



PHYLOGENETIC STUDY OF *STREPTOMYCES* SP. ISOLATED FROM POTATOES WITH COMMON SCAB DISEASE IN SINALOA, MEXICO

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Introduction. Common scab is an important worldwide disease of potatoes caused mainly by *Streptomyces* species. For many years the causal agent of the disease was *Streptomyces scabies*, however, new species of *Streptomyces* have been worldwide reported as scab pathogens. Common scab is characterized by a superficial or a deep corky lesion on the tubers and some reports suggest that the disease maybe associated with the pathogen.

Methods. In the present study, nineteen putative strains of *Streptomyces* were isolated from potatoes with visible common scab lesion. The samples were collected from five different States of Mexico but the majority of them came from the state of Sinaloa. The isolates were characterized by combining both phenotypic and genotypic methods based on molecular biology techniques. For the first one, evaluation of the LL-diaminopimelic acid in the cell wall, growth onto six ISP media and Scanning Electron Microscopy were evaluated. For the second one, BOX-PCR, amplification and sequencing of 16S rRNA and its corresponding phylogenetic study was employed.

Results. The isolates showed a wide range of spore mass color on the ISP media, all the isolates contained the characteristic LL-diaminopimelic acid. Typical straight or spiral spore chains of smooth or irregular ornamentations were also noticed. The corresponding phylogenetic study showed that the isolates belong to the genus *Streptomyces*, five of them are associated to the *S. acidiscabies* subclade and may well represent new species as this was also confirmed with fingerprinting patterns for the isolates and the reported pathogen.

Conclusions. All the isolates belong to the genus *Streptomyces*, three are associated to known species, six of them are close to species that produce antibiotics, five are *Streptomyces* sp. and

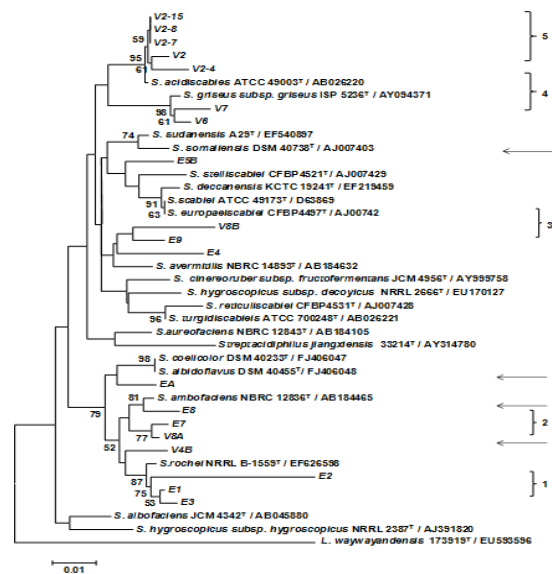


Fig. 1. Phylogenetic tree based on 16S rRNA gene sequences of *Streptomyces* and the isolates studied.

the other five are highly related to pathogenic *Streptomyces*, notably to *S. acidiscabies*. Studies on the microbial activity of the isolates against other pathogens are currently underway.

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