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Uncovering seed biology traits of new hybrids of interest in wheat

Sara Belcapo, PhD Molecular and Cellular Biology, 39° cycle

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Background: Agriculture development is necessary to improve the quality of crops in order to cope with human food necessities and climate changes. Wheat is a worldwide staple food, and it is one of the most produced cereals. However, studies have shown that wheat yield should double by 2050 to feed almost 10 billion people. A solution suggested to meet the challenge of having more productive and resistant plants is the generation of hybrids.
Despite the fact that seed germination and development are crucial processes in the successful establishment of the plant, leading to healthy crop stands, the biological and genetic basis of seed development in heterosis (the improvement of any biological quality in a hybrid offspring) is still limited and poorly understood.
In this project, we intend to describe better this phenomenon at early seed stages by characterizing the seed biology of hybrids under control and stress conditions. Moreover, in the future we would like to uncover the genetic and epigenetic bases related to seed quality and germination by performing genome-wide analysis and NGS.

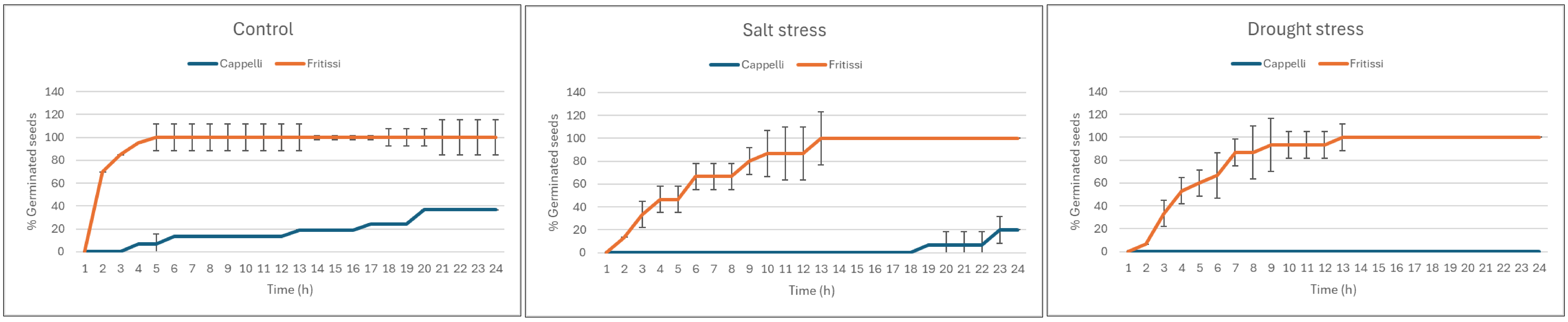


Figure 1: Germination analysis under control and stress conditions. We performed germination tests on several varieties. Here are represented the two lines with the most extreme phenotypes: Fritissi (FRI) and Cappelli (CAP). Under stresses condition we could observe a slower germination rates for both the lines. Salt stress (9g/l NaCl) and drought stress (80g/l PEG 6000).

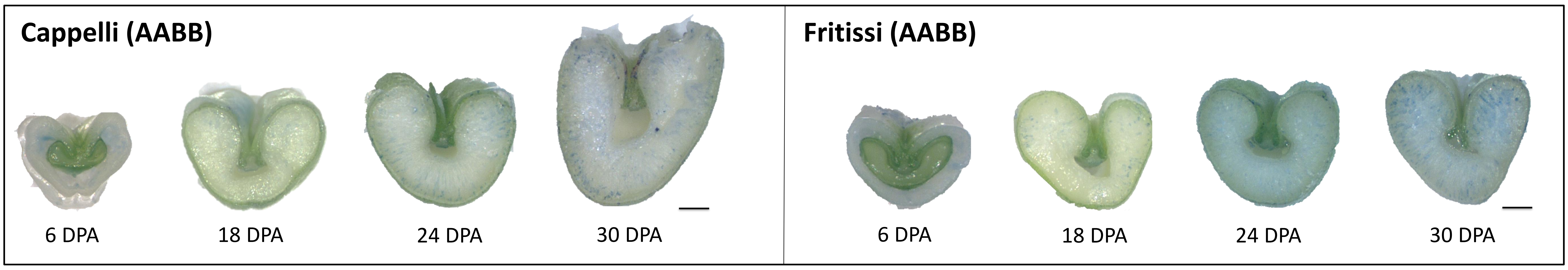


Figure 2: Seed development study. Seeds have been collected at 6, 18, 24 and 30 DPA (days post-anthesis) and then colored with Evans blue dye. This staining is used to check the integrity of the cell membrane. Also in this experiment, we have analyzed several lines. Here are represented Cappelli and Fritissi. The bar is 1 mm.

