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Emerging pathotypes in cereals

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RAMULARIA LEAF SPOT IN DENMARK: DISTRIBUTION, YIELD LOSSES, VARIETAL RESISTANCE & CHEMICAL CONTROL, EPIDEMIOLOGICAL ISSUES

Hans O. Pinnschmidt
University of Århus, Faculty of Agricultural Sciences
hans.pinnschmidt@agrsci.dk

High severity levels of Ramularia leaf spot (RLS), caused by *Ramularia collo-cygni*, have been observed in Denmark since 2002 in many spring- and winter barley varieties on many occasions. The fungus was also isolated from several grass species. However, the importance of RLS for Danish barley production is still unclear although trial results indicated that 1000-grain weight and yield decrease as the RLS severity level increases. Host plant resistance appears to have a great potential for disease prevention and control. A number of spring and winter barley cultivars appeared relatively resistant against RLS under variable environmental conditions in Denmark during the past years. Strikingly, the spring barley cultivars exhibiting the highest RLS severity levels possess *mlo* resistance against powdery mildew while those displaying the lowest RLS severity levels do not have this resistance. Among winter barley cultivars, the most severely attacked ones are two-rowed while six-rowed cultivars appear more resistant. Best disease control was achieved in Danish field trials by foliar applications of fungicide mixtures containing boscalid plus epoxiconazole. Seed dressing with prothioconazole plus tebuconazole seems promising. As visual diagnosis and quantitative assessment of RLS severity can be difficult, a quantitative real-time PCR method has been developed to make quantitative assessment of disease severity and varietal resistance expression more reliable and objective. Successful artificial inoculation was achieved on adult plants in the screen house. The inoculation methodology will be improved further to facilitate the testing of varietal disease resistance as well as of the efficiency of fungicides and fungicide application schemes. Future progress in disease management depends on resistance breeding, the optimisation of fungicide applications and, last not least, progress in epidemiological research addressing the role of various inoculum sources, cultural disease management practices and specificity and variation of virulence of the pathogen.

IMPORTANCE OF *RAMULARIA COLLO-CYGNI* – ON BARLEY PLANTATIONS IN POLAND

Jerzy H. Czembor
IHAR Radzików
j.h.czembor@ihar.edu.pl

Fungus *Ramularia collo-cygni* is causing *Ramularia* leaf spot. Until recently it was considered a minor disease of barley. However in recent years it has become increasingly important in many barley growing areas, especially in central Europe (Austria, Bavaria, Czechy, Moravia). In 2003, first incidence of this disease was observed in Poland. It was observed on production fields in Upper Silesia (Southern part of Poland). The disease symptoms are small dark brown spots on barley leaves. These symptoms can easily be confused with damage symptoms caused by abiotic stresses (Physiological Leaf Spots - PLS) and other pathogens. The reasons for the recent shift of the status of the disease are largely unknown. Effective varietal resistance to the disease exists and can be exploited in disease resistance breeding and practical disease control. However, further investigations are needed concerning the effective control measurements. Several control strategies of *Ramularia* leaf spot will be discussed.

Because lack of epidemiological studies of this pathogen concerning major areas of barley production in Poland - the importance of *R. collo-cygni* on barley plantations in Poland can be only a matter of speculations. However, experimental and survey data from neighbouring countries like Denmark and Germany suggests that this disease should be considered as important emerging disease in Poland.

NET BLOTCH OF BARLEY- NOVEL RESULTS ON EPIDEMIOLOGY, AND VIRULENCE

Marja Jalli

MTT Agrifood Research Finland, Plant Protection
marja.jalli@mtt.fi

Recently, Finnish farmers have been increasingly interested in no-tillage systems due to the economical and environmental reasons. Plant protection in no-tillage systems brings new challenges for research. In Finland, the most important fungal pathogen of barley is *Pyrenophora teres*. Two distinct pathogenic forms of *P. teres* exist: *P. teres* f. *teres* (net form) and *P. teres* f. *maculata* (spot form). To manage net blotch successfully, both the knowledge on the virulence spectrum and the recognition of the possibilities for changes in virulence spectrum are important. No-tillage system might offer an excellent environment for sexual reproduction. If *P. teres* is able to survive and to cross on barley stubble during the long and cold Finnish winter there could be an ever changing virulence spectrum that would impact negatively on barley plant protection efforts.

Our research was conducted in Jokioinen in Finland. In 2006 and 2007, random barley leaves were collected from the barley monoculture field established in 2001. The field was divided in two parts; in tillage and in no-tillage part. 536 single-spore *P. teres* isolates were obtained. Barley genotypes Annabell, Kunnari, Pirkka, CI9819 and CI2330 were selected to be used in greenhouse virulence screenings as test cultivars based on their different resistance to Finnish *P. teres* net type isolates. Two weeks after sowing relative humidity in the greenhouse was raised to 100% and the plants were inoculated with conidial suspension at 0.3 ml per pot (40 000 spores/ml). A control set of genotypes inoculated with distilled water was included in each replicate. Ten days after the inoculation, infection response and the form of the *P. teres* isolate were recorded for the second leaf using the 10 point scale of Tekauz.

The preliminary results from the *P. teres* population studies indicate that both the crop rotation and the cultivation method have a significant effect on the structure of the *P. teres* pathogen population. The frequency of *P. teres* f. *maculata* (spot type, close to 100 %) was highest in the populations collected from the no-tillage barley monoculture field. The tillage method had no effect on the population structure when turnip rape was used as a pre-crop.

Based on the virulence studies in the greenhouse, there were significant differences in the virulence spectrum of the net and spot type populations. The most important difference was the interaction of the spot type isolates with barley genotype CI9819 which is known as a very resistant genotype against barley net type isolates. However, most of the tested spot type isolates were virulent on CI9819. No-tillage together with barley monoculture may cause novel disease risks and will demand new efforts in barley resistance breeding programs and in plant protection strategies.

