106, 111, 114, and 127), the production of type B trichothecenes was completely suppressed.

PUCCINIA STRIIFORMIS ANALYSIS BY SEQUENCE RELATED AMPLIFIED POLYMORPHISM

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Yellow rust, caused by the fungal pathogen *Puccinia striiformis*, is a major disease of wheat in temperate-cool climates. The pathogen exists as a large number of 'physiologic races' possessing virulence for different resistance genes in host cultivars. The traditional method used for testing rust populations using a set of differential cultivars is time-consuming. As such, any molecular tool that offers a quick method for primary screening yellow rust populations would be welcomed. Ideal markers used for pathogen identification would be based on the genes responsible for virulence. Here we present the use of a promising molecular approach for identifying and developing race-specific markers. The technique, SRAP, is based on the use of degenerate random primers. It has been shown that the primers used, preferentially target the exon–intron junction of genes in plants. To identify markers that can be useful to differentiate races of the pathogen, a subset of twelve single pustule isolates was first tested for pathogenicity and secondly analysed for their molecular profile obtained using the SRAP technique with 9 primer combinations. It was possible to generate a 30% higher level of polymorphism compared to AFLP and it was possible to identify bands specific for single isolates that differ for the avirulence genes. These results suggest that SRAP may be suitable for the identification of pathogencity-related markers in pathogens such as yellow rust and represents the first application of the technique to the order Uredinales.

COMPARISON OF *FUSARIUM* GENETIC CHEMOTYPING METHODS.

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Fusarium chemotyping is an essential tool for characterizing *Fusarium* populations causing Head blight on wheat and other cereals. The chemotype determination of *F. graminearum* and *F. culmorum* was shown to improve the precision of prediction of *Fusarium* toxin contamination in the field. Moreover, it is useful for defining the population structure of the pathogens within a field. Chemotyping methods for trichothecene type B discrimination in *Fusarium* have been developed for *F. graminearum* and *F. culmorum.* All methods are based on differences in the *tri* cluster that encodes the genes necessary to synthesize toxin variants (nivalenol, 3 acetylated deoxynivalenol and 15 acetylated deoxynivalenol). Three methods were compared, using DNA obtained from previously isolated *F. graminearum* strains as developed by Ward *et al*. (2002), Quarta *et al*. (2006) (derived from Jennings *et al*., 2004), and Li *et al*. (2008). The methods, all based on polymorphisms of the *tri* cluster between the three known chemotypes are targeting *tri 3*, *tri 7*, *tri 12* and *tri 13*. In order to verify specificity of the chemotyping tests and consistency of the markers, a set of 110 isolates from the CRP-GL collection belonging to *F. graminearum*, *F. culmorum* as well as control strains belonging to *F. poae* and *F. avenaceum* were analysed using the three above cited methods. PCR programs were modified to increase specificity of Phusion Taq, raising temperature of the annealing and denaturing steps. The three methods were not always consistent in chemotype attribution. In particular, differences were observed at the level of amplification specificity. When primers were used to amplify *F. poae* and *F. avenaceum* DNAs aspecific products were seldom amplified by Ward *et al*. (2002) and Quarta *et al*. (2006) methods. Wang's method showed a lack of specificity being unable to distinguish correctly all the 3ADON and 15ADON isolates. This suggests that *tri13* intron size cannot be used to distinguish acetylated chemotypes. This work highlights the fact that genetic chemotype determination requires a continuous monitoring of markers and that targeting different regions of the cluster may be the most reliable strategy for correct chemotype attribution. Moreover, none of the tested markers can be used on direct plant extracts that are often contaminated by multiple *Fusarium* species, giving raise to aspecific cross reaction products.

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PATHOGENICITY AND MYCOTOXIN PROFILE OF *FUSARIUM TEMPERATUM*, AN EMERGENT PATHOGEN OF MAIZE IN EUROPE[#].

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In a recent study, a population of *Fusarium* strains isolated from maize, closely related to *F. subglutinans,* was described as a new species, *Fusarium temperatum* J. Scauflaire et F. Munaut. In several temperate regions of Europe, the *F. temperatum:F. subglutinans* ratio is very high in the fields, suggesting that *F. temperatum* competes with its sister species *F. subglutinans*. This raised the question of the contribution of this novel species to the final ear rot or stalk rot symptoms observed on maize plants at harvest, as well as to the potential mycotoxin contamination. The pathogenicity of *F. temperatum* to maize plant has been tested in greenhouses and preliminary results confirm its ability of to cause stalk rot and seedling malformation with a virulence similar to that of *F. subglutinans*. Currently, studies are in progress to elucidate the mycotoxigenic potential of *F. temperatum*.

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