

Table S1: antiSMASH results for publicly available full genome assemblies of *Phoma* sp. in NCBI (Feb 2019).

Species	Accession number	
<i>Phoma herbarum</i>	GCA_001599375.1	
https://fungismash.secondarymetabolites.org/upload/fungi-bfd8ee4b-2d68-4d85-ae11-d4fcc2bf1c1/index.html		
<i>Phoma koolunga</i>	GCA_004151575.1	
https://fungismash.secondarymetabolites.org/upload/fungi-fb1774d6-1352-4ae6-b2c1-69e101f6c2a5/index.html		
<i>Phoma koolunga</i>	GCA_004151145.1	
https://fungismash.secondarymetabolites.org/upload/fungi-fb080fce-3824-4c69-82e1-40b66a3a89d1/index.html		
<i>Phoma koolunga</i>	GCA_004151165.1	
https://fungismash.secondarymetabolites.org/upload/fungi-ec1b5e37-13ca-42d5-8b4b-b195dedc1485/index.html		

Initially, there was only one publicly available full genome assembly of *Phoma* in NCBI. The assembly belongs to *Phoma herbarum* (GenBank assembly accession: GCA_001599375.1, Genome coverage:462x; Genome size: 39.26 MB; Scaffolds: 218 and Contigs:498). We have run antiSMASH webserver for fungal sequence to detect any potential biosynthetic cluster but the results do not show the presence of any complete cluster which could be predicted to synthesize Phomafungin.

The antiSMASH run results could be found at the given link:

<https://fungismash.secondarymetabolites.org/upload/fungi-bfd8ee4b-2d68-4d85-ae11-d4fcc2bf1c1/index.html>

Recently in 2019, three more assemblies of *Phoma koolunga* were submitted to NCBI. We have performed the antiSMASH analysis of all these assemblies. The links to the antiSMASH run are given below. Similar to *Phoma herbarum* genome, we do not see the presence of any complete cluster in these genomes as well.

1. *Phoma koolunga* (Genbank accession number: GCA_004151575.1, Genome coverage: 70.0x; Genome size: 50.29 MB, contigs:27,692)
<https://fungismash.secondarymetabolites.org/upload/fungi-fb1774d6-1352-4ae6-b2c1-69e101f6c2a5/index.html>
2. *Phoma koolunga* (Genbank accession number: GCA_004151145.1, Genome coverage: 40.0x; Genome size: 43.76 MB, contigs:23,210)
<https://fungismash.secondarymetabolites.org/upload/fungi-fb080fce-3824-4c69-82e1-40b66a3a89d1/index.html>
3. *Phoma koolunga* (Genbank accession number: GCA_004151165.1, Genome coverage: 140.0x; Genome size: 50.46 MB, contigs:21,3995)
<https://fungismash.secondarymetabolites.org/upload/fungi-ec1b5e37-13ca-42d5-8b4b-b195dedc1485/index.html>