INCREASE OF NET BLOTCH INFECTION ON SPRING BARLEY IN LITHUANIA

Roma Semaskiene, Grazina Stankeviciute
Lithuanian Institute of Agriculture
roma@lzi.lt

Spring barley is the most important cereal crop in Lithuania and was sown on 366 900 ha in 2007. Foliar diseases, e.g. net blotch and powdery mildew are common barley diseases. New barley disease ramularia is on the increase. Rust and scald are rare. During recent years was recorded higher incidence of net blotch. This disease of barley is caused by *Pyrenophora teres* Drechsler. (anamorph *Drechslera teres* [Sacc.] Shoemaker syn. *Helminthosporium teres* Sacc.). Net blotch requires high humidity and wet weather to infect a plant, but develops faster at higher temperatures. Heavy pressure of this disease was recorded in 2006 and especially in 2007 in Lithuania. Crops showed severe infection from beginning of stem elongation. Net blotch in untreated with fungicide crops affected 50—80% leaf area at milk growth stage. Single application of triazoles gave poor control. Best control showed only on strobilurine based fungicides.

P. teres is known to produce two different symptoms, and based on these Smedegård-Petersen (1971) differentiated the forms of *P. teres* as *P. teres* f. *teres*, which produces brown netted lesions and *P. teres* f. *maculata*, which produces brown spot lesions. Net blotch is found across the world; however the occurrence of the two forms of net blotch in different regions varies. Both forms are common in some countries, whereas in other countries prevalent spot form or net form of net blotch. The occurrence of spot and net forms of net blotch is differing in the countries geographically close to Lithuania (Denmark, Sweden, Finland) too. The population of fungi *P. teres* was investigated in Lithuania during 1990-1993. Unfortunately, forms of this pathogen were not examined. Current knowledge of the spot and net forms of *P. teres* remains limited, therefore future research on the variation of pathogenic fungi *Pyrenophora teres* population will focus on these topics:

- to identify the dominating form of *P. teres* according to visual symptoms and by using molecular assay method;
- to identify the structure of *P. teres* populations using PCR method;
- to estimate the effects of different agroecosystems on *P. teres* population diversity;
- to identify seasonal and inter-seasonal variation of *P. teres* population;
- to establish the influence of genotype on population structure of *P. teres*.

HAPLOTYPE CHARACTERIZATION AND MARKERS AT THE BARLEY *MLO* POWDERY MILDEW RESISTANCE LOCUS AS TOOLS FOR MARKER-ASSISTED SELECTION

Gianni Tacconi

CRA-GPG Genomich Research Center, Fiorenzuola d'Arda

tacconig@yahoo.com

Recessive *mlo* alleles of the barley *Mlo* gene confer resistance to almost all known isolates of the powdery mildew fungal pathogen targeting barley (*Hordeum vulgare*). To characterize haplotypes present in the *Mlo* chromosomal region of cultivated *Mlo* and *mlo* barley genotypes, we conducted a polymorphism search in 3 predicted low-copy sequence regions adjacent to the *Mlo* gene by examining a sample of 4 *Mlo* and 3 *mlo* cultivars. Eight single nucleotide polymorphisms (SNPs) and 1 insertion–deletion (indel) were detected, and easy to use PCR-based markers (named om) were developed for typing the SNPs. The PCR markers were used to characterize a collection of 46 *Mlo* and 25 *mlo* barley cultivars, identifying 3 distinct *mlo-11* haplotypes, 1 *mlo-9* haplotype, and 4 *Mlo* haplotypes. We summarized the haplotype and marker information obtained here and in a previous study to help breeders identify strategies for *mlo* marker-assisted selection.

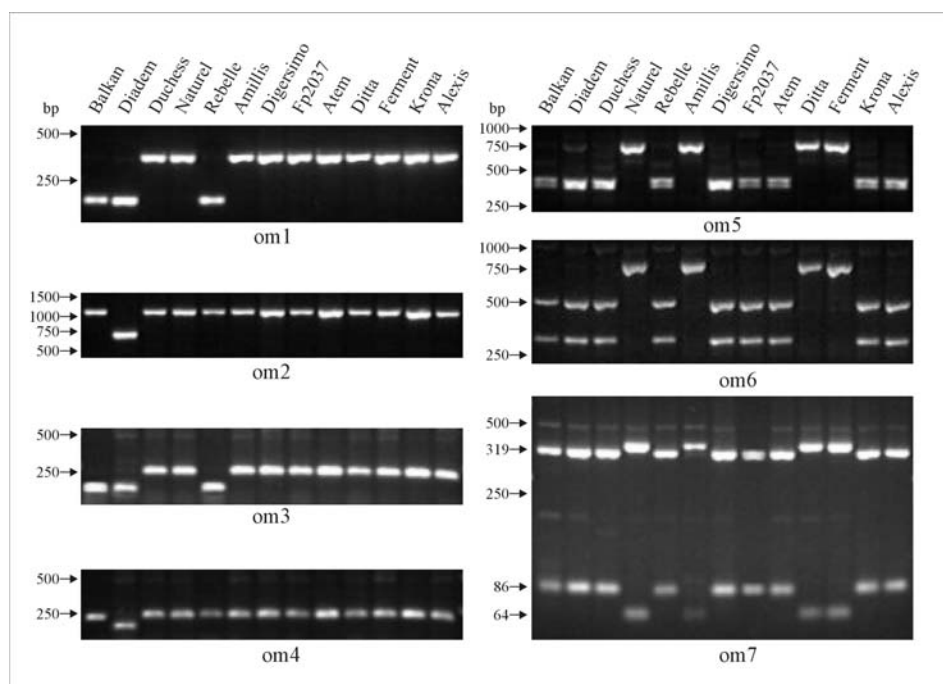


Fig. 1. Agarose gel images of CAPS (om1 and from om3 to om7) and indel (om2) markers closely linked to *Mlo*. Eight *Mlo* (from ‘Balkan’ to ‘Fp2037’) and 5 *mlo* (from ‘Atem’ to ‘Alexis’) cultivars were analysed. The SNP (or insertion, in; deletion, del) allele of each marker is indicated for the first 4 barley cultivars. Molecular mass marker sizes (bp) are indicated on the left.