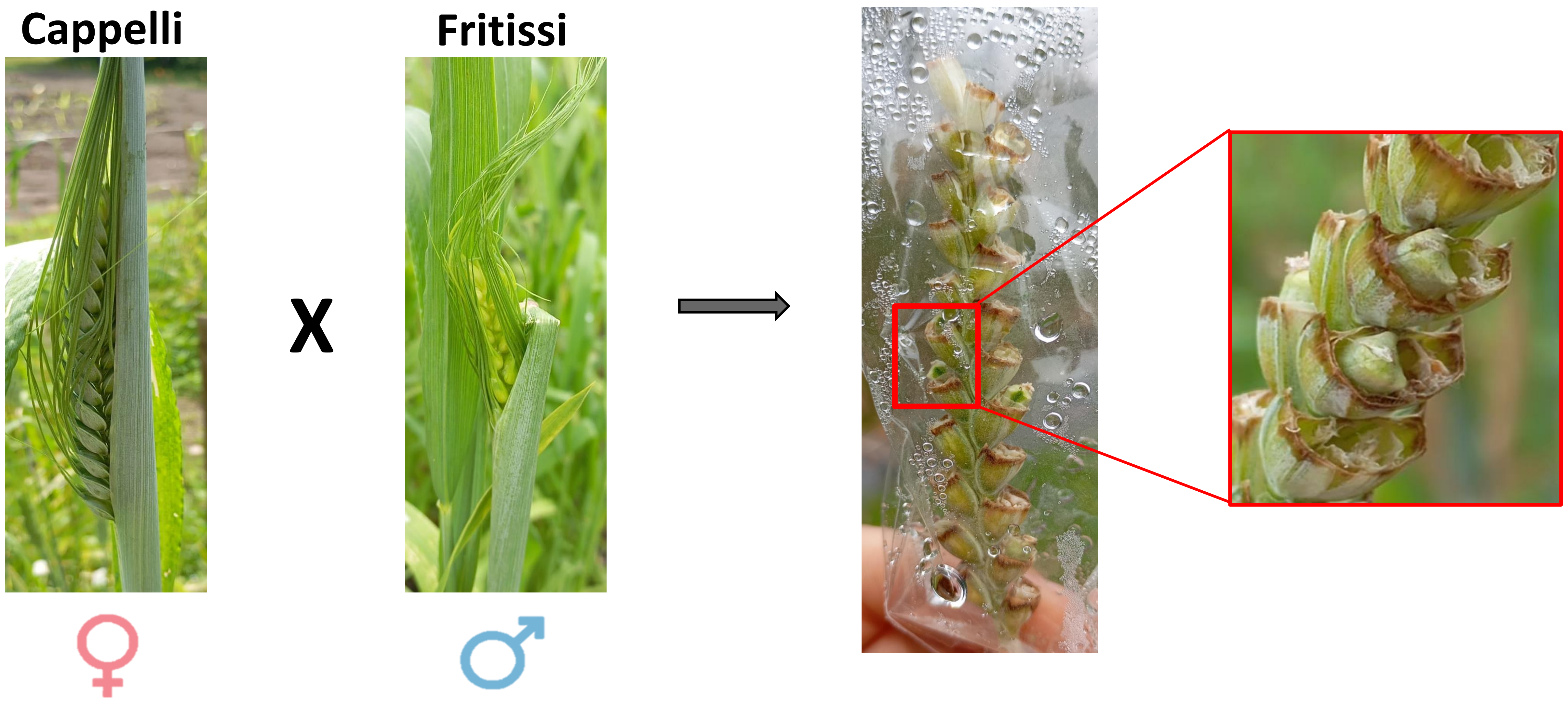
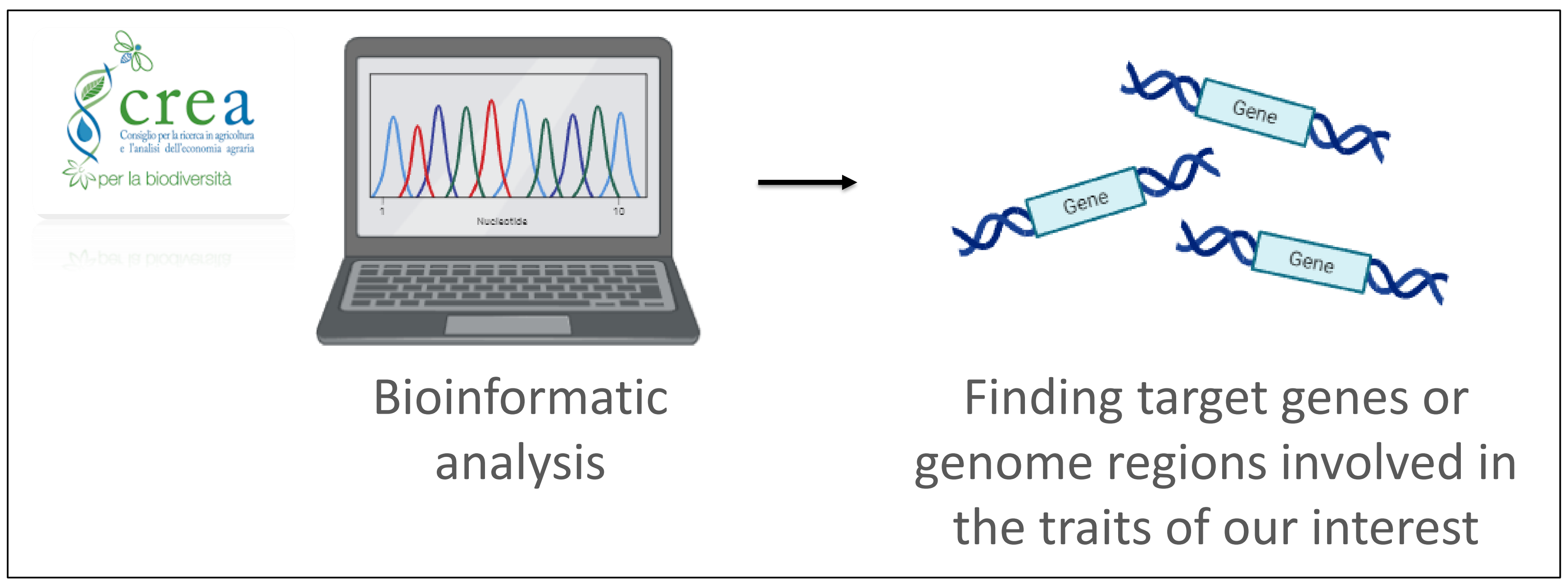


