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Alternaria is a cosmopolitan fungal genus comprising many saprophytic, endophytic and pathogenic species. Pathogenic *Alternaria* species cause major pre- and post-harvest losses on diverse agricultural crops including vegetables. Understanding the mode of reproduction in a plant pathogenic fungus is essential because it affects the population genetic structure, evolution and epidemiology, and so will influence effective disease management. Plant pathogenic fungi in general have different means of reproduction, including sexual, asexual and parasexual mechanisms. Sexual reproduction in ascomycetes is controlled by a mating type (*MAT*) locus. In this study, the complete genomes of two randomly selected strains of *Alternaria alternata* from onion were sequenced, and two genes (*MAT1-1-1* and *MAT1-2-1*) at the MAT locus were identified and characterized. The high mobility group (HMG) and alpha-1 (α-1) box are highly conserved and the genes are, respectively, 1083 and 1217 base pairs in length. The flanking region of both idiomorphs contained DNA lyase. These results suggest that this fungus is heterothallic, since the two opposite mating type genes were found from two different strains. Sexual structures have not been observed in *A. alternata* and the presence of both mating types indicates the existence of cryptic sexual process. This would result in an increase in the genetic diversity of the pathogen and complicate the management practices used. A more detailed study of the frequency and distribution of the two genes in major onion growing locations is necessary to determine how frequent recombination occurs in these populations.

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PRATYTECH: Biotechnological approaches towards control of the root lesion nematode *Pratylenchus penetrans*. C.S.L. VICENTE[1], J. BRANCO[2], J. FIGUEIREDO[3], I. ESTEVES[3], J. CARDOSO[3], A.C. FIGUEIREDO[2], J. BARROSO[2], I.L. CONCEIÇÃO[3], I. ABRANTES[3], M. MOTA[1], P. VIEIRA[1]*. [1]*ICAAM – Instituto de Ciências Agrárias e Ambientais Mediterrânicas, Universidade de Évora, Pólo da Mitra, Ap. 94, 7006-554 Évora, Portugal.* [2]*CESAM Lisboa, Faculdade de Ciências da Universidade de Lisboa, CBV, C2, Campo Grande, 1749-016 Lisboa, Portugal.* [3]*Centre for Functional Ecology, Universidade de Coimbra, 3004-517 Coimbra, Portugal.* [*]*E-mail: pvieira@uevora.pt*

Root lesion nematodes (RLN) are ranked third worldwide as plant parasitic nematodes with economic impacts. *Pratylenchus penetrans*, one of the most damaging species of this group, affects more than 400 hosts, and is considered a limiting factor in production of important crops (e.g. corn, potato), ornamentals (e.g. lily, roses) and fruit trees (e.g. apple, cherry orchards). Surveys conducted in Portugal have revealed different RLN species associated with important crops, with *P. penetrans as* one of the most abundant species found in potato fields. Host resistance to RLN is very limited, as only a few genetic loci have been linked to resistance/tolerance to some species. Effective and long-lasting control strategies based on current pesticide compounds are hampered by increasing regulations, due to their non-specificity and potential toxic effects to ecosystems and human health. A promising research area is the identification of critical metabolic and parasitism-related genes of these plant pathogens, in which silencing through RNA interference (RNAi) can promote lethal or inhibitory effects on nematode development or parasitism strategy. The main goal of the project PratyTech is to identify protein-coding genes in *P. penetrans* which may be established as new nematode targets for the development of specific and efficient crop resistance strategies. Another relevant aspect of this project is the study of the host gene expression profile and cellular changes upon *P. penetrans* infection in potato, which should provide important insights into the molecular mechanisms involved in RLN parasitism.

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Tolerance of olive (*Oleae europaea*) cv. Frantoio to *Verticillium dahliae* relies on differential basal and pathogen-induced transcriptomic responses.

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Verticillium wilt (VW) is one of the most serious biotic constraints for olive trees. Knowledge of the genetics of tolerance/resistance to this disease is very limited. To analyze the susceptibility/tolerance of olive cultivars Frantoio (tolerant) and Picual (susceptible) to *Verticillium dahliae,* a comparative transcriptomic analysis (RNA-seq) was carried out in host root tissues. Results showed that a large number (27,312 unigenes) of differentially-expressed genes (DEGs) were found between 'Frantoio' and 'Picual' non-manipulated control roots. Dissimilar root system architecture was also observed between the two cultivars. Upon infection with *V. dahliae*, 'Picual' and 'Frantoio' plants also responded in completely different ways. Genes induced in 'Picual' roots were basically different to the DEGs observed in 'Frantoio' non-manipulated/uninoculated roots. Transcriptome changes occurring in each cultivar at early stages of *V. dahliae* infection were also very dissimilar. When targeting for tolerance/resistance-related genes, the most noticeable expression differences between the cultivars were: i) a pathogenesis-related protein of the Bet v I family, likely encoding a major latex protein; ii) a dirigent-like protein involved in lignification; iii) several *BAK1* (Brassinosteroid insensitive 1-Associated receptor Kinase) and *NHL1* (Harpin-INduced protein-like) unigenes; iv) six unigenes involved in ROS stress response (stronger in 'Picual' but no expression in 'Frantoio'); and v) an overall induction of *BAM* unigenes (involved in starch degradation) in 'Picual' in contrast to 'Frantoio'. These results show that tolerance of 'Frantoio' plants to VW is a complex polygenic plant trait.

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Expressional and positional candidate genes for resistance to *Didymella pinodes* in pea. S. FONDEVILLA, M.D FERNANDEZ-ROMERO, D. RUBIALES. *Institute for Sustainable Agriculture, CSIC, Alameda del Obispo s/n, 14004, Córdoba, Spain. E-mail: sfondevilla@ias.csic.es*

Didymella pinodes, causing Ascochyta blight, is the most destructive foliar pathogen of dry peas. Resistance identified so far is incomplete, and more frequent in wild pea relatives than in cultivated pea. One of these wild relative resistant accessions is the *P. sativum* ssp. *syriacum* accession P665. Quantitative Trait Loci (QTLs) associated with resistance to Ascochyta blight have been identified in the recombinant inbred lines (RIL) population P665 × Messire and in other crosses, but the resistance genes underlying these QTLs are unknown. expressional and positional candidate genes for resistance to *D. Pinodes* were identified by selecting 15 candidate genes to be mapped in the P665 × Messire RIL population. They were differentially expressed in resistant reactions in previous transcriptomic studies, or putatively located into QTLs associated with resistance to this disease according to other pea maps. Thirteen QTLs were successfully amplified in the parental lines. Two were monomorphic, direct polymorphism was found for another, and CAP markers were developed for the remaining ten genes. Therefore, eleven genes could be analysed and mapped in the available P665 × Messire map. Four genes were located within the confidence interval of previously described resistance QTLs or highly associated with resistance parameters. These are therefore suggested as putative candidate genes for resistance to Ascochyta blight.

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Genomic analysis of nontoxigenic strains of *Pseudomonas syringae* pv. phaseolicola. P. LLOP[1], L. BARDAJI[1], M. ECHEVERRÍA[1], P. RODRÍGUEZ-PALENZUELA[2], J. SÁNCHEZ-COLMENERO[2], C. RAMOS[3], J. MURILLO[1]. [1]*Departamento de Producción Agraria, ETS Ingenieros Agrónomos, Universidad*