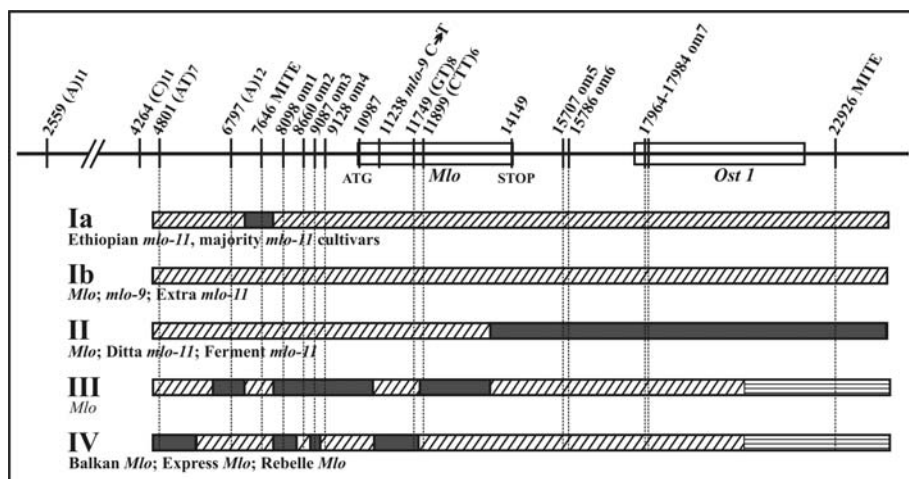


Fig. 2. Representation of the haplotype groups in Table 3 identified in the *Mlo*-region using the om markers and the data of Piffanelli et al. (2004). The upper section indicates the positions within the Y14573 sequence of marker polymorphisms, *Mlo* and *Ost1* genes (rectangles), and the *mlo-9* resistance-causing mutation. Haplotype sections containing the same marker sequence variant(s) are indicated by the same shading pattern.

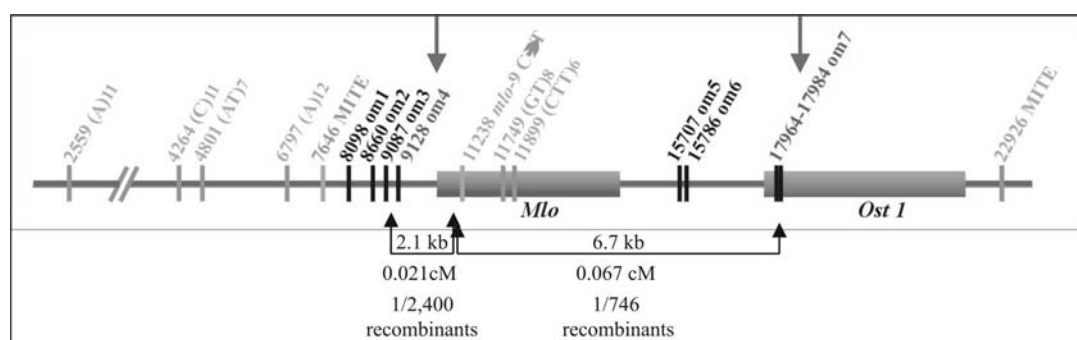


Fig 3. The om markers are useful for MAS due to their close linkage with *Mlo*: the physical distances of the nearest and farthest om markers from *mlo-9* resistance gene and the corresponding genetic distances indicate the expected recombination frequency in MAS

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IN VITRO ANTIFUNGAL ACTIVITY OF THE TEA TREE (*MELALEUCA ALTERNIFOLIA*) ESSENTIAL OIL AND ITS MAJOR COMPONENTS AGAINST PLANT PATHOGENS

Gianni Tacconi

CRA-GPG Genomich Research Center, Fiorenzuola d'Arda
tacconig@yahoo.com

In this study the effect of *Melaleuca alternifolia* essential oil (TTO) and its principal components was examined on four cereal-pathogenic fungi. The antimycotic properties of TTO and of terpinen-4-ol, gamma-terpinen and 1,8-cineole (eucalyptol) were evaluated in vitro on *Fusarium graminearum*, *Fusarium culmorum* and *Pyrenophora graminea*. Moreover, barley leaves infected with *Blumeria graminis* were treated with whole TTO. All the tested fungi were susceptible to TTO and its components. TTO exerted a wide spectrum of antimycotic activity. Single TTO purified components were more active than the whole oil in reducing in vitro growth of fungal mycelium and, among the tested compounds, terpinen-4-ol was the most effective. TTO and its components can be considered potential alternative natural fungicides.

