



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

### **Open Call fiche**

*Open Call #1: Marker-Assisted Selection (MAS) in strawberry*



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Marker assisted selection is a method used to select desirable individuals in a breeding programme based on DNA molecular marker patterns in addition to their trait values. This can serve as a valuable tool to assist breeders to select new genotypes more efficiently. In this project, we will evaluate the predictive capacity of molecular markers and their usefulness for MAS. The selected markers are either already published or currently under research within the BreedingValue consortium, and have been validated in diverse strawberry germplasm for a reduced number of cases. We will focus on identifying molecular markers for the traits listed in the annex at the end of the document, such as disease resistances, fruit quality as well as vegetative and production traits.

For the project, a low-density SNP array for Marker Assisted Selection (MAS) is currently under development in cooperation with an external facility, that will perform the genotyping for the breeders selected in this Open Call. The genotyping costs will be covered by the BreedingValue consortium. The objective of this Open Call #1 is to share this easy-to-use tool with the selected external breeders to facilitate the selection of superior breeding material. In return, the results obtained by the breeders will allow the BreedingValue consortium to validate the low-density SNP array in larger genetic backgrounds.

In this Open Call, we will fund **3 projects à 20,000€**.

### Who are we looking for?

We are looking for breeders and pre-breeders working on cultivated strawberry (*F. xananassa*), who are interested in training on marker-assisted selection but currently have no or little experience with this.

Applicants will need to provide during the course of the project phenotyping data on some (as many as possible) of the traits listed in the annex. Phenotyping protocols will be provided by the BreedingValue project. Genotyping will be done using the array under development for at least 300 lines of strawberries. The exact number of lines will depend on the number of traits recorded by the breeder. The breeder must also be able to provide extracted DNA (the technique can be provided by the BreedingValue consortium if needed) and have an interest to develop and apply MAS on own breeding material.

### Your benefits

If you are selected for this Open Call, you will

- ✓ Receive training on marker-assisted selection
- ✓ Obtain support for phenotyping and genotyping of selected material
- ✓ Obtain support in setting up and conducting marker-assisted selection on your own material.

### Eligibility criteria

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

- ✓ 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 a breeding selection programme for cultivated strawberry (*F. xananassa*).
- ✓ You are willing to undertake training for MAS, including sending one person to be trained in a lab of a BreedingValue partner (in France or Spain);
- ✓ You include into the proposal a list of at least 300 genotypes from a pre-breeding programme, GenRes and breeding programmes chosen for the MAS approach. The exact number of lines will depend on the number of traits recorded by the breeder. Criteria of genotype selection has to be explicit.
- ✓ You already have experience in collecting phenotyping data linked to specific traits such as the traits listed in the annex, as well as environmental data (temperature, humidity etc.)
- ✓ You include into the proposal a list of the traits you will score (from the list of traits in the annex). For these traits, you will follow the phenotyping protocols provided by the BreedingValue project.
- ✓ You are able to provide phenotyping data on two seasons of production: 2022 and 2023. As the project will begin at April 2022, participants from Southern Europe should be able to start the phenotyping at the beginning of 2022 before official project start.
- ✓ You will produce appropriate excel files of this phenotyping data (including environmental data) and give the correspondence between the genotyping number and the phenotyping data.
- ✓ You are able to extract high quality DNA from leaves of at least 300 samples (number depending on the number of traits recorded). The DNA extracted will be sent to the external facility that will perform the genotyping for all breeders selected in this Open Call;

## 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, phenotyping, genotyping, attending trainings, travel etc.). For more details, please consult the Proposal Template and the Guide for Applicants.

