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Analysis of the genome sequence of *Phomopsis longicolla* type strain TWH P74 causing Phomopsis seed decay in soybean

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Phomopsis seed decay is one of the most devastating diseases reducing soybean seed quality worldwide. This disease is primarily caused by the seed-borne fungal pathogen *Phomopsis longicolla* (syn. *Diaporthe longicolla*). To facilitate investigating the genetic basis of fungal pathogenicity and to understand the mechanism of the disease development, the genome of P. longicolla type strain TWH P74 was sequenced, de novo assembled, and analyzed. The resulting draft genome was estimated to be approximately 64 Mb in size with an overall G+C content of 48.1%. There were 16,606 annotated genes identified from the genome. A total of 12,624 SSRs with di-, tri-, and tetranucleotide repeats of five or more were identified in the TWH P74 whole genome sequence (WGS) which included 1,972 SSRs consisting of repeat units of di- (≥9) (919), tri- (≥8) (369), and tetranucleotide (≥7) (684). Among the 1,972 SSRs, (AT)n, (ATT)n and (AAAT)n were the most abundant motifs among di-, tri-, and tetranucleotide SSRs, respectively. The SSR markers developed from WGS will be used to determine the phylogenetic relationships and genetic diversity among *P. longicolla* isolates collected from different geological origins. The genome of *P. longicolla* type strain TWH P74 represents one of the important fungal pathogens in the Diaporthe-Phomopsis complex. The *P. longicolla* genome sequence contains valuable molecular resources for developing genetic markers of the pathogen, enhancing our understanding of the mechanism of fungal infection, and facilitating development of new control strategies for this pathogen.