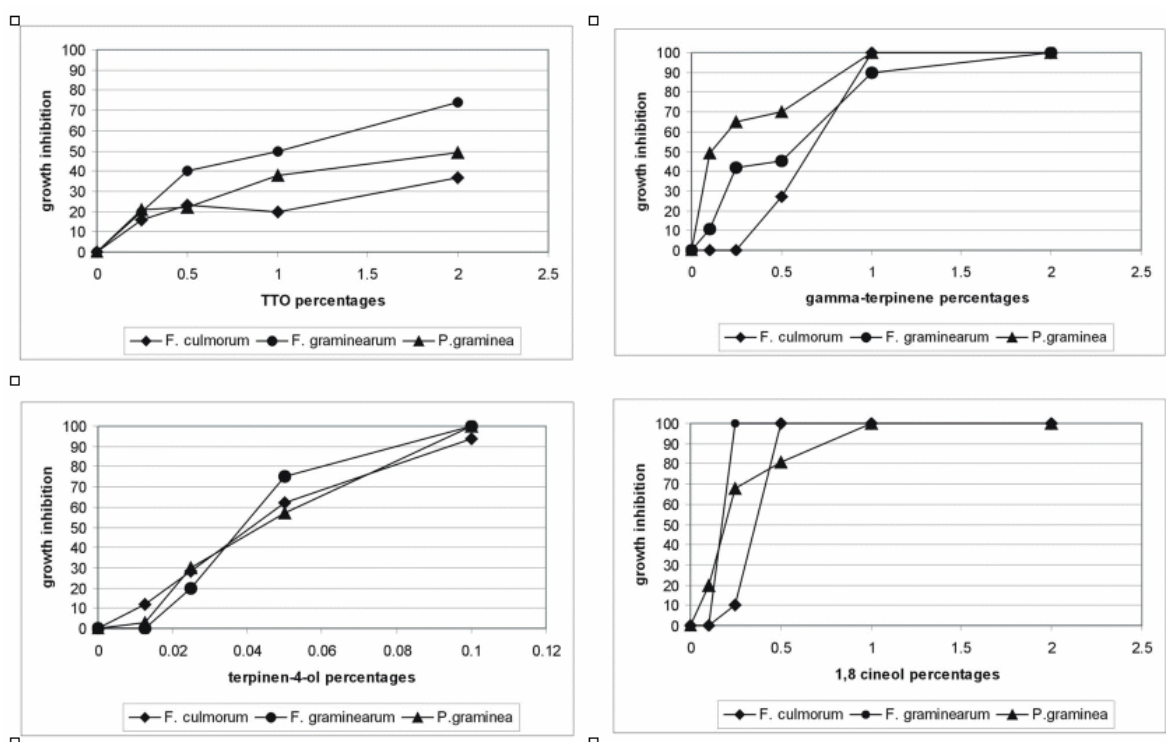


Fig. 1 The effect on *F.graminearum*, *F.culmorum* and *P.graminea* was evaluated by measuring the mycelial growth of the three fungi in solid medium amended different oil percentage. TTO > 0.25% *F.culmorum* *F.graminearum* and *P.graminea* Terpinen-4-ol > 0.0125% *F.culmorum* Terpinen-4-ol > 0.025% *F.graminearum* and *P.graminea* Gamma-terpinene > 0.1% *F.culmorum* *F.graminearum* and *P.graminea* 1,8Cineole > 0.25% *F.culmorum* *F.graminearum* and *P.graminea*

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MARKERS FOR BARLEY LEAF STRIPE RESISTANCE GENE: FROM FINE MAPPING TO MARKER ASSISTED SELECTION TOWARD POSITIONAL CLONING

Gianni Tacconi

CRA-GPG Genomich Research Center, Fiorenzuola d'Arda
tacconig@yahoo.com

Leaf stripe, caused by the fungus *Pyrenophora graminea* is an important seed-borne disease of barley. The objective of this study was to verify the reliability of a PCR-based marker (MWG2018) associated with the resistance gene *Rdg2a* and to assess the leaf stripe resistant phenotype in barley breeding programs. A large number of barley cultivars and accessions were thus evaluated for their reaction to a highly virulent monoconidial isolate (Dg2) of the pathogen and genotyped for the allele of the molecular marker. Several resistant genotypes were identified and four were shown to possess the same allele as the cultivar Thibaut (the resistant parent of the original mapping population in which was identified) at the marker locus. One of them, cv. Rebelle, is being used as a source of leaf stripe resistance in winter barley programs. The allelic composition at the MWG2018 locus was verified in several resistant lines bred from five crosses, in which Rebelle acted directly or indirectly as donor of the resistance. The results showed that the resistant phenotype of the lines was always associated with the resistance allele of the molecular marker, thereby demonstrating its reliability for selecting leaf stripe resistance. The MWG2018 PCR-based marker can therefore be proposed as a tool to assess the resistant phenotype.

Rdg2a is located in the distal region of chromosome arm 1 (7H)S. As the first step towards isolating the gene, a high-resolution genetic map of the region was constructed using an F2 population of 1,400 plants (ThibautRdg2a_Mirco). Additional markers were generated using the sequence from the corresponding region on rice chromosome 6, allowing delimitation of the *Rdg2a* syntenic interval in rice to a 115 kbp stretch of sequence. Analysis of the rice sequence failed to reveal any genes with similarity to characterized resistance genes. Because the rice-barley synteny is disrupted in this region, a Morex BACs library was used in order to physical mapping *Rdg2a*. Due to the absence of the resistance gene in Morex, a Thibaut cosmid library, of 5.12 haploid genome equivalents, was constructed and screened with the developed *Rdg2a* markers. The identification and sequencing of positive cosmid clones allow to identification of three NBS-LRR candidate *Rdg2a* gene.

