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Resistance behaviour to *Gnomonia leptostyla* (Fr.) Ces. in various species and provenances of *Juglans*

N. Anselmi¹, M. Gras²

¹Department for Innovation in Biological, Agro-food and Forest systems (DIBAF), University of Tuscia, Viterbo (Italy); ²CRA (Agricultural Research Council) – PLF (Research Unit for Intensive Wood Production), Rome (Italy). E-mail: anselmi@unitus.it

The aim of this work was to evaluate the response of various species and provenances of *Juglans* to the anthracnose agent *Gnomonia leptostyla*. The research was carried out in the 15-year-old experimental plantation Cesurni Farm (CRA) near Tivoli, Rome, during the 2014 vegetative seasons, characterized by a high anthracnose incidence. The considered material consisted of four *Juglans* species originated from USA, i.e. *J. cinerea* (8 genotypes), *J. microcarpa* (18), *J. sieboldiana* (16) and *J. nigra* (66) and of *J. regia* plants of different provenances, from France (27), Russia (16), Israel (28), Iran (9), northern Italy (32), central Italy (36), southern Italy (42). Both the average number of necrosis spots and the percentage of leaf necrotic area were useful tools to evaluate disease susceptibility. *J. cinerea* and *J. sieboldiana* showed only small (2–4 mm diameter) necrotic spots, while the other species exhibited necroses larger than 1 cm², with stronger severity (in descending order) on *J. regia*, *J. nigra* and *J. microcarpa* and, among *J. regia*, for the provenances from France, Russia, Italy, Israel and Iran. *J. cinerea*, *J. sieboldiana*, *J. microcarpa*, *J. nigra*, resulted more resistant to anthracnose than *J. regia*. Among *J. regia*, the genotypes of French origin were discreetly resistant, those from Russia and Israel were tendentially susceptible, those from Iran were very susceptible, whereas the genotypes from Italy ranged from very susceptible to moderately resistant. These results represent an important starting point for the selection and genetic improvement of walnut for fruit and wood production.

Wheat associated microbial community changes due to the activity of *Trichoderma gamsii* T6085 as a biocontrol agent to mitigate Fusarium Head Blight disease in wheat

A.S. Alukumbura¹, W.G.D. Fernando¹, S. Sarrocco², A. Bigi², G. Vannacci², M.G. Bakker³

¹Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada; ²Department of Agriculture, Food and Environment, University of Pisa, Via del Borghetto 80, 56124 Pisa, Italy; ³Department of Microbiology, 45 Chancellor's Circle, Winnipeg, MB R3T 2N2, Canada. E-mail: matthew.bakker@umanitoba.ca

Beneficial microbes can help mitigate plant diseases through competition with pathogens. *Trichoderma gamsii* T6085 is a biocontrol agent capable of mitigating Fusarium head blight (FHB) in wheat. This study assessed the impact of *T. gamsii* T6085 on wheat-associated microbiome and on *Fusarium graminearum* in field. Cultivar Tirex was seeded in a RCBD with four treatments. *T. gamsii* was applied on: i) crop debris at stalk stage; ii) on spikes at anthesis and iii) on both crop debris at stalk stage and on spikes at anthesis. Untreated plots were used as control with five replicates. Crop residue (wheat from the previous growing season), wheat spikes, and wheat kernels were collected at different time points from T6085 application for DNA extraction and qPCR. The microbial community structure showed an apparent variation over time. The most abundant taxa in wheat spikes and kernels were *Pseudomonas*, *Enterobacter*, and *Pantoea*, while *Alternaria* and *Fusarium* were the most abundant fungi. The *F. graminearum* density was significantly higher in crop residue initially and decreased over time. *F. graminearum* density increased over time in wheat spikes, reaching the highest densities at harvest. Application of *T. gamsii* did not significantly affect the microbial community composition. There was a significant reduction in FHB disease index and severity 28 days post inoculation with *T. gamsii*, the changes

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Fusarium verticillioides* and *Aspergillus flavus* co-occurrence influences plant and fungal gene expression in maize kernels and *in vitro

P. Giorni, A. Lanubile, A. Marocco, P. Battilani

Department of Sustainable Crop Production, Università Cattolica del Sacro Cuore, Via Emilia Parmense 84, 29122 Piacenza, Italy. E-mail: paola.battilani@unicatt.it

