should ideally be taken from a replicated field trial. If, however, an un-replicated trial is used, a set of control lines should be planted in every 10th plot. Spatial information (row and column numbers) must be presented in order to correct for spatial variability through the field. The pesticide treatment must be relaxed after field establishment to allow for powdery mildew to establish. The scoring of powdery mildew susceptibility must be done using Simpson's 1 to 5 ordinal scale. This scoring must be done at least five times between planting and first harvest in order to calculate area under the disease progress curve (AUDPC). Additional phenotype data, e.g., date of flowering, etc., can be supplied and is regarded positively.
- ✓ You can ensure consistency of the phenotypic data provided. This implies that the phenotypic scores are taken by the same person over time and that this person is trained.

Please note: Breeders are encouraged to share the pedigree of the studied genotypes.

Funding criteria

In order to qualify for financial assistance within this call breeders will be asked to give an outline on how the money will be spent to meet the outlined criteria (DNA extraction, attending meetings, travel etc.). For more details, please consult the Proposal Template and the Guide for Applicants.

- ✓ **Milestone 1:** Completion of contracts and introductions to researchers. Initial traits of interest and phenotypic data collection are recorded (*December 2021*).
- ✓ **Milestone 2:** Suitable leaf samples (and if possible/agreed upon pedigree information) have been collected (*July 2022*).

The **first payment** will be made after an **interim report** confirming the milestone achievement has been submitted and approved (*July 2022, 50% of total funding*).

- ✓ **Milestone 3:** Suitable phenotypic data has been received for the selected material (*November 2022*).
- ✓ **Milestone 4:** Supply of supplementary phenotypic data from the second year (*July 2023*).
- ✓ **Milestone 5:** Completion of training (*Fall 2024*).

The **final payment** will be made after a **final report** has been submitted and approved (*Fall 2024, 50% of total funding*).

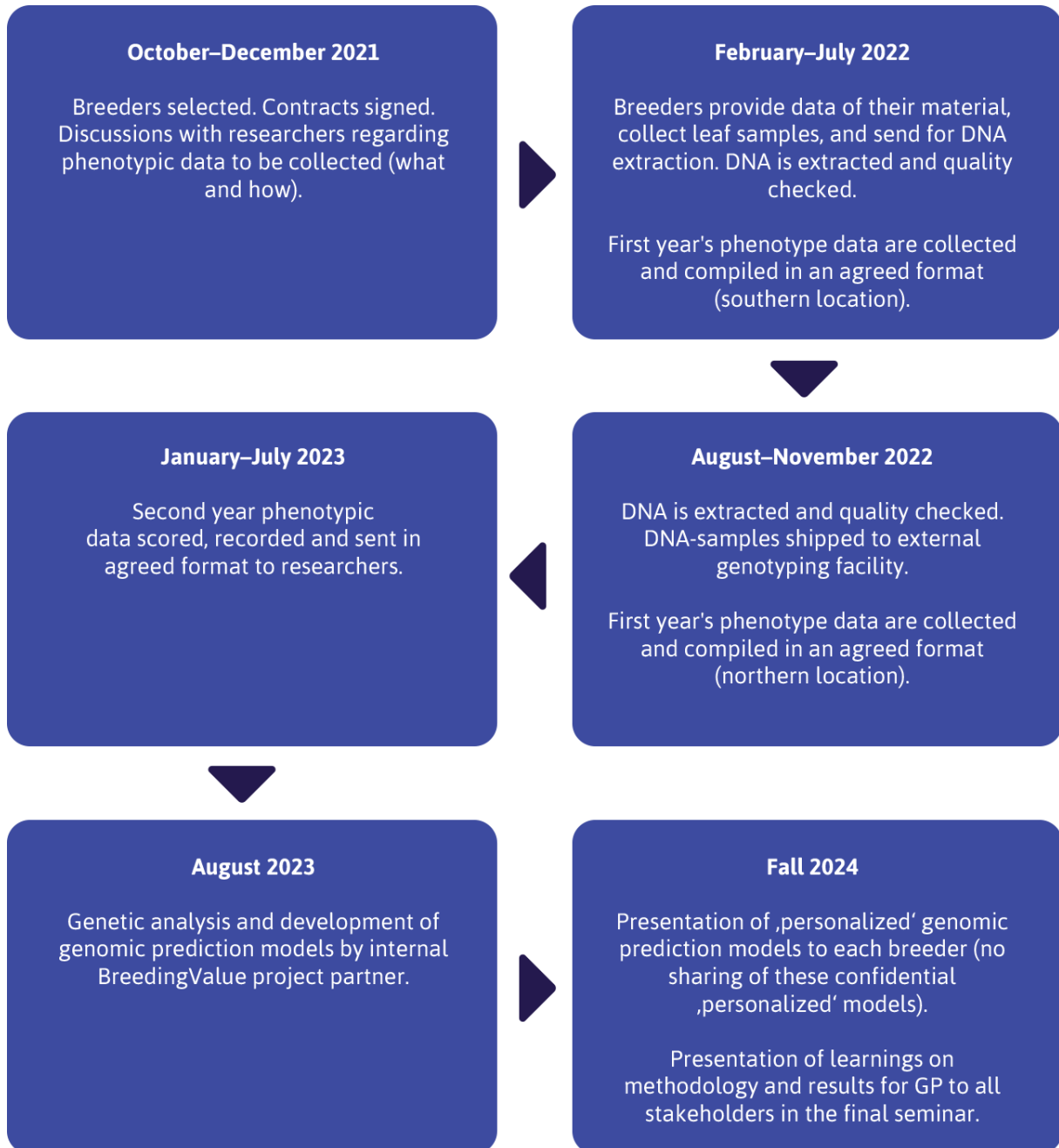
Please note that in case ethical issues were identified in the application phase, additional deliverables for monitoring of these issues will be added as contractual requirements during the Sub-Grant-Agreement negotiation.

Application, evaluation and project preparation timeline



Timeline of project implementation

The Open Call project will run for 4 years, from 2021 to 2024. The detailed timeline is described below.



How to apply

Applications can only be made via e-mail and have to be submitted under the following address: opencalls@breedingvalue.eu.

Please observe the instructions for formatting and submissions in the Guide for Applicants.

Deadline

The deadline for submissions is **30th June 2021 at 17:00 CET**. Applications received after the deadline will not be considered for evaluation.

Documents to be filled in the application process

- ✓ Proposal template
- ✓ Declaration of Honour

- ✓ SME Status Confirmation
- ✓ Data protection statement

Further information for the application is provided in the Guide for Applicants.

Contact Info

In case of questions, please consult the BreedingValue helpdesk: info@breedingvalue.eu