

ORAL PRESENTATIONS

WHOLE-GENOME SEQUENCING IDENTIFIES A NEW *Aspergillus tubingensis* STRAIN FROM *Eremostachys isochila* WITH INTRASPECIFIC VARIATION IN PHARMACEUTICALLY RELEVANT BIOSYNTHETIC GENE CLUSTERS

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Endophytic fungi are a well-documented source of pharmaceutically active secondary metabolites, yet few isolates have had their biosynthetic potential characterized at the whole-genome level against a proper comparative background. We report the whole-genome sequencing and comparative analysis of isolate S23, a filamentous fungal endophyte recovered from healthy tissue of *Eremostachys isochila* (Lamiaceae) in Uzbekistan. Six convergent lines of evidence; ITS barcoding, three protein-coding loci, multi-locus phylogeny, genome-scale ortholog-based phylogenomics, CAZyme content, and biosynthetic gene cluster (BGC) content, identify S23 isolate as *Aspergillus tubingensis*, genetically typical of the species. Genome-wide anti SMASH mining detected 95 BGCs, and dedicated comparative analysis against a 13-genome reference panel of close relatives revealed striking intraspecific variation at two BGCs. The yanuthone D antifungal meroterpenoid pathway is complete and functionally intact in S23