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

Open Call fiche

Open Call#3: Marker-Assisted Selection (MAS) and Genome wide association

Open Call#3: Marker-Assisted Selection (MAS) and Genome wide association studies (GWAS) in Raspberry

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 more efficiently. In this BreedingValue project, we will identify molecular markers which can be useful to breeders across all raspberry breeding programmes for traits such as fruit size, softening, timings of fruit development stages, cane diseases or fungal diseases such as yellow rust.

The objective of this Open Call is to offer breeders an opportunity to screen and select their genotypes of interest against a suite of markers, which can help breeders to better select parental material depending on the trait of interest. Genome wide association studies (GWAS) delves further into the genetic variants within screened markers across different individuals to determine if any of these variants are associated with a particular trait or disease such as yellow rust susceptibility.

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

Who are we looking for?
We are looking for breeders with robust phenotypic information (or with the ability to obtain such within the call's time frame) on a diverse range of around 450 raspberry material. The breeder must also be able to provide extracted DNA or leaf material for genotyping and have little or no experience with MAS and GWAS with an interest in developing this approach further.

Your benefits
If you are selected for this Open Call, you will benefit from
- ✓ Support (including seminars) on MAS and GWAS and their application in breeding.
- ✓ Support on setting up and conducting MAS and GWAS across diverse germplasm, genetic information on marker results, such as yellow rust susceptibility, to better inform breeders with their parental choices.

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 fours 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 established raspberry breeding program with selections of five years or older.
- ✓ You can collect suitable leaf samples from 450 lines and store at -20°C prior to sending to a genotyping platform that can extract high quality DNA. (Advice will be given to selection of appropriate leaf material and where to send samples for extraction if required). This is likely to involve: 1) Collection, accurate labelling, and immediate flash-freezing in liquid nitrogen of

juvenile leaves as instructed by genotyping facility. 2) Storage of leaf samples (at least -20°C following flash freezing) until DNA extraction in-house or shipment to extraction sub-contractor in frozen condition as close to collection as possible. 3) Extract/provide DNA of a high-quality grade required by the genotyping assay. 4) Shipment of DNA in frozen condition to genotyping facility.

✓ You are able to perform phenotyping on the 450 genotypes selected; the phenotyping to be performed will include the date of flowering, the quality of the fruit (visual aspect e.g., size, softening, total soluble solids), the susceptibility to diseases of interest such as yellow rust and any available environmental data (temperature, humidity etc.), subject to agreed priorities. 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 to correct for spatial variability through the field.

✓ You can produce appropriate excel files for selected raspberry lines complete with the phenotypic data collected.

✓ You can ensure consistency of the phenotypic data provided and detail how the data was collected.

✓ You are willing to undertake training for MAS and GWAS.

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 *(May 2022).*

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

✓ **Milestone 3**: Receipt of the phenotypic data for the 450 selections (*November 2022*).

✓ **Milestone 4**: Supply of supplementary phenotypic data from year 2 for the 450 selections (*November 2023*).

✓ **Milestone 5**: Completion of training (*Fall 2024*).

