

An overview of the whole genome single nucleotide polymorphism based phylogenetic relationships and population structure of global isolates of *Colletotrichum coccodes*

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Black dot, caused by *Colletotrichum coccodes*, is an economically important disease of potato and has been reported from most potato-growing regions worldwide. Understanding the phylogenetic relationship and genetic structure among *C. coccodes* isolates collected from five continents provides insight into genetic variations of the population that could lead to the identification of resistant potato cultivars functional across most pathogen genotypes. We studied phylogenetic relationships and population structure of 42 global *C. coccodes* isolates using whole-genome sequence (WGS) based single nucleotide polymorphisms (SNPs). The WGS-SNP based phylogenetic tree placed isolates into two major clades, from which they were further divided into four fundamental subclades. Analysis of molecular variance (AMOVA) resulted in 52 and 48% within and among population variations, respectively. Discriminant analysis of principal components (DAPC) grouped isolates in four clusters which supported the clustering of the phylogenetic tree. The majority of Australian and European populations (83%) were in cluster one and the rest were placed in clusters two and three, 85% of isolates from Chile were in cluster two and 15% were in cluster one, and South African isolates were in cluster three and four. The USA isolates were scattered into cluster one, two and four. Results of these analyses indicated that South Africa was the most differentiated population while the USA population was not significantly distant from other populations except those from Chile. Low variation among most of the tested populations could be due to the increasing dissemination of the isolates throughout the world from the place of their origin.