

## PhD proposal: Genetic bases of adaptation in wheat wild relatives

### Context

Modern crops harbor limited potential for improvement due to recurrent selection for few traits such as increased biomass, in detriment of traits for adaptation to biotic and abiotic stresses. In comparison, crop wild relatives (CWR) have evolved under diverse and often extreme ecological contexts and carry greater levels of genetic diversity that can be deployed in crop breeding (Dempewolf *et al.*, 2017). In the quest for new targets for yield, sustainability and climate resilience (Krug *et al.*, 2023), there is a major interest in understanding CWR adaptive strategies.

Cereals are the world's most significant sources of calories and nutrients. Within the grasses (family Poaceae), the Triticeae includes worldwide staples wheat, barley and rye. In the last decades, transfer of alleles from CWR into the crop gene pool have improved yield, quality, and tolerance to biotic and abiotic stresses (Feuillet *et al.*, 2008). More potentially useful traits have been identified, but, with approximately 500 species, the extent of adaptive diversity within the Triticeae is largely unknown and virtually untapped so far (Kilian *et al.*, 2011; Leigh *et al.*, 2022).

It has been recently shown that the probability that the same genetic variants are mobilized in response to selection depends on populations and species divergence (Bohutinská *et al.*, 2020). Thus, to identify adaptive variants for future agriculture, a relevant strategy is to investigate the signatures of selection in a multispecies comparative setting, which may give insights on the probability of evolution repeating itself.

### Objectives

**This PhD proposal aims at studying the genetics of adaptation in wheat wild related species to leverage CWRs in an agroecological context.**

The objectives are:

- identifying genes under selection in wheat wild relatives,
- associating these selection footprints with environmental constraints,
- identifying among those selected genes those that can be leveraged for wheat breeding.

### Available data

The student will build up on already available whole transcriptome data (Glémin *et al.*, 2019; Burgarella *et al.* 2023), which provides i) full transcriptome sequences for 103 individuals of 19 Triticeae species, ii) the level of expression of the different genes in these individuals, iii) polymorphism data ( $\geq 7$  individuals for 5 species).

Additionally, high-quality whole genome sequences of wild, domesticated and modern wheat accessions are publicly available and large-scale sequencing projects are currently underway, as well as gene expression studies in domesticated wheat under stress. These data will be suitable for assessing the relevance of further investigating identified candidate genes in cultivated species.

### Methodology

The doctoral candidate will have some freedom to decide the direction of the thesis and therefore the analyses to be performed, such as:

- Searching for genes/branches under selection using a dN/dS approach relying on the phylogeny published by Glemin *et al.* (2019).
- Searching for species specific selection footprints using tests comparing polymorphisms and divergence for species for which polymorphic data are available. Recent method developments allow these approaches to be applied to gene expression analysis (reviewed in Price *et al.*, 2022).
- Identifying genes under selection for specific environmental constraints (e.g. higher temperature) using methods such as those described in Pease *et al.*, 2016 and Wu *et al.*, 2017.
- Identifying genes in cultivated species homologous to adaptive genes in the wild compartment.
- Documenting indicators that could influence the transfer of relevant wild allele/genes (recombination rates, degree of similarity between domesticated and wild alleles, etc.).

## Hosting environment

The PhD student will be hired by INRAE and hosted by the team GE2pop (*Evolutionary genomics and population management*), UMR AGAP Institut (<https://umr-agap.cirad.fr/en>). Supervisors will be Concetta Burgarella (population geneticist, INRAE), Nathalie Chantret (evolutionary genomicist, INRAE) and Vincent Ranwez (molecular phylogeneticist, Institut Agro Montpellier).

GE2pop research on wheat wild relatives aims at understanding species evolutionary history and adaptive potential. Our recent works have disentangled the evolutionary history of the *Triticum/Aegilops* species complex (Glémin *et al.*, 2019), and shown the effect of mating systems on genomic diversity and patterns of selection (Burgarella *et al.*, 2023).

Montpellier has one of the largest communities of crop geneticists and evolutionary biologists in Europe, and a large student community, and provides a very stimulating scientific environment.

## Applicant's profile

Strong expertise in either (or combined) evolutionary biology, phylogenetics, genomics, and data analysis.

## Eligibility and application procedure

- Applicants from all countries are eligible, provided that they have a MSc. Degree.
- Please provide: (1) a motivation letter with a statement of research interests, skills and experience relevant to the position, (2) a CV, (3) contact details of two referees, (4) copies of previous degrees and transcripts of records and (5) a copy of the master thesis. All materials should be emailed to [concetta.burgarella@inrae.fr](mailto:concetta.burgarella@inrae.fr), [nathalie.chantret@inrae.fr](mailto:nathalie.chantret@inrae.fr) and [vincent.ranwez@supagro.fr](mailto:vincent.ranwez@supagro.fr).

## Relevant references of GE2pop team

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## Other references

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