

Revisiting Green Revolution Genes in Cereals to Address Agroecological Challenges

Join us in a multidisciplinary project!

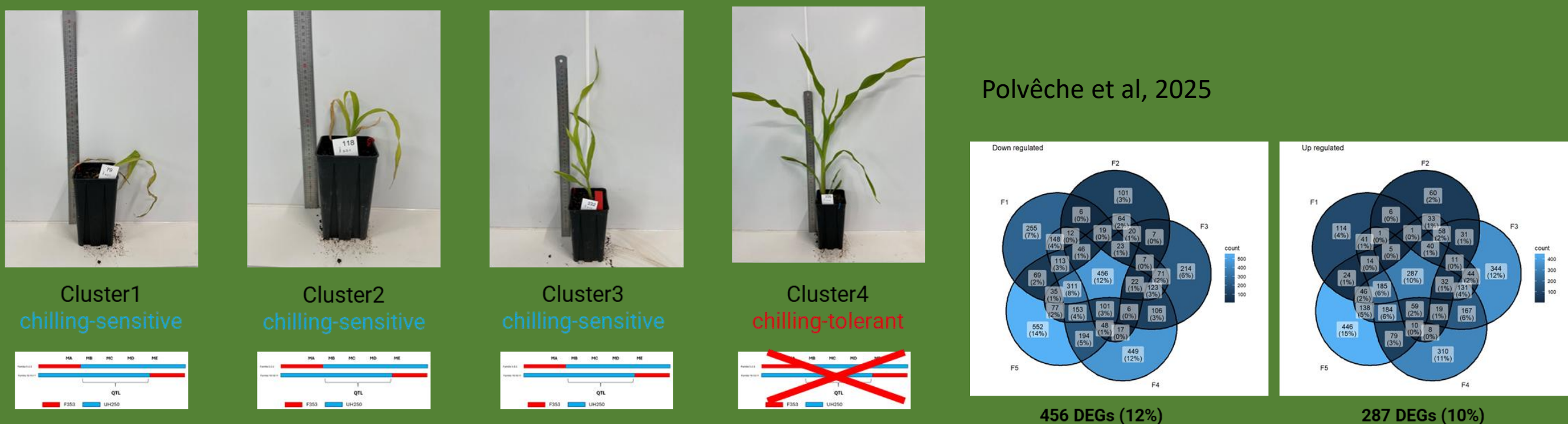


Catherine Giauffret and AGAP colleagues
catherine.giauffret@inrae.fr

The European Union is a major importer of maize (15 millions tons in 2021) (USDA, 2022). In France, maize is the second most widely grown crop after bread wheat, but it suffers from a negative reputation due to its high water consumption during summer. In a context of reduced irrigation opportunities and lower fertilizers inputs, sorghum appears as a good alternative. However, sorghum often fails to survive when exposed to low temperatures at early stages. This extreme chilling susceptibility strongly limits sorghum expansion in Europe. Previous genetic studies in sorghum and maize have found a tight link between chilling susceptibility and the semi-dwarfism genes widely used in breeding. If this result is confirmed, breeding programs will have to search for new sources of short stature.

Fine-mapping of a stress tolerance QTL and genomic sequences analysis

In a previous study, five heterogeneous inbred families (HIF) were used to validate and refine the position of a causal region for chilling tolerance. Multivariate analyses were applied to classify plants according to chilling symptoms severity. Several clusters of chilling-sensitive plants, differing in symptom severity, were identified, but only a single cluster of tolerant individuals. Based on the phenotyping, the interval was narrowed to a 455 kb segment containing nine positional candidate genes.