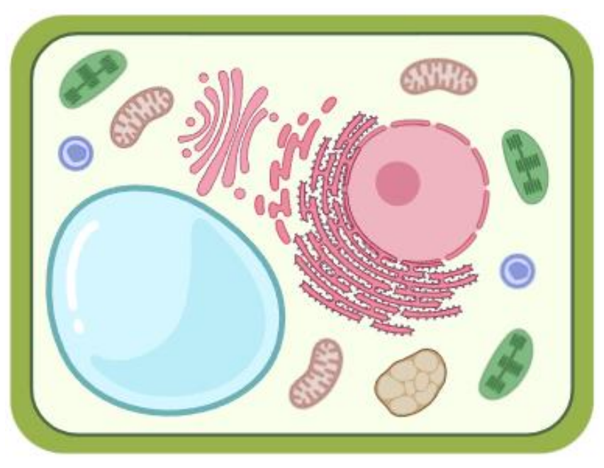
Figure 3: Crossings. The scheme of the crossing between Cappelli and Fritissi to obtain hybrids. In the next years we are going to check first the F1 whose lines are expected to show the same phenotype being in heterozigosis and the next year the F2 (in which we should start seeing different phenotypes).



Bioinformatic analysis

Finding target genes or genome regions involved in the traits of our interest

We would like to carry out a detailed functional characterization of the signaling events leading to heterosis dynamics, as well as an analysis of the metabolome, hormone profiling and cell wall changes during development of the different seed generations.



Conclusions: Overall, the output of this project will lead to the identification of novel genes and traits potentially involved in increasing seed quality and resilience in next-generation cereals and therefore helping to meet the challenge of reaching food security.