PhD School on Agriculture, Environment and Bioenergy

(http://sites.unimi.it/dottorato_aab/)

(XXXIX cycle, 2023-26)

Project draft

1.Field of interest

Wheat genetics, plant breeding, plant molecular biology

2.Project title

Wheat breeding assisted by biomolecular tools

3.Tutor (membro del Collegio dei Docenti)

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co-tutor

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4.Relevance of the topic and state of the art:

Wheat is one of the most important staple crops in the world and plays a vital role in feeding the global population: it is a highly nutritious cereal grain, providing carbohydrates, proteins, dietary fiber, vitamins (such as B vitamins), and minerals (such as iron and zinc) and it can be processed into a wide range of food products, including bread, pasta, noodles, pastries, cakes, and cereals. Its accessibility and affordability make it an essential component of diets in both developed and developing countries.

Modern wheat varieties, including those produced and commercialized by the partner of this project Apsov sementi S.p.A., have been optimized for several traits such as yield potential, grain quality, resistance to biotic and abiotic stresses and adaptation to diverse growing conditions.

Nevertheless, wheat still presents a certain degree of susceptibility to various diseases caused by pathogens, such as fungi, bacteria, and viruses that can be targeted by breeding programs. Disease-resistant varieties can minimize yield losses caused by infections, contributing to overall food security and can also help reducing the need for chemical treatments.

Recently, climate change has been posing significant challenges to agriculture, affecting crop productivity and geographical distribution: breeding can adapt varieties to different environments by modulating their photoperiod sensitivity, their temperature requirements and their resistance to drought, and salinity.

Finally, breeding targets also traits that match consumer demands and market preferences, that evolve over time, to help maintaining the competitiveness of wheat in the global market and the economic viability of wheat production for farmers.

Breeding based on phenotypic selection, supported by large experimental fields in different locations, has been traditionally and successfully performed in Apsov sementi S.p.A. This can be coupled to molecular tools like Marker-Assisted Selection (MAS) that offers several benefits and can enhance the efficiency of the breeding process. Indeed, it allows breeders to screen for parental lines carrying the genotype of interest and identify and select plants with desired traits at an early stage, even before they express those traits phenotypically. MAS enables breeders to select also for complex traits such as yield potential, quality attributes, and resistance to multiple diseases and to pyramid genes more easily. Identifying the plants that carry the desired markers for each trait allow the rapid incorporation of multiple traits into a single variety, leading to the development of improved wheat varieties.

5.Layout of the project (draft)

5.1. Materials & Methods:

DEVELOPMENT OF MOLECULAR MARKERS:
Molecular markers (from literature and from experimental data) for the traits of interest will be developed and tested, markers can range from CAPS, dCAPS, KASP or SNPs detectable by HRM real time PCR. Traits: disease resistance, photoperiod sensitivity, others…

VALIDATION OF MARKERS, GENE FUNCTION AND MULTIPLE LOCI INTERACTION:
Genome editing might be used to validate gene function or interaction of different loci that can be the target of gene pyramiding.

PARENTAL SELECTION AND CROSSING:
Parental lines might be chosen by genotyping and appropriate F1 populations created.
Crossings will be preferentially performed in the field.
Multi-parental crossings could be also used.

BACKCROSS/ SELFING AND GENOTYPING:
F1 lines will be backcrossed to recurrent parental lines following the desired molecular markers.
If segregating populations would be chosen, these could also be genotyped.

FIELD PHENOTYPING:
Accurate plant phenotyping will be performed in the fields at different locations and after harvest for grain quality traits under the supervision of expert Apsov sementi S.p.A. breeders.

5.2. Schedule and major steps (3 years)

Year 1 – Literature review, molecular markers development, parental lines genotyping and F1 production.

Year 2 - eventually genome editing targeting one or multiple genes as functional validation before editing. Backcrosses and genotyping.

Year 3 – Backcross, genotyping, and field phenotyping.

6. Available funds

Progetto di Co-Sviluppo fondazione Bussolera Branca

Erogazione liberale Lugano Leonardo s.r.l.