

PhD School on Agriculture, Environment and Bioenergy
(http://sites.unimi.it/dottorato_aab/)

(XXXIV cycle, 2018-20)

Project draft

1. Field of interest

Patologia Agraria AGR/12, Genetica Agraria, AGR/07

2. Project title

Valorization and exploitation of maize biodiversity

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Co-tutor Gabriella Consonni

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

The maize species, which has always been considered as a model for its long history of genetic and cellular analysis, since the advent of genomic technologies, has become even more attractive. With a fully sequenced genome and the availability of different tools it is considered one of the more accessible higher plant system. Numerous gene models and molecular markers are available, along with seed stocks of genetic variants (<http://www.maizegdb.org>). Maize is also a species of agronomic and cultural importance. The history of maize breeding and cultivation is very long and gave rise to several local varieties, which were later abandoned when mechanized farming practices became more common in the second half of the twentieth century. These varieties constitute a source of desirable traits for nutritional quality of the grain and pathogen resistance, and many efforts are made to recover the genotypes of these populations. Programs for the genetic improvement of maize are starting to study landraces with the aim of identifying novel alleles and haplotypes, to be used in a context of low-input, sustainable agriculture.

This research project aims to contribute to the characterization of the agrobiodiversity in maize for what concerns the capability to recruit endophytes and tolerate drought stress condition.

5. Layout of the project (draft)

5.1. Materials & Methods:

1. Functional studies of genes involved in drought stress. A list of candidate genes involved in the drought stress response is available in the laboratory of the proponents. Their expression profile will be determined through quantitative RT-PCR analysis during early stages of development in plants grown under well-watered condition and subjected to drought stress.

Genetic variants of these genes will be recruited from mutant as well as germplasm collections, and introgressed in suitable genotypes to obtain segregating populations. The function of these genes and interaction among them will be studied through a detailed phenotypic analysis of this material.

2. Effect of isolated endophytes on seedling and plant growth. Specific bacterial strains isolated from local maize varieties will be inoculated to plants of the maize reference line B73 and other maize lines and the effect of the treatment will be determined at early stages of plant development. Plants will be grown both in well-watered and under water stress conditions. Treated and non-treated plants will be compared for plant growth and physiological parameters. The expression of selected genes will be also evaluated.

5.2. Schedule and major steps (3 years): mezza pagina max

First year activities.

Studies of candidate genes.

Expected results

List of genes involved in drought stress response and related genetic variants.

Second year activities:

1. Analysis of the effect of isolated endophytes on seedling growth in controlled condition
2. Plant material reproduction

Expected results:

Detection of bacterial strains beneficial to plant growth and response to drought.

Production of F₂ populations segregating for the genetic variants

Third year activities

1. F₂ population studies
2. Analysis of the effect of isolated endophytes on drought response

Expected results

Detailed phenotypic descriptions of variants in genes involved in drought stress response

Role of genes involved in drought response

Detection of bacterial strains beneficial for the response to drought.

6. Available funds (source and amount)

Harnessing Plant Reproduction for Crop Improvement (PROCROP) H2020-MSCA-RISE-2014
4.000 Euros

6. Literature: max 10 citazioni

Brandenburg J.T., Mary-Huard T., Rigai G., Hearne S.J., Corti H., et al. (2017) Independent introductions and admixtures have contributed to adaptation of European maize and its American counterparts. *PLOS Genetics* 13(3): e1006666

Castorina G, Persico M, Zilio M, Sangiorgio S, Carabelli L, Consonni G (2018) The maize *lilliputian1* (*lil1*) gene, encoding a brassinosteroid cytochrome P450 C-6 oxidase, is involved in plant growth and drought response, *Annals of Botany*, <https://doi.org/10.1093/aob/mcy047>

Kroll S., Alger M.T, Kemen E. (2017) Genomic dissection of host-microbe and microbe-microbe interactions for advanced plant breeding. *Current opinion in Plant biology* 36, 71-78

La Rocca N, Manzotti P, Cavaiuolo M, Barbante A, Dalla Vecchia F, Gabotti D, Gendrot G, Horner D, Krstajic J, Persico M, Rascio N, Rogowsky P, Scarafoni A, Consonni G (2015) The maize *fused leaves1* (*fdl1*) gene controls organ separation in the embryo and seedling shoot and promotes coleoptile opening. *J Exp Bot* 66:5753-5767.