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Multilocal resistance assessment against common bunt of wheat (*Triticum aestivum*)

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Abstract

Bunt is one of the most devastating diseases of wheat, in Europe and Northern America mainly caused by *Tilletia caries* and *T. controversa,* in the warmer climates of the Near East by *T. foetida*. The generally obligate biotrophic pathogen is transmitted by contaminated seeds or can persist in the soil. Infection occurs at the very first moments after germination of the grain. Once penetrated into the plant, the fungus grows endophytically, remaining undetected until early maturity stages when grains are replaced by spores. Besides yield losses, the malodorant spores contaminate the grains impairing their use as seeds or as food, thereby leading to serious economic losses.

Usually the disease is controlled by the use of seed dressings and the use of certified seeds. For organic farming, however, resistance of wheat varieties to bunt is crucial as seed treatments with chemical pesticides are not allowed and several proposed alternatives, *e.g*. treatments with bacteria, hot water, vaccum-steam, steam-ultrasound or electrons, are expensive and lack efficiency. Major and some minor genes conferring resistance to *Tilletia* infections are described, however, the performance and stability and, therefore, usefulness of these resistances are under debate.

Common bunt resistance is based on Flors' gene for gene principle with an effector of the pathogen and a resistance gene in the host plants, able to detect the effector and to unleash the appropriate resistance mechanisms. To efficiently use this type of resistance, it is important to characterize the effectors in the pathogen population as well as to monitor the presence and the efficacy of the resistance genes. While many of this information is available at local and regional level, only little is known at an interregional or even continental dimension.

In order to obtain a better overview on the efficacy of resistance genes and the presence and distribution of pathogen races, the European *Tilletia* ringtest (ETR) was established including also the USA and Iraqi Kurdistan. The ringtest consists of a set of 65 wheat accessions including differentials to characterize the pathogen strains and 40 modern varieties and landraces with specific resistance features. The ringtest took place in 2015 and 2016.

First results display a wide diversity of pathogen strains, allowing to recommend the deployment of the most appropriate resistance genes in the different cropping areas. Important differences in disease severity were observed among sites. Resistance was not always linked to the postulated resistance genes. Across all test sites no susceptible plant was observed in PI636170, a breeding line selected from a Turkish landrace. Low infection levels (≤25%) were observed in some breeding lines/genetic resources and also in released cultivars, e.g. Stava and SW Magnifik.

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Keywords

Genotype by environment interaction · pathogen races · resistance genes · *Tilletia* · *Triticum aestivum*

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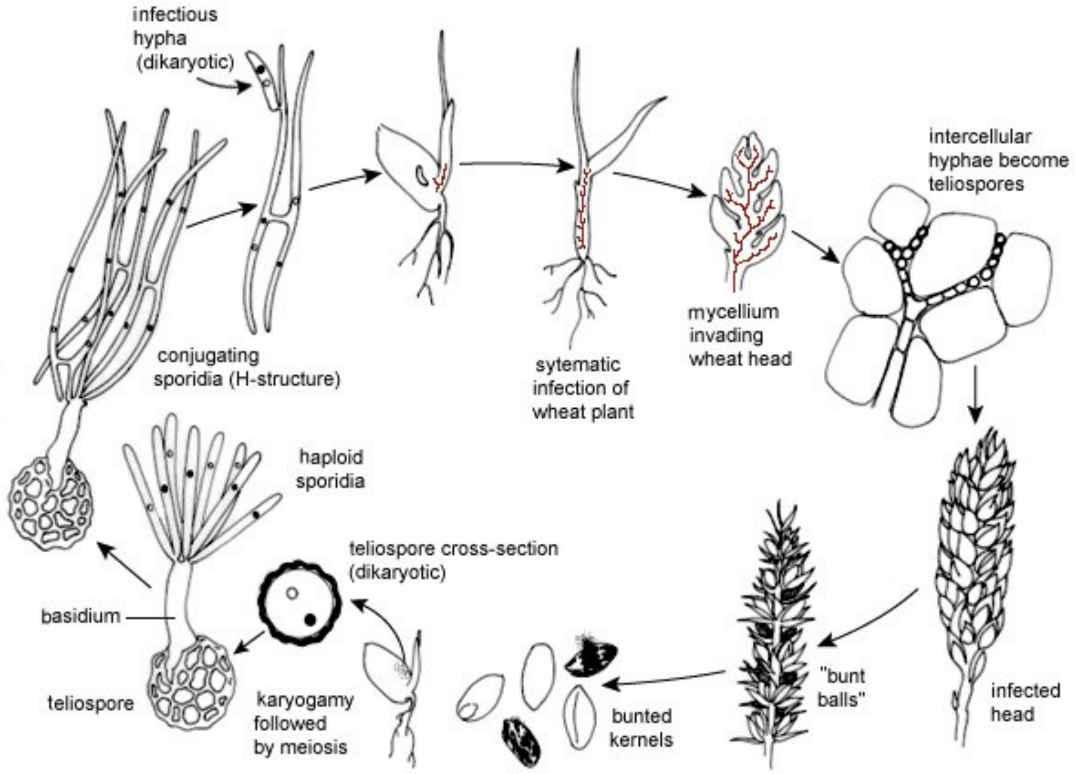

Figure 1: Disease cycle of common bunt. Survive between growing seasons is guaranteedby teliospores on the surface of healthy seed or in the soil where they can remain viable in for a number of years (Source: MATHRE 2005)