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Multilocus molecular characterization of a *Penicillium* strain isolated from maize in Nigeria

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Aims

Access the phylogeny of *Penicillium* strain (MUM 14.07) within the *P. sclerotiorum* complex and the relationship with *P. mallochii*.

Methods and results

The *Penicillium* strain (MUM 14.07) was subjected to multilocus molecular phylogenetic analysis using partial β-tubulin (*BenA*), calmodulin (*CaM*), cytochrome c oxidase subunit 1 (*cox1*), internal transcriber spacer (ITS) region and translation elongation factor 1-α (*tef1-α*).

The multilocus phylogenetic analysis revealed that the *Penicillium* strain (MUM 14.07) clustered closely with *P. mallochii* (1), revealing an unconditional position within the section Sclerotia. The sole exception was for the *BenA* gene where the studied strain did not show good homology with any particular *Penicillium* species. The Basic Local Alignment Search Tool (BLAST) of the sequence obtained of *BenA* gave a higher similarity with species from the section Citrina.

Conclusions

With this result we cannot state that our strain is a *P. malochii* but we can consider that they are two related species that were separated geographically. It would be interesting to be able to isolate more strains.

Significance of study

This case study shows that many species have a common ancestor and that *Penicillium sp*. MUM 14.07 and *P. mallochii* might belong to the same monophyletic group.

References

(1) Rivera KG, Díaz J, Chavarría-Díaz F, Garcia M , Urb M, Thorn RG, Louis-Seize G, Janzen DH, Seifert KA (2011). *Penicillium mallochii* and *P. guanacastense*, two new species isolated from Costa Rican caterpillars. Mycotaxon **119**:315-328.