359 and KFB 363) induced hypersensitive reactions in tobacco leaves. They grew at 41°C and produced beige to tan-coloured, nonmucoid, convex colonies on yeast extract-dextrose-CaCO₃ agar. All strains studied used L-arabinose, did not reduce nitrate, nor utilized sucrose. Conventional PCR was performed using A. citrulli-specific primers BX-L1/BX-S-R2. The 16S rRNA gene sequence from two strains (KFB 343 and KFB 344) showed 100% identity to strains of Acidovorax citrulli from China, Thailand and the USA. These results identified the causal organism as A. citrulli. Genetic relatedness among strains was investigated by rep-PCR, using BOX and REP primers. All tested strains except one (KFB 358), showed the same BOX-PCR profiles. In addition, all strains were assigned to the same REP-PCR group. These results show that A. citrulli strains isolated in Serbia during three years belong to an homogeneous population. These occurrences of bacterial fruit blotch are considered to be of seed-borne origin, but is not known whether the pathogen will survive from season to season in Serbian climatic conditions.

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Screening of mycotoxin profile and mycotoxin gene clusters in toxigenic fungi of food crop plants reveals phenotypic and genetic variability at intraspecific levels. A. SUSCA, A. LOGRIECO, M. HAIDUKOWSKI, A. VILLANI, A. MORETTI. Institute of Sciences of Food Production, Italian National Research Council (ISPA-CNR), Via Amendola 122/O, 70126, Bari, Italy. E-mail: antonio.moretti@ispa.cnr.it

There is concern regarding occurrence of toxigenic fungi on food and feed crops, since mycotoxin accumulation in the final products represents serious risks for human and animal health. Among the plant pathogens that produce mycotoxins in planta, Aspergillus and Fusarium spp. are the most common, and show great variability of their mycotoxin profiles, even in closely related species or at intraspecific levels. We report here results from studies conducted using HPLC/FLD and LC-MS/MS measurements and whole genome sequencing: i) variability of Ochratoxin A (OTA) production related to the occurrence of the ota gene cluster in the Aspergillus niger clade, where both the intact and deleted clusters coexist; ii) variability of beauvericin (BEA) production and occurrence of the BEA gene cluster in Fusarium subglutinans and F. temperatum, two phylogenetic sister species where toxigenic potential is not related to real production capacity in vitro; iii) variability of fumonisin production and FUM gene cluster occurrences in F. proliferatum isolated from fig and maize, two populations with the same toxigenic potential but different fumonisin production capacity; iv) variability of trichothecene production in the F. equiseti/ incarnatum species complex and related variability in the trichothecene gene cluster. Taken together, these data show that mycotoxin gene clusters can differ within a single species, or among very closely related species. The lack of a given mycotoxin production, at least in in vitro conditions, is frequently, but not always, related to the absence of gene clusters.

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Identification of pathotypes and analysis of the genetic structure of Fusarium oxysporum f. sp. lentis populations. H.R. POURALIBABA¹, Z. SATOVIC², M.J. COBOS³, D. RUBIALES³, S. FONDEVILLA³. ¹Dryland Agricultural Research Institute, Education and Extension Organization (AREEO), Maragheh 119, Iran. ²Faculty of Agriculture, Department of Seed Science and Technology, Svetošimunska 25, 10000 Zagreb, Croatia. ³Institute for Sustainable Agriculture, CSIC, 14004 Córdoba, Spain. E-mail: hpouralibaba@ias.csic.es

Lentil cultivation is threatened worldwide by Fusarium wilt, caused by Fusarium oxysporum f. sp. lentis (Fol). Knowledge on pathogenic diversity and genetic structure of Fol populations is fundamental for breeding for resistance and managing the disease. We therefore studied virulence diversity within a collection of Fol isolates. Twenty-eight resistant lentil accessions were inoculated with six Fol isolates from different geographical origins. The lentil accession × Fol isolate effect was highly significant, which allowed four accessions to be selected as a differential set. Inoculation of this set with 48 Fol isolates from Iran, Syria and Algeria, allowed the identification of seven different virulence patterns, designated pathotypes 1 to 7. In addition, the genetic structure of this Fol collection was analyzed using twelve SSR markers, eight of which were designed in this study.

