

PhD School on Agriculture, Environment and Bioenergy

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(XXXVII cycle, 2021-24)

Project draft

1. Field of interest

AGR07

2. Project title

Fusarium diseases of maize associated with mycotoxin contamination: genetic aspects

3. Tutor (membro del Collegio dei Docenti)

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- Eventually: co-tutor/s

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

The contamination of maize kernels by fumonisins is due to *Fusarium* infection, in particular by *F. verticillioides* and *F. proliferatum*. *Fusarium* hyphae have been reported to spread within the pericarp, colonizing the kernel in a radial pattern: the starburst symptoms of the colonization appear subsequently, in correspondence with the extensive dissolution of the pericarp walls [1].

Fumonisin contamination is implicated in various serious animal diseases such as porcine pulmonary edema, equine leukoencephalomalacia, hepatotoxicity and carcinogenicity in rats, and seems to be related to human oesophageal cancer [2]. To reduce fumonisin exposure, several official agencies such as the FAO/WHO Expert Committee on Food Additives, U.S. Food and Drug Administration and the European Union, have established maximum levels of fumonisin content in non-processed maize (4 ppm), and maize meal (2 ppm) for human consumption. The chronic exposure to mycotoxins represents a critical factor for human health, especially in the case of malnourished populations in low income countries [3]. In fact in rural subsistence regions of Southern Africa, where maize is the major staple crop, even when the level of mycotoxin contamination is under the maximum level, the exposure to mycotoxin can exceed the safe levels because of the undiversified maize-based diet. Maize cultivated in these areas is often prone to pre- and post-harvest mycotoxin contamination because of poor agricultural practices such as sowing untreated seeds from the previous season, late planting, incomplete drying of grains, or long storage of crops in facilities without adequate aeration, moisture and temperature control [3]. Important results on the reduction of pre-harvest fumonisin contamination came from genomic assisted breeding programs, that allowed the identification of QTL and candidate genes for the selection of resistant maize lines [4], and the development of the transgenic *Bt* maize, where the expression of the insecticidal Cry protein from *Bacillus thuringiensis* allows the reduction of insect damage, *Fusarium* infection and fumonisin accumulation [5]. Crop growing techniques can reduce the risk of *Fusarium* infection but there are no definitive strategies to prevent fungal infection and fumonisin accumulation in maize kernels. In 2017 in Italy about 37% of the sample analysed showed a level of fumonisin contamination higher than the legal limit [6].

5. Layout of the project (draft)

Objective of the project is to analyze corn germplasm to identify sources of resistance to *Fusarium* *ssp.* Mycotoxin contamination of corn grain is an important challenge for Italian agriculture. A multidisciplinary approach is necessary to solve the problem. Known agronomic practices can reduce the occurrence of high levels of fumonisin; although there is also evidence of genetic effects, there is a lack of knowledge regarding the genetic base of the resistance.

In this project will be used QTL analysis to discover molecular marker associated with fusarium resistance. Analysis of a set of inbreds, will allow us to identify additional sources of resistance and speed up developing resistant inbreds. For this study is also planned to use double haploid (DH) populations.

The project will start by creating a preliminary list of the selected genetic materials. Through artificial inoculations will be evaluate the fusarium resistance of the different inbred lines. The experiment will be carried out for two following seasons and in different locations. The use of a multi-location and multi-year approach will permit the proper statistical data elaboration. The field experimental activities will be performed by Pioneer facilities.

For the data collection will be used a scoring system based on values ranking from 1 to 9, where higher values indicate greater resistance level. The value will be assigned based on the % of ears covered by the mycelium or with starburst symptoms. All the genetic material selected will be

For the molecular analysis will be use SNPs obtained by Pioneer platform. GWAS and QTL analysis will permit the identification of the genomic regions useful for the genetic improvement programs for this trait.

5.1. Materials & Methods:

- Experimental field at Pioneer facilities.
- Fusarium artificial inoculation
- Genotyping by sequencing (SNPs detection) at Pioneer facilities
- Data elaboration: GWAS and QTLs analysis

5.2. Schedule and major steps (3 years):

| | YEAR | 2021 | | | 2022 | | | | | | | | | | | | 2023 | | | | | | | | | | | | 2024 | | | | | | | | | | | |
|--------|--|-------|----|----|------|---|---|---|---|---|---|---|---|---|----|----|------|---|---|---|---|---|---|---|---|---|----|----|------|---|---|---|---|---|---|---|---|---|----|--|
| | | MONTH | 10 | 11 | 12 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | |
| Task 1 | Selection of genetic materials | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Task 2 | multi-location and multi-year experimentation | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Task 3 | Genotyping and GWAS/QTLs analysis | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Task 4 | Production of scientific papers and education activity | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

6. Available funds

Pioneer funding, SOCIAAALP, GEMMA, MIND HUBS. Private funding

6. Literature:

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- [4] Gaikpa, S. & Miedaner, T. Genomics-assisted breeding for ear rot resistances and reduced mycotoxin contamination in maize: methods, advances and prospects. *Theor. Appl. Genet.* 132, 2721–2739 (2019).
- [5] Pellegrino, E., Bedini, S., Nuti, M. & Ercoli, L. Impact of genetically engineered maize on agronomic, environmental and toxicological traits: a meta-analysis of 21 years of field data. *Sci. Rep.* 8, 3113, <https://doi.org/10.1038/s41598-018-21284-2> (2018).
- [6] Locatelli, S., Mascheroni, S. & Lanzanova, C. Micotossine in mais: campagna 2017. <http://mangimiealimentari.it/articoli/2331-micotossine-in-mais-campagna-2017> (2018).