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Poster Communication Abstract - 1.44

IDENTIFICATION OF QTLS WITH A KEY ROLE IN RESISTANCE AGAINST FUSARIUM HEAD BLIGHT IN DURUM WHEAT

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Durum wheat (*T. turgidum* ssp. *durum*) is one of most susceptible cereals to *Fusarium* head blight (FHB, scab) which is annually responsible for serious economic threats due to huge losses in yield, and for decay in qualitative characteristics of the grain (destruction of cell walls, alteration of the lipid fraction and the reduction of the protein fraction). FHB is also responsible to produce mycotoxins mainly deoxynivalenol (DON), a powerful inhibitor of eukaryotic protein synthesis and very harmful to human and animal health. The most effective strategy to manage FHB disease and gain a more economically and ecologically sustainable wheat production is the use of genetic resistance, which is controlled by the combined effects of several quantitative trait loci (QTL) and environment.

Resistance to FHB is a complex and quantitative trait controlled by multiple genes, largely influenced by plant architecture and genotypeenvironment interactions, and characterized by large genetic variation in wheat gene pool. Resistance to FHB is of quantitative nature and its inheritance includes many genes and is affected by environmental conditions.

Cell wall is the first line of plants defense against fungal pathogens and several lines of evidence indicate that structural components of the cell wall are involved in plant resistance against such pathogens. Understanding biological mechanisms associated biomarkers driving the and wheat development and adaptation relies on an urgent understanding of the continuum between structural, expressional and epigenetic variations. A specific activity has been conducted for *Fusarium* Head Blight (FHB), reported QTL identification and the map-based cloning of a new FHB QTL located on 2A chromosome from a resistant bread wheat line deriving from Sumai 3. New functional marker genes conferring durable plant resistance against Fusarium were developed and efficiently used in a marker-assisted selection program for the constitution of resistant superior durum wheat genotypes to be used for a sustainable agriculture and food security.