415 BIOLOGICAL AND GENETIC CHARACTERISTICS OF COLLECTIONS OF SEVERAL POLYPORE MUSHROOMS (BASIDIOMYCOTA)

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Polypore mushrooms (Basidiomycota, Polyporales) are wood inhabiting fungi with significant biotechnological potential. Many polypores, such as species of genera Ganoderma, Fomes and Fomitopsis produce different bioactive substances (polysaccharides, terpenoids, phenolics, etc) with immune-modulating, antimicrobial and other activities. Polypores are also known as producers of lignin and cellulose degrading enzymes (laccases, peroxidases), and proteolytic enzymes, applicable in biotechnological processes. Establishment of culture collections of polypores with different geographical origin are of great importance to study their biological (morphological, ecological, physiological, biochemical) and genetic characteristics, as well as to estimate their biotechnological potential. In our study variability in morphological, physiological and ecological characteristics of mycelial collections of several polypores with different origin, particularly species of Ganoderma (G. lucidum, G. applanatum, G. adspersum, G. resinaceum), Fomitopsis (F. annosa, F. pinicola) and Fomes (F. fomentarius) at different temperatures and pH was revealed. Colony morphology and growth parameters on different agar media were described. Mycelial microstructures, such as hyphal clamps, loops, cystidia, anamorphic sporulation (oidia), chlamydospores (oval, round) and others were observed in polypores' cultures. Formation of pellets and their morphology (filamentous, smooth) during submerged cultivation of studied collections were described. Taxonomic significance of observed cultural characteristics was evaluated. The highest proteolytic (milk-coagulating) activity was detected in cultural liquid of F. fomentarius and G. resinaceum, whereas activity of others was weaker. High antifungal/antagonistic activity against different test-fungi (plant pathogenic and their antagonists, potentially pathogenic for humans/animals) was observed in G. resinaceum. The genetic analysis of Ganoderma collections from Armenia, France, Iran, Italy and China show that the sequences of G. lucidum collections from European, Trans-Caucasian and Iranian regions are closely related and phylogenetically separated from the East-Asiatic sequences. DNA-markers based genetic analysis of Russian collections revealed higher polymorphism in G. applanatum, rather than F. fomentarius and F. pinicola isolates. The reported study was partially supported by SCS RA, joint armenian-russian research project № 13AR-110.

416 CHARACTERIZATION OF A NEW PARTITIVIRUS ISOLATE IN VERTICILLIUM DAHLIAE PROVIDES FURTHER EVIDENCE OF THE SPREAD OF THE HIGHLY VIRULENT DEFOLIATING (D) PATHOTYPE THROUGH NEW INTRODUCTIONS

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Verticillium dahliae is a cosmopolitan soil fungus which causes important vascular diseases in a variety of crops, including olive trees, cotton and horticultural crops. The widespread of a highly virulent defoliating (D) pathotype has greatly increased the threat posed by V. dahliae in certain crops like olive trees. In olive orchards in Spain and Turkey, it has been proposed that the spread of the D pathotype can be connected to the previous existence in the same areas of infected cotton crops in which the D pathotype was frequently found. Since V. dahliae has been, until now, described as an asexually-reproducing fungus, vegetative compatibility is a prerequisite for genetic exchange. Compatible isolates are placed within the same vegetative compatibility group (VCG). Isolates from the D pathotype are all placed in the VCG1A. Extracromosomal double-stranded RNA (dsRNA) molecules (mycoviruses) have been detected in all major taxonomic groups of filamentous fungi. In this study, we have identified two dsRNAs in a Turkish D isolate of V. dahliae infecting olive. Sequencing and phylogenetic analysis of these dsRNAs confirmed that they corresponded to a micovirus and clustered it with members of the family Partitiviridae, being most closely related to a partitivirus identified in a V. dahliae cotton isolate from China (VdPV1). Sequence identities between these two viral isolates are 94% and 91% at the nucleotide level for RNA1 and RNA2, respectively, and 96% and 93% at the deduced amino acid sequence levels for RNA1 and RNA2, respectively. This high similarity indicates that the new virus identified in the Turkey isolate could correspond to a strain of the established species VdPV1. For this reason, we have designated it VdPV1-ol (from olive). Our results support the hypothesis that the spread of the D pathotype in different regions could be associated to new introductions from distant geographical areas, and that once introduced in a crop, it can affects other crops in the same region. Although no information is available about the VCG (or pathotype) of the cotton isolate in which VdVP1 was identified, our results indicate that it is probably a D isolate (VCG1A). We propose that the characterization of micoviruses can serve as fingerprints to study the geographical flow of V. dahliae isolates.