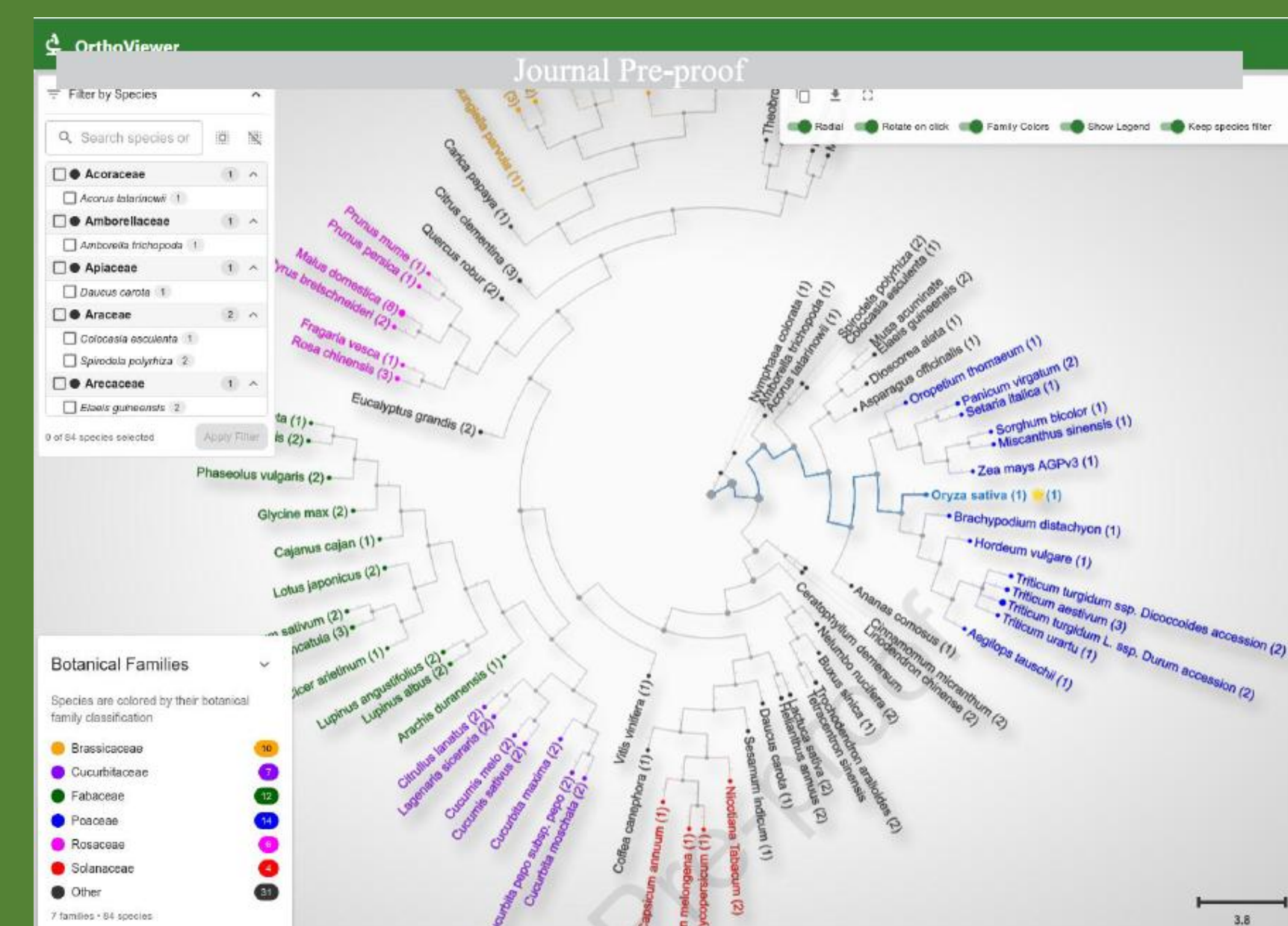
At the transcriptomic level, sensitive clusters could not be distinguished. Comparison between sensitive and tolerant individuals within each HIF family revealed 456 upregulated and 287 downregulated genes. None of the nine positional candidates were among these differentially expressed genes shared across families.



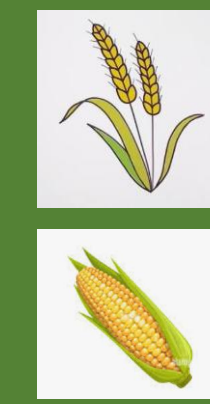
An analysis of targeted genomic and transcriptomic sequences of various lines differing in chilling tolerance (including the HIFs' parents) will help link DNA/RNA polymorphisms to stress tolerance.

Identification of dwarfism orthologous genes in cereals

Dwarfism genes have been widely used in cereals, but dwarfism is obtained through various pathways depending on the species. Hormones (auxin, gibberellin, BR...) are often involved although an increasing amount of studies document their role in stress response. In sorghum, the reduction of plant height through dw1 and dw3 is associated with a reduced chilling tolerance (Marla et al., 2021).



Signet C., Olivier M., Huneau C., Sow M.D., Stenger P.-L., Klopp C., ... Salse J. (2026) Reconstruction of ancestral plant genomes for inter-crop translational research. *Molecular Plant*, S1674205226002194.