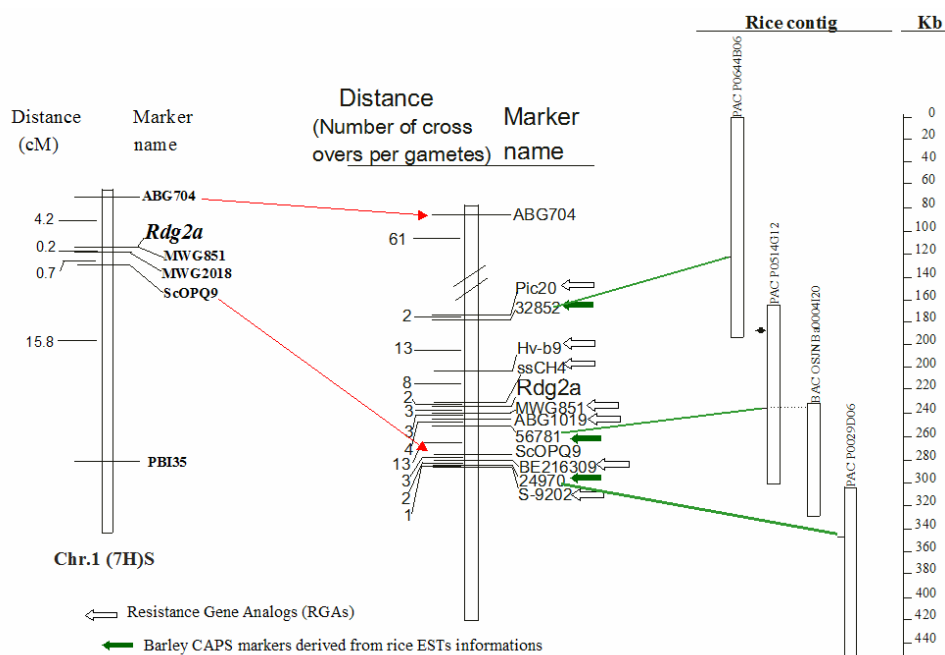


Fig. 1. Fine mapping of *Rdg2a* gene: the map included six classes of resistance gene analogues (RGAs) tightly associated with *Rdg2a* that was delimited to a genetic interval of 0.14 cM between the RGAs ssCH4 and MWG851.

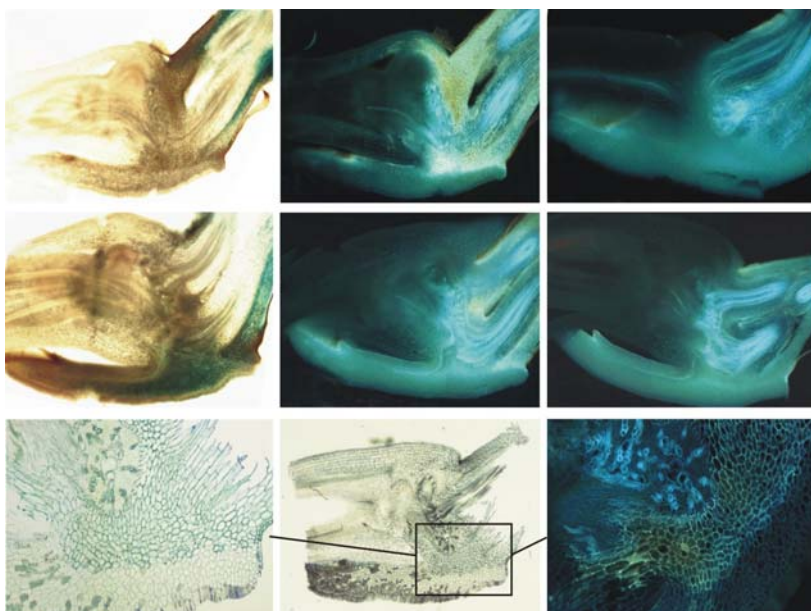


Fig. 2. Microscopic analysis of the *Rdg2a*-mediated embryo defense responses at 20 d.a.i. with *P. graminea* Dg2-uidA transformed: upper resistant NIL, middle susceptible Mirco, bottom magnification of resistant NIL; on the left GUS assay under visible light and, on the right, under UV light.

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ASSESSMENT OF FUSARIUM INFECTION IN WHEAT HEADS USING A QUANTITATIVE POLYMERASE CHAIN REACTION (QPCR) ASSAY

Gianni Tacconi

CRA-GPG Genomich Research Center, Fiorenzuola d'Arda
tacconig@yahoo.com

The accuracy of a quantitative polymerase chain reaction assay in quantifying the DNA of trichothecene-producing *F. culmorum* and *F. graminearum* within harvested wheat grains and head tissue was evaluated in comparison with incidences of infected kernels and deoxynivalenol levels. In a first experiment, six durum and bread wheat varieties were grown in randomized plots for a 2-year period, and inoculated with *Fusarium* macroconidia at six growth stages between heading and dough ripening, to obtain a wide range of Fusarium head blight incidences. There was a close relationship between fungal DNA and the amount of deoxynivalenol, and this relationship was consistent over *Fusarium* species, wheat species and varieties, and over a wide range of Fusarium head blight infection. In a second experiment potted wheat plants were grown under environmentally controlled conditions and inoculated with the two *Fusarium* species at full flowering; head samples were collected before inoculation and after 6 h to 12 days, and processed by the quantitative polymerase chain reaction assay. This assay made it possible to detect the dynamic of fungal invasion in *planta* after infection had occurred, and to single out the presence of infection before the onset of the disease symptoms: A robust detection of the infection occurred within 18–24 h for *F. culmorum*, and within 2–9 days for *F. graminearum*.

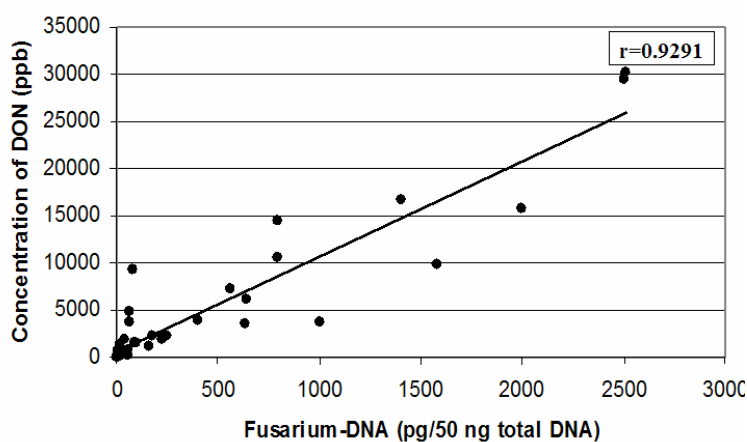


Fig. 1. The correlation between DON concentration surveyed by ELISA and the Fusarium DNA concentration evaluated by quantitative-PCR is consistent and allow to estimate Fusarium head blight incidences.