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AMOVA showed that there was large molecular variation within groups but also between groups, showing that the Iranian populations were different from non-Iranian populations. STRUCTURE and Fitch-Margoliash tree analyses concluded the presence of two ancestral Fol lineages, one distributed in all regions while the other was only present in Iran. Our results suggest that Iran could be the origin of the diversity demonstrated in this study.

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Comparison of microbial quality of lettuce grown under three crop systems in Cyprus. C. MENEL-AOS CHRISTODOULO, E. SAVVA, D. TSALTAS. Department of Agricultural Sciences, Biotechnology and Food Science, Cyprus University of Technology.E-mail: dimitris.tsaltas@cut.ac.cy

Leafy greens, which are usually consumed raw, are increasingly recognized as important vehicles for transmission of foodborne pathogens. Contamination with pathogenic bacteria can occur at different stages of the production and distribution chain, making food safety of vegetables an important priority. Lettuce is the most commonly consumed vegetable worldwide, growing in close proximity to soil, while rain and irrigation water facilitate microbial movement and contamination. It is of scientific and public interest to explore how different production systems affect the presence of foodborne pathogens, since there is skepticism about safety of organic produce, hydroponics is increasing, aquaponics is a new appealing production trend. Lettuce and irrigation water samples of four years (2013-2016) were used for analysis. Three hundred and sixty lettuce samples (110 conventional (C), 105 organic (O), 90 hydroponic (H) and 55 aquaponics (A)), were collected and analyzed. For water analysis, 64 irrigation water samples (39 C/O, 15 H and 10 A) were analyzed. Total aerobic microbe counts, and Enterobacteriaceae for aquaponics, was 2 log less than in other samples. Escherichia coli were 0.61 log_{10} cfu g^{-1} for C, O, 1.24 log_{10} cfug for H, while E. coli in aquaponics was below the detection limit. All Salmonella counts were also below detection limits. Enterococcus counts were 3.5-4.5 log_{10} less in aquaponics, while E. coli in irrigation water for aquaponics was under the detection limit. This study indicates that the microbiological quality of organic and aquaponics vegetable growing systems are equal to, or in better than, other systems. Some concerns, however, may rise for hydroponic systems, probably due to specific practices.

Genetic diversity of Botrytis cinerea between tomato greenhouses in Northern Algeria. A. ADJEBLI*, C. LEYRONAS2, K. AISSAT1, P.C. NICOT2.

To estimate the genetic diversity for a better understanding of the spread of Botrytis cinerea, we genotyped with nine microsatellite markers 174 isolates collected from four greenhouses during three growing seasons in the region of Bejaia. Four of these isolates were identified as Botrytis pseudocinerea according to the allele size at locus Bc6. For all other isolates further studied, all loci were polymorphic, with the mean number of alleles per locus ranging from 2.77 to 5.22. Considerable genetic variability was detected in all subpopulations (D* > 0.87; Hnb > 0.40). Based on standardized index of association analysis, significant but low levels of clonality occurred, not excluding the possibility of recombination (Rd = 0.07, P < 0.001). A total of 109 haplotypes were characterized among the isolates, few of which were shared between subpopulations. This, together with moderate genetic differentiation among subpopulations according to the geographical origin (0.080 < F_{ST} < 0.167), suggested a low level of inoculum exchange among greenhouses, and little carry-over of inoculum from one sampling season to the next. The importance of genetic structure of B. cinerea populations should be taken into consideration for management of grey mould in tomato greenhouses.

Postharvest fungal diseases of loquat cv. ‘Algerie’ in Spain. L. PALOU, P. SANCHEZ-TORRES, C. MONTESINOS-HERRERO, V. TABERNER. Laboratori de Patologia, Centre de Tecnologia Postcollita (CTP), Institut Valencià d’Investigacions Agràries (IVIA), Aparat Oficial, 46113 Montcada, València, Spain. E-mail: palou_llu@gva.es