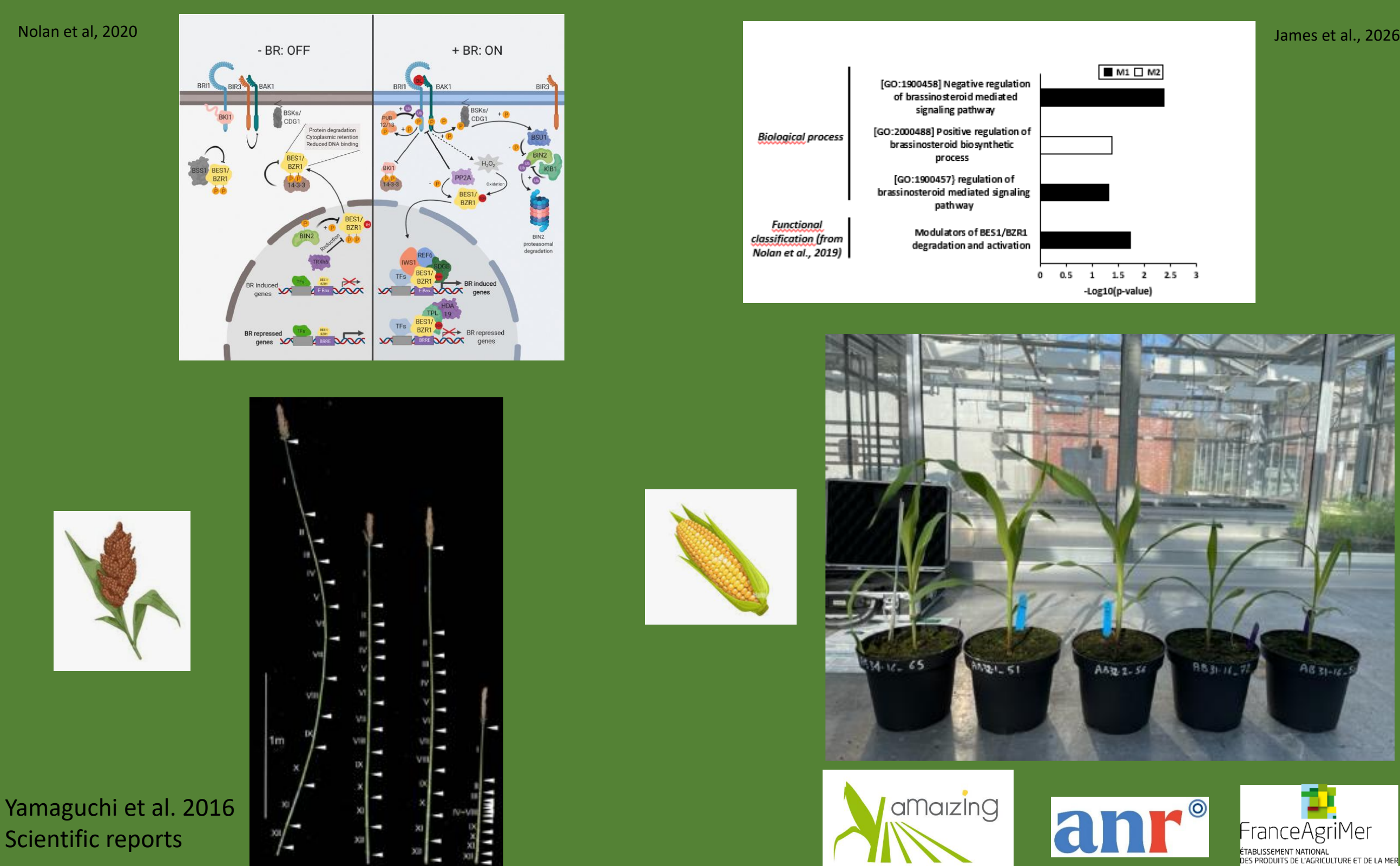


A translational analysis of dwarfism genes in cereals will open new avenue for short but resilient high yielding genotypes in sorghum



Functional analysis of brassinosteroid-related dwarfism genes

Chilling tolerance in maize and sorghum appears to be associated with hormonal pathways, especially brassinosteroid signalling genes. Some of these genes are known to be involved in plant height.



The study of EMS mutants (sorghum) or edited plants (maize) will elucidate the link between brassinosteroid genes and chilling stress.

Phenotyping of near-isogenic lines and mutants

For sorghum, near-isogenic lines or mutants for various well-known dwarfism genes (dw1, dw3) or new candidates have been obtained.

The AGAP-PhenoME team has strong expertise in conducting experiments under controlled conditions or in field networks to study the effects of isolated, repeated, or combined environmental stresses. To analyse the determinants of phenotypic variability, the team develops cutting-edge phenotyping methods and software, including image and spectral analyses using artificial-intelligence pipelines.



Characterising the effects of environmental stresses on short versus normal-stature plants (HIFs, mutants) will guide the choice of dwarfism targets in sorghum breeding programmes.

Within this project, M1 and M2 students will have the opportunity to experience ecophysiology, biochemistry, genetics, genomics and/or bioinformatics methods to solve an agronomic problem. While contributing to an agroecological challenge, it offers them a way to choose their specialisation. The detailed program of each internship can be adapted to student's preference.

Please come and discuss with us