- ✓ **Milestone 1:** Validation of the lists of genotypes and traits to be scored (*April 2022*)
- ✓ **Milestone 2:** Training (1-2 days) in France or Spain on the MAS approach (phenotyping protocols for MAS validation, steps for array development) (*April – May 2022*)
- ✓ **Milestone 3:** Phenotyping 1<sup>st</sup> year of the material studied in this project (at least 300 genotypes) with a complete excel file (list of genotypes and their corresponding phenotyping data). Phenotyping in Southern Europe will start before official project start (*April – October 2022*)
- ✓ **Milestone 4:** Send the DNA material to the genotyping facility after the DNA extraction of at least 300 genotypes (*September – December 2022*)

The **first payment** will be made after an **interim report** confirming the milestone achievement has been submitted and approved (*January 2023, 50% of total funding*).

- ✓ **Milestone 5:** Pre-genetic analysis based on genotyping data and phenotyping data of the 1<sup>st</sup> year. Collaboration between BreedingValue partners (INRAe, IFAPA) and the breeders (*April – December 2023*)
- ✓ **Milestone 6:** Phenotyping 2<sup>nd</sup> year of the material studied in this project (at least 300 genotypes) for 2 years (*January – October 2023*)
- ✓ **Milestone 7:** Final genetic analysis based on genotyping data and phenotyping data of both years. Collaboration between BreedingValue partners (INRAe, IFAPA) and the breeders (*October 2023 – May 2024*)
- ✓ **Milestone 8:** Final workshop (1-2 days) in France or Spain (*June - August 2024*)

The **final payment** will be made after a **final report** has been submitted and approved (*September 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 2.5 years, from 2022 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](mailto:opencalls@breedingvalue.eu)

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

## Deadline

The deadline for submissions is **31<sup>st</sup> December 2021 at 17:00 CET**. Applications after the deadline will not be considered for evaluation.

## Documents to be filled out for application

- ✓ Proposal template
- ✓ Declaration of Honour
- ✓ 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](mailto:info@breedingvalue.eu)

## Annex:

Table 1. Traits targeted in the BreedingValue MAS array

### RESISTANCES TO PESTS

Resistance to *Pythophtora cactorum*  
Resistance to *Coletotrichum acutatum*  
Resistance to *Fusarium oxysporum* f. sp.  
Resistance to *Colletotrichum gloesporioides*  
Resistance to *Verticillium dahliae*  
Resistance to *Xanthomonas fragariae*  
Resistance to Powdery mildew (*Podosphaera aphanis*)  
Resistance to *Macrophomina phaseolina*  
Resistance to *Tetranychus urticae*

### VEGETATIVE TRAITS

Day neutrality, Everbearing  
Flowering time

### PRODUCTION TRAITS

Fruit weight  
Fruit number  
Total Yield  
Class one yield specific

Total Fruit Number & Marketable Number

Total Fruit Number, class 2 mass

## FRUIT QUALITY

Fruit firmness

Bostwick consistency

Vitamin C (L-ascorbic acid)

Soluble solids content (SSC)

Acidity (TA) / pH / acidity perception

Sucrose

Raffinose

Succinic acid

Malic acid

Fruit color (quantitative), pelargonidins and Eriodictyol

Internal fruit color (qualitative)

Fruit color (internal and external; qualitative)

Total anthocyanins

Total anthocyanins + Pelargonidin-3-Glucoside

Yellow flesh color and carotenoids

epicatechin glucuronide, kaempferol hexose, cyanidin hexose and rutin

propelargonidin dimer and kaempferol hexose

pelargonidin-3-O-malonylglucoside

Ellagic acid hexose

ellagic acid deoxyhexoside

cinnamoyl glucoside

Galloyl-bis(HHDP)-glucose

Caramel aroma (Mesifurane)

Peach aroma (gamma-declactone)

Grape aroma (Methyl anthranilate)

Fruity aroma (Methyl butanoate)

Fruity aroma: decyl, hexyl, octyl and nonyl acetates, octyl butanoate

Butyl, hexyl, octyl, nonyl, decyl, cinnamyl acetates, butyl and octyl butanoate, butyl and octyl hexanoate

Aroma: Terpenes