Climate change will increase the co-occurrence of *Fusarium verticillioides* and *Aspergillus flavus*, so as of their mycotoxins, in European maize. In this study, the expression profiles of two pathogenesis-related (PR) genes and four mycotoxin biosynthetic genes, *FUM1* and *FUM13* (fumonisin pathway) and *AFLR* and *AFLD* (aflatoxin pathway), were examined in kernels and in artificial medium after a single inoculation with *F. verticillioides* or *A. flavus* or with the two fungi in combination, in different temperature regimes (20, 25 and 30 °C) over a time-course of 21 days. In maize kernels, PR genes showed the strongest induction at 25 °C in the earlier days post inoculation (dpi) with single fungi. A similar behavior was maintained with fungi co-occurrence, but with enhanced defense response at 9 dpi under 20 °C. Regarding *FUM* genes, in the kernels inoculated with *F. verticillioides* the maximal transcript levels occurred at 6 dpi at 25 °C, decreased with the co-occurrence of *A. flavus*, while the highest gene induction was detected at 20 °C. Similar results were observed in fungi grown *in vitro*. Concerning *AFL* genes, considering both *A. flavus* alone and in combination, enhanced up-regulation levels were reached at 30 °C during all time-course both in infected kernels and in fungi grown *in vitro*. Regarding mycotoxin production, no significant differences were found among temperatures for kernels contamination; *in vitro* the highest production was registered at 25 °C for AFBs and at 20 °C for FBs in case of single inoculation. In fungal co-occurrence, both mycotoxins resulted reduced at all the temperatures considered compared to the amount produced with single inoculation.

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Draft genome sequence of a new *Fusarium* isolate collected from hazelnut in central Italy

A. Grottoli¹, S. Turco², L. Faino³, M. Reverberi³, V. Cristofori², A. Mazzaglia²

¹Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Centro di ricerca difesa e certificazione (CREA-DC), Via C.G. Bertero 22, 00156 Roma; ²Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, Via S. Camillo de Lellis snc, 01100 Viterbo, Italy; ³Dipartimento di Biologia Ambientale, Sapienza, Università di Roma, Piazzale Aldo Moro 5, 00185 Roma. E-mail: angmazza@unitus.it

Fusarium lateritium, already known as the causative agent of hazelnut twig cankers and fruit rot on walnuts and olives, since 2000 has been also associated in Italy to a serious disease, the nut grey necrosis as well (NGN). Indeed, in several hazelnut orchards located in the Latium Region, in central Italy, symptoms like brown greyish necrotic patch on the nutshell, bracts, and less frequently on the petioles, have been observed together with a severe fruit drop. The disease impacts the Italian hazelnut production cultivation, which is the second largest world hazelnut producer, after Turkey.

To date, the only genome of *F. lateritium* available on the public database is an American strain isolated from elm tree with canker and dieback of branches, arranged in 1,404 contigs. Thus, a more complete representation of an Italian strain isolated from hazelnut could represent a first important step towards a better understanding of the biology, epidemiology, and infection mechanisms of this pathogen. Here we evaluated different *de novo* assembly algorithms, and a combined approach that takes advantage of the long but quite inexact reads obtained by Oxford Nanopore Technology, and of the precision of the short reads obtained by Illumina technology, to reach a complete and precise genome sequence. This resource could be a milestone to further disentangle the phylogeny of the *F. lateritium* complex and to develop a focused and specific control disease strategy.

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Evolution of mini chromosomes in *Fusarium verticillioides*

A. Grottoli^{1,2}, L. Faino¹, M. Beccaccioli¹, V. Scala², N. Ferrante¹, B. Massimo³, M. Aragona², R.S. Fratini¹, M. Reverberi¹

¹Department of Environmental Biology, University of Rome "La Sapienza", p. le Aldo Moro 5, 00185 Rome, Italy; ²Research Centre for Plant Protection and Certification, Council for Agricultural Research and Economics (CREA), Via C.G. Bertero 22, 00156 Roma, Italy ; ³Department of Agricultural, Forest and Food Science,

University of Turin, largo Braccini 2, 10095 Grugliasco (TO).
E-mail: luigi.faino@uniroma1.it