The **final payment** will be made after a **final report** has been submitted and approved (F*all 2024*, 50% of total funding).
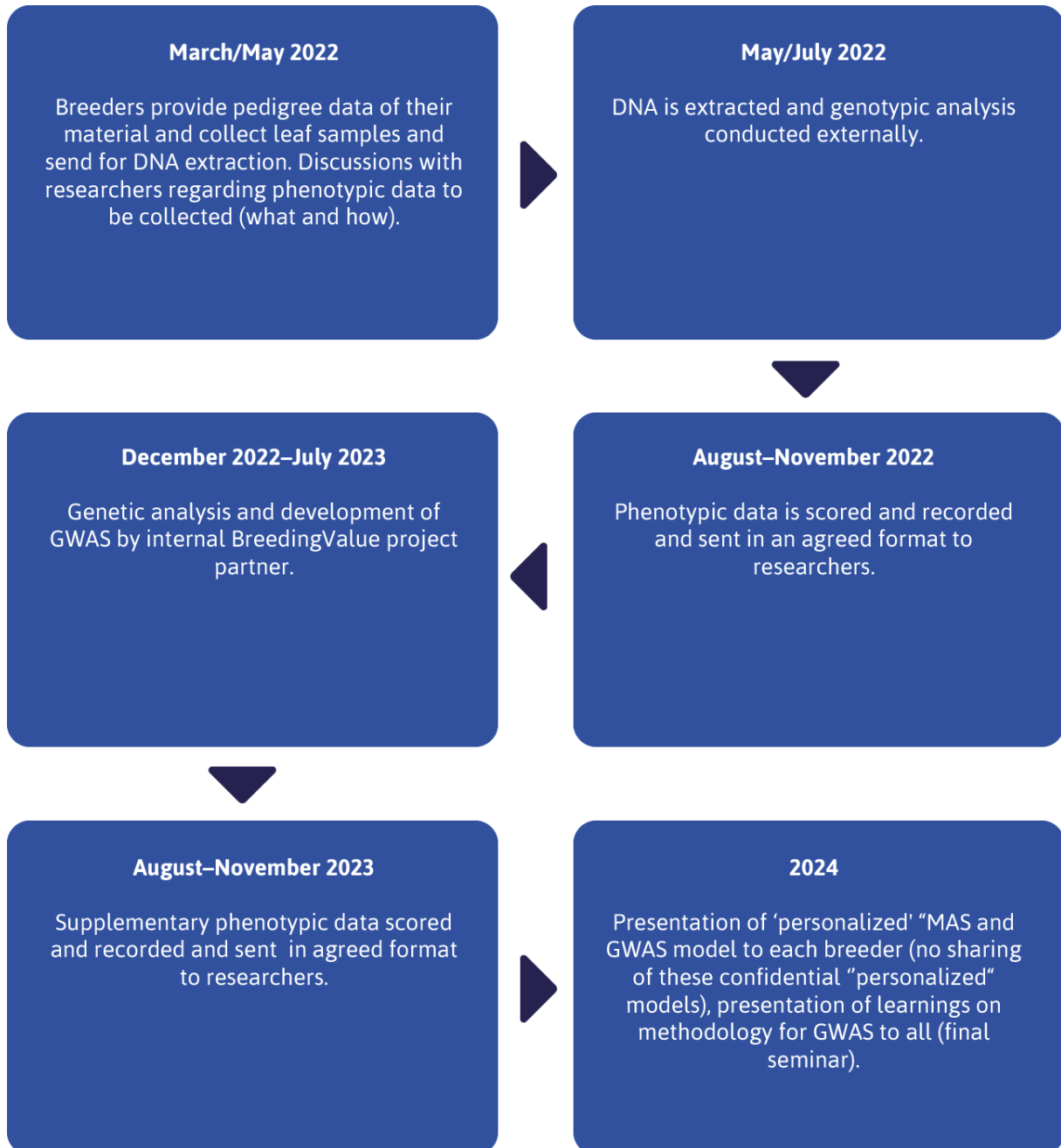
Please note that in case ethical issues were identified in the application phase, additional deliverables for monitoring of these issues will be added as contractual requirements during the Sub-Grant-Agreement negotiation.

Application, evaluation and project preparation timeline

Timeline of project implementation

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

March/May 2022

Breeders provide pedigree data of their material and collect leaf samples and send for DNA extraction. Discussions with researchers regarding phenotypic data to be collected (what and how).

May/July 2022

DNA is extracted and genotypic analysis conducted externally.

December 2022–July 2023

Genetic analysis and development of GWAS by internal BreedingValue project partner.

August–November 2022

Phenotypic data is scored and recorded and sent in an agreed format to researchers.

August–November 2023

Supplementary phenotypic data scored and recorded and sent in agreed format to researchers.

2024

Presentation of 'personalized' "MAS and GWAS model to each breeder (no sharing of these confidential "personalized" models), presentation of learnings on methodology for GWAS to all (final seminar).

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 of Applicants.

Deadline

The deadline for submissions is **30th June 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
- ✓ 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