

## ***Phytophthora porri* Foister VKLJUČUJE DVE RAZLIČNI GOSTITELJSKO SPECIFIČNI VRSTI**

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### **IZVLEČEK**

Glivo *Phytophthora porri* smo izolirali iz obolelih rastlin iz rodu *Allium* in iz rodu *Brassica*. *Phytophthora porri*, izolirana iz rastlin iz rodu *Allium*, ne more okužiti rastlin iz rodu *Brassica* in obratno. Morfološke razlike med izolati iz rastlin iz rodu *Allium* in iz rastlin iz rodu *Brassica* so komaj opazne in se prekrivajo. Razlike med posameznimi izolati v njihovi sposobnosti za okužbo pa močno nakazujejo, da *P. porri sensu lato* najverjetnejše vključuje dve različni gostiteljsko specifični vrsti. Da bi preverili, če *Phytophthora porri* predstavlja eno samo homogeno vrsto, smo uporabili izoencimske analize in sekvenciranje neprevedljivih sekvenc ribosomske DNA (ITS, sestavljen iz ITS1, 5.8S in ITS2). Pri 16 sojih, izoliranih iz rodu *Allium*, in desetih sojih, izoliranih iz rodu *Brassica*, smo analizirali izoencime malat dehidrogenaze (MDH), izocitrat dehidrogenaze (IDH) in laktat dehidrogenaze (LDH), ki skupno zajemajo 4 domnevne lokuse. Pri sojih, izoliranih iz rastlin iz rodu *Allium*, smo odkrili samo 5 izoencimskih alelov, medtem ko so imeli soji, izolirani iz rastlin iz rodu *Brassica*, 6 drugačnih alelov. Očitno reproducija med obema populacijama ni mogoča zaradi genskih zaprek, ki onemogočajo prosti pretok genov. Sekvenčna analiza ITS regije je dodatno pokazala izrazite in dosledne razlike med izolati iz rastlin iz rodu *Allium* in izolati iz rastlin iz rodu *Brassica*. Podobno je restrikcijska analiza mitohondrijske DNA pokazala dosledne razlike med mitohondrijsko DNA izolatov iz rastlin iz rodu *Allium* in mitohondrijsko DNA izolatov iz rastlin iz rodu *Brassica*. Na osnovi rezultatov izoencimskih analiz, sekvenciranja ITS regij in restrikcijske analize mitohondrijske DNA ter na osnovi morfologije in patogenosti zaključujemo, da *Phytophthora porri* Foister ni homogena vrsta, ampak dejansko vključuje dve vrsti in sicer *Phytophthora porri sensu stricto* in *Phytophthora brassicae* sp. nov.

### **ABSTRACT**

## ***Phytophthora porri* Foister HARBOURS TWO DISTINCT HOST SPECIFIC SPECIES**

*Phytophthora porri* has been isolated from diseased *Allium* and *Brassica* plants. *Phytophthora porri* isolated from *Allium* is not capable to infect *Brassica* plants and

vice versa. Morphological differences between isolates obtained from *Allium* and isolates obtained from *Brassica* are subtle and show overlap. The differential infection capability, however, strongly suggests that *P. porri sensu lato* possibly contains two different host specific species. Isozyme analysis and sequence analysis of the internal transcribed spacer regions (ITS, consisting of ITS1, 5.8S and ITS2) of the ribosomal DNA gene repeat were used to examine whether *Phytophthora porri* represents a single homogeneous species. Sixteen strains isolated from *Allium*, and ten strains isolated from *Brassica*, were analyzed with malate dehydrogenase (MDH), isocitrate dehydrogenase (IDH) and lactate dehydrogenase (LDH), comprising altogether four putative loci. Five isozyme alleles were only detected in strains isolated from *Allium*, whereas in strains obtained from *Brassica* six other alleles were observed. Apparently the two populations are reproductively isolated from each other by genetic barriers to gene flow. In addition sequence analysis of the ITS regions showed marked and consistent differences between isolates from *Allium* and isolates from *Brassica*. Similarly, restriction enzyme analysis of mitochondrial DNA revealed that mtDNA patterns of strains obtained from *Allium* differed consistently from those isolated from *Brassica*. Based on isozyme data, ITS sequence analysis, restriction enzyme analysis of mitochondrial DNA, morphology and pathogenicity, it was concluded that *Phytophthora porri* Foister is not a homogeneous species, but actually contains two species, *Phytophthora porri sensu stricto* and *Phytophthora brassicae* sp.nov.

Do konca redakcije nismo prejeli integralnega besedila.