The maize pathogen *Fusarium verticillioides* causes huge economic losses per year due to the production of fumonisins. *Fusarium verticillioides* ITEM 10027 (*Fv*10027) isolated in Italy shows a reduced fumonisins synthesis when compared to the *F. verticillioides* reference strain 7600 (*Fv*7600). Although the difference in fumonisins production, the pathogenicity tests on maize stalk did not show any difference in infection levels. Additionally, using knock-out mutant in *FUM1* gene did not show any compromised virulence in stalk rot assay. To better understand *Fv* virulence, the genome of *Fv*10027 was sequenced and assembled. Comparative genomics between *Fv*7600 and *Fv*10027 showed a difference in genome size of about 1.4 Mb despite 99% nucleotide identity. Genome assembly of *Fv*10027 showed that two mini-chromosomes of about 1 Mb and 750 Kb were unique to *Fv*10027 while a mini-chromosome of about 400 Kb to *Fv*7600. To determine the presence of these mini chromosomes in the Italian *Fv* population, 24 strains, sampled in the Po valley, were sequenced; presence/absence analysis showed that only three *Fv* strains had those chromosomes. The analysis of *Fv*10027 dispensable chromosomes showed an enrichment of secreted proteins and a higher level of repetitive elements. Intriguingly, BLAST analysis on the *Fv*10027 proteome showed that proteins codified on mini chromosomes have the best identity to *F. oxysporum* proteins located at dispensable chr3 and chr6. Moreover, synonyms substitution analysis suggests that mini chromosomes of *F. verticillioides* were not probably acquired through a horizontal chromosomal transfer from *F. oxysporum* but rather originated before the split of the two species.

First report of *Venturia asperata* in Trentino Region (northern Italy)

V. Gualandri^{1,2}, D. Prodorutti^{1,2}, L. Delaiti¹, M. Zaffoni¹, C. Panizza¹, F. Pedrazzoli¹, G. Angeli¹

¹Fondazione Edmund Mach, Center for Technology Transfer, Via E. Mach 1, 38010 S. Michele all'Adige, Trento; ²Center of Agriculture, Food and Environment (C3A), University of Trento, I-38010 San Michele all'Adige, Italy. E-mail: valeria.gualandri@fmach.it

Venturia inaequalis (Cooke) G. Winter is known to be responsible for apple scab, a very harmful disease reported in almost all apple-growing regions worldwide. Apple industry constitutes an important cornerstone for the economy of Trentino (northern Italy). As the demand for a reduction of chemical treatments in agriculture is increasing, the development of resistant cultivars plays a crucial role. During the late summer of 2018 and 2019, atypical symptoms of apple

scab were observed on a resistant cultivar carrying the *Vf* resistance gene to *V. inaequalis*. Symptoms were observed in a commercial orchard in Adige Valley. To identify the pathogen involved in this symptomatology, small pieces of brownish suberose patches (collected from fruits) and dusty patches (collected from leaf tissue) were plated on potato dextrose agar. DNA was extracted from mycelia originated from monoconidial cultures and the ITS region was amplified using the primer Vasp (5'-GTCTGAGAAACAAGTAATAG-3'), specific for *Venturia asperata* Samuels & Sivan., in combination with ITS4. Amplicons of the expected size were generated, gel purified, and sequenced (MT459450 and MT459451). A BLAST search was performed in the NCBI database and one isolate showed 100% of identity with *V. asperata*. These data suggest that, besides *V. inaequalis*, another species of *Venturia* may occur in Trentino region, confirming what has already been reported in France, Emilia Romagna and Piedmont. The presence of *V. asperata*, which causes a minor disease so far, might represent an emerging problem on apple tree. Epidemiological studies on a wider scale could improve the knowledge of this Ascomycetes, leading to specific control strategies aimed reducing fruit losses especially in sustainable and organic orchards, where treatments against apple scab are usually reduced.

Fusarium oxysporum hyphal penetration depends upon physical rather than chemical stimuli

V.M. Guastaferrò¹, S. Vitale², R. Marra¹, D. Turrà¹

¹Department of Agricultural Sciences, University of Naples "Federico II", Via Università 100, 80055 Portici (Na), Italy; ²IPSP, Istituto per la Protezione Sostenibile delle Piante, sede secondaria di Portici, Piazzale Enrico Fermi 1, 80055 Portici (NA), Italy. E-mail: valentinomaria.guastaferrò@unina.it

Fusarium oxysporum (*Fo*) is a soil dwelling fungal ascomycete and the causal agent of wilt disease in a large number of economically important crops. A crucial step for plant infection relies on hyphal-mediated penetration of epidermal root cells. In order to identify if chemical or physical stimuli trigger *Fo* invasive growth we characterized *Fo* penetration using different nutrient sources, plate orientations or cellulose-based poreless membranes (cellophane) or chemically inert membranes of known pore size (nylon; 0.45 µm and 0.22 µm). Here we show that while gravity or nutrient sources do not alter *Fo* penetration, pore size does affect hyphal invasive growth. In *Fo* there exist three mitogen-activated protein kinase (MAPK) signalling cascades responsible for invasive growth (FMK1) and cell wall integrity (MPK1) or high osmolarity (HOG1) responses. Interestingly, we observed that while *Mpk1Δ* or *Hog1Δ* knock-out mutants did not show differential growth and