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EVOLUTIONARY FORCES AND EMERGING PATHOTYPES OF BARLEY POWDERY MILDEW

Antonin Dreiseitl
Agricultural Research Institute Kromeriz Ltd
dreiseitl@vukrom.cz

Current changes in the Czech population of *Blumeria graminis* f.sp. *hordei* can be considered gradual. It is mostly due to the mentioned prevailing area of cultivars that do not induce directional selection, but as well as the absence of dominant cultivars with other genes for specific resistance. It results in gradual decrease in the virulence complexity for many of 12 earlier significant *Ml* resistance genes (*a1*, *a3*, *a6*, *a7*, *a9*, *a12*, *a13*, *k1*, *La*, *g*, *at* and *Bw*). The virulence complexity for these 12 resistance genes was about 0.90 in 1971 and culminated (9.27) in 2000, and since that time it has been decreasing to a present level of 7.32 (2007). However, it takes place along with increasing the population diversity because some of the virulences, at their frequency decline, approach to the level of 50% (optimum level with respect to maximizing the population diversity). However, at the same time the virulence frequency for newer resistance genes (whose frequency is mostly below 50%) has been gradually rising. Therefore, the increase in these virulence frequencies induces not only the growth of the virulence complexity but also the growth of the population diversity.

The present Czech (Central European) population of *Blumeria graminis* f.sp. *hordei* is characteristic of both gradual extending the spectrum of virulences (increasing the virulence complexity due to a larger number of present virulences) and optimization of their frequencies (approaching the frequencies of individual virulences to the level of 50%). It leads towards the increase in the population diversity as a whole, i.e., the increase in the number of existing pathotypes as well as their even proportions (decreasing the frequency of the most abundant pathotypes and increasing the value of evenness). A result is the increase in adaptation potential of the current pathogen population to resistance genes in grown cultivars. It can decrease the efficiency of intraspecific diversification of barley with regard to protection against powdery mildew infection. It can be assumed that the suggested trend in the development of Czech population will continue also in next years.

POWDERY MILDEW, OUTLINE OF THE NEW MENACE ON TRITICALE PRODUCTION

Fabio Mascher¹, Marcello Zala², and Celeste Linde^{2,3}

¹Agroscope Changins-Wädenswil research station ACW, ²Federal Institute of Technology (ETHZ), ³School of Botany and Zoology, Daley Road, The Australian National University, fabio.mascher@acw.admin.ch

Triticale is a recent cereal species originated from an interspecific cross between durum wheat (*Triticum turgidum* spp. *durum*) and rye (*Secalis cereale*). First commercial varieties were released in Western Europe during the 1980s. During the first years of cultivation, triticale excelled due to its disease resistance, robustness and frugality. It was argued that the thorough mixture of genes and traits might have generated durable resistance.

In 2001, first symptoms of powdery mildew, caused by *Blumeria graminis*, have been observed on breeding lines in Switzerland. In the following year, the disease, for the first time, occurred on the commercial varieties Timbo, Trimaran and Tricolor. As these 3 varieties share a common genetic background, only little practical importance was attributed to this observation. Two years later, a first pan-European epidemic affected further varieties. In particular, the high-yielding winter triticale variety Lamberto has been heavily affected in Switzerland, leading to a yield loss of up to 30%. Since then, the fungus has overcome the resistances of several more varieties. It appears that, once broken through the species-specific resistance barrier, the fungus adapts rapidly to new host varieties. This raises questions on which strategies to adopt for resistance breeding in triticale.

In a first step, representative numbers of Swiss powdery mildew isolates from triticale, wheat, rye and barley have been characterized with cross-infection studies and with differential tests. Results show that cross-infections are not very frequent. Under optimal infection conditions in vitro, triticale isolates infect wheat but wheat isolates hardly infect triticale. Rye and barley isolates can infect their respective species of origin, but fail infections on other cereals. This gives a first hint that powdery mildew on triticale might originate from wheat. When testing triticale isolates on powdery mildew differentials for wheat, an amazing diversity of virulence genes are evidenced, that corresponds largely to the diversity in wheat. These findings raise new questions about the relatedness of powdery mildew of wheat and of triticale. These questions have been addressed through molecular comparisons of the structure of conserved genes. Further studies have evidenced the presence of quantitative resistance sources that might allow breeding for durable resistance.

FUSARIUM SPECIES IN FINNISH CEREALS AND INFECTION DEVELOPMENT UNDER DIFFERENT CULTIVATION PRACTICES

Päivi Parikka, Sari Rämö and Veli Hietaniemi
MTT Agrifood Research Finland
paivi.parikka@mtt.fi

In 2004-2006, *Fusarium* infection and mycotoxins of cereals were investigated in two studies. A survey of *Fusarium* infection and mycotoxins on dried cereal grain was carried out in 2005-2006. Altogether 388 samples were collected from farms in different locations in Finland. The aim of the study was to get an up-to-date view of the situation of *Fusarium* infection on cereals and the species forming mycotoxins in grain. In 2005, the deoxynivalenol (DON)-producing species *Fusarium culmorum* and *F. graminearum* were common on oats and barley, less common on spring wheat. The T2/HT-2-producing species *F. sporotrichioides* and *F. langsethiae* were most often detected on oat cultivars, less on barley. In the dry conditions of 2006, DON-producing species were not so common as in 2005, but T2/HT-2-producing species and *F. poae* occurred more abundantly. Especially *F. langsethiae* was quite often detected on certain oat cultivars, also in samples derived from northern locations. This species seems to be the most important T2/HT-2 producer on Finnish cereals, and these toxins were analysed particularly on oats where, in fact, also the highest DON contents were detected. In 2005, some samples of barley and spring wheat also had higher DON contents, but in 2006 the contents analysed did not exceed the limits set in the EU regulations.

A study of cultivation practices, autumn ploughing and direct drilling as well as disease control versus no control was carried out in a field trial in 2004-2006. The aim of this study was to find out, whether direct drilling is a risk for grain quality and safety. Other objectives were to determine whether oat and barley cultivars exhibited differences in the development of *Fusarium* infection and mycotoxin contents. Both cultivation practices were applied to grow four cultivars of malting barley and food oats. The first *Fusarium* infections were detected on oat cultivars at panicle emergence. Infections were detected also on barley, but not so often as on oats. *Fusarium langsethiae* was the first *Fusarium* species observed after ear/panicle emergence. Its abundance was gradually reduced as the grain was ripening. The other species detected in early stages in flowers and kernels of oats was *F. poae*. *F. avenaceum* and *F. sporotrichioides* infected kernels in July to early August while *F. culmorum* and *F. graminearum* infections became more prevalent in August during rainy weather.

The mycotoxin contents detected were mainly low in the trial material. The deoxynivalenol-producing species *F. culmorum* and *F. graminearum* were quite common in the grain, but the DON contents remained well below the EU limits. The highest DON contents were below 1000 µg/kg. The barley cultivar 'Barke' seemed to be most susceptible to DON-producing *F. culmorum* and it also had the highest toxin contents. Among oats, 'Roope' had the highest DON contents and it was also susceptible to *F. culmorum* and *F. graminearum*. *F. langsethiae* infections resulted in T2/HT-2 formation on oat cultivars. The highest contents were detected on cv Belinda which also had the highest infection levels until harvest. Also barley cultivars had T2/HT-2 in the grain, but the contents were lower. *F. langsethiae* and *F. sporotrichioides* both produce type A trichothecenes T2 and HT-2. Direct drilling did not increase the DON contents of oats and barley compared with autumn ploughing. Disease control at flag leaf stage did not have any effect either on *Fusarium* infection or mycotoxin contents. However, direct drilling is a risk in oat production. These results, although from a short period of time, indicate that *F. langsethiae* may become a serious problem in cereal cultivation, of oats in particular, where no tillage and crop rotation are used. However, more information is needed about the survival of *F. langsethiae* in the field.

Fusarium-species are common in Finnish cereals, especially oat and barley cultivars. The analysed DON contents are normally below the maximum contents defined by EU, but the problem may become of T2/HT-2 toxins on oats. There are differences in susceptibility to *Fusarium* infection and mycotoxin formation among cereal cultivars, but at the moment we do not know enough of that. Especially infection of *F. langsethiae* on oats needs more research. However, there is no *Fusarium*-resistance known in cultivated oats. This means new challenges for plant breeding.

CONTRIBUTIONS TO THE IMPROVEMENT OF RESISTANCE TO *FUSARIUM* HEAD BLIGHT IN WHEAT AND TRITICALE AT NARDI- FUNDULEA, ROMANIA

M. Ittu¹, N. N. Saulescu ² and G. Ittu³

^{1,2,3} National Agricultural Research Development Institute (NARDI) Fundulea

ittum@ricic.ro/gittu@clicknet.ro

Wheat is one of the most traditional staple food crops in Romania, while triticale is an expanding crop, of higher concern mainly in hilly regions with acid soils, where it is more performant than other small grains. The most of bread wheat and triticale varieties released in the past decades at NARDI-Fundulea combines improved desirable agronomic traits with a better resistance to foliar (rusts & powdery mildew) and seed diseases (*Fusarium* head blight, FHB and common bunt). From the perspective of increasing demand of consumers for safer end use products became obvious that resistance to FHB has to be emphasized.

High attacks of FHB with damaging effects are registered only in some environments from Romania. A survey of *Fusarium* head blight performed from 1998 to 2002, on 1464-2067 thousand hectares/yr, revealed on average incidence values ranging from 19 to 37%, from which only 1-5% could be considered as significant.

The main goals of FHB researches were to search for new sources of resistance and to introduce them into modern Romanian germplasm. Yearly, are evaluated in experimental fields under point artificial inoculation with 2-6 *Fusarium* isolates, around 1500 entries of winter wheat and 500 of triticale, respectively, from preliminary, advanced and regional trials with the both crops.

Bread wheat. In a first stage was established the methods for screening of the both, pathogen aggressiveness and host resistance. As result of the first researches has been identified the line *Fundulea 201R*, a source of resistance, not related with Chinese germplasm, in which resistance is already very well documented. Furthermore, a progress in selecting of advanced breeding lines with higher resistance to FHB, combined with improved agronomic type has been registered. The close significant correlation found between DON concentrations in grains from heads, artificially inoculated at anthesis with *Fusarium* and *Fusarium* diseased kernels, *FDK*, % suggests the possibility to select concomitantly for the both FHB traits.

Marker-assisted introgression of the donor-QTLs alleles 3B (*Sumai 3*) and 3A (*F 201R*) into Romanian winter wheat germplasm combined with phenotypic selection, is a promising component of the strategy to reduce the vulnerability to FHB epidemics of the new cultivars in conventional and low inputs systems from Romania.

Triticale. Following a long term screening of resistance to FHB, in the breeding triticale germplasm a large variability for this trait was noticed. This was the background to the continuous improvement of the level of resistance in the new registered cultivars (*Gorun* and *Stil*). As compared with bread wheat, the initial level of resistance to FHB in Romanian breeding triticale was better. Our data revealed that similarly with bread wheat, the same criteria, respectively, area under disease progress curve (AUDPC) and relative weight of heads (RWH, % of control), are reliable in respect of assessment for resistance, being in a very close correlation ($r=-0.82$).

BREEDING EFFORTS TO IMPROVE RESISTANCE TO COMMON BUNT IN WHEAT AT NARDI-FUNDULEA, ROMANIA

M. Ittu¹, N. N. Saulescu ² and G. Ittu³

¹²³ National Agricultural Research Development Institute (NARDI) Fundulea
ittum@ricic.ro/gittu@clicknet.ro

Common and dwarf bunt (*Tilletia caries* (DC) Tul & C. Tul, *T. foetida* (Wallr.) Liro and *T. controversa* (Kuhn) are potentially important wheat diseases in Romania, especially in organic farming and on small farms, unable in most cases to properly treat the seed.

The resistance researches to common bunt are focused at NARDI Fundulea on multi-environmental screening of breeding germplasm under field inoculation with isolates, previously evaluated and selected for aggressiveness from the local *Tilletia* populations.

A small breeding program have been started in 1972, by crossing the old Turkish wheat PI 178383 (a *Bt*, *Bt 8* and *Bt 10* carrier) with adapted cultivars. Later, in an attempt to diversify the resistance genes used in the program, several original gene sources (including *Bt 5*, *Bt 8*, *Bt 11*, *Bt 12* etc.), primarily received from Bob Metzger (Oregon State University, U.S.) and more recently obtained, by the courtesy of Blair Goates (National Small Grains Germplasm Research Facility, West Aberdeen, U.S.), were used as parents in order to improve resistance to common bunt of the modern bread wheat germplasm obtained at NARDI-Fundulea.

Current research efforts are focused on: 1) survey of efficiency of known bunt resistance genes against local populations (isolates) of bunt; 2) screening of resistance in germplasm derived of repeated selection cycles for combining the bunt resistance with valuable agronomic traits and 3) searching and use of new sources with bunt resistance.

Results showed that constantly, *Bt 5*, *Bt 8*, *Bt 10*, *Bt 11*, *Bt 12* expressed a high level of resistance to local *Tilletia* populations originated from Romania. Promising results were obtained following the latest cycles of selection. Presently available bunt resistant lines are semi dwarf and powdery mildew resistant, being better adapted to local conditions. The high level of resistance in some lines was also confirmed in different environments from Romania and abroad.

Accelerated progress is expected by use of advanced lines with resistance derived probably from the cultivar Colonias (Brasil) and rye genome. The use of molecular markers for some of the bunt resistance genes is under way.

INFLUENCE OF CLIMATE CHANGE ON VIRUS VECTORS OF FIELD CROPS

Roland Sigvald
Swedish University of Agricultural Sciences
roland.sigvald@ekol.slu.se

Aphids play an important role in the epidemics of both persistently and non-persistently transmitted plant viruses. There are several viruses of cereals, potatoes, sugar beet, oilseed rape, which are transmitted by aphids. These viruses cause extensive damage to several crops in most countries, but there is a great difference between different regions and years. These differences could partly be explained by different weather conditions, occurrence of virus sources and timing between growing period of crops and flight periods of virus vectors. The future climate will have a great influence on the vectors as well as the crops.

Potato virus Y (PVY) seems to be more important in the northern regions of Europe than potato leaf roll virus (PLRV), which can be explained by differences in vector populations. In the northern regions of Sweden the spread of PVY is minimal because vectors are uncommon. By contrast, in southern regions the spread of PVY has led to serious problems for seed potato growers during some years. In the future climate we can expect increased problems with PVY also in Northern Sweden and probably with PLRV in southern and central Sweden. Although, PVY can be transmitted by aphids that feed preferentially on potatoes, other species that do not colonize potatoes, seems to be far more important, e.g. *Rhopalosiphum padi*, *Brachycaudus helichrysi*, *Acyrtosiphon pisum*, and *Phorodon humuli*. Totally about 40 aphid species are known to be vectors of PVY. Most aphid species overwinter as an egg, but in the future they will probably also survive during the winter on different winter crops and weeds.

Barley yellow dwarf (BYD) is another example of virus, which cause great damage to several cereal crops all over the world. In Sweden BYD seems to be very important in spring cereals in some regions of the country, but during the last 10 years BYDV is also of importance in winter cereals. In 2006-2007 the mild winter in southern Sweden was very favourable to aphids, which are vectors of BYDV. In April 2007 symptoms of BYDV was very common in winter cereals in southern Sweden and in some fields yield reduction was estimated to more than 20%. In the future warmer climate the main vectors, *Rhopalosiphum padi* and *Sitobion avenae* will probably survive during the winter on winter cereals and grasses. Increased growing of maize and warmer climate will probably favour such vectors as *Rhopalosiphum maidis*. Occurrence of BYD will probably increase partly because of timing between growing period of winter cereals and aphid migration and that maize will act as a green bridge between spring and winter cereals. There are also viruses of economic importance on oilseed rape and sugar beet and it is likely that vectors of these viruses also will be favoured by the future warmer climate.

In Sweden and several other countries suction traps have been used in aphid monitoring and forecasting. Suction trap catches from southern, central and northern parts of Sweden has partly been analysed in relation to post harvest testing of samples from seed potato fields. A number of factors were considered, such as proportion of virus sources in seed potato fields, planting date, number of aphids, number of vectors, aphid flight in relation to mature plant resistance, data from field inspection and date of haulm destruction. In Sweden strong relationship was found between suction trap catches of aphids and proportion of PVY infected progeny tubers ($r^2=0,47$), but even better when taking into account mature plant resistance, number of main vectors and proportion of virus sources ($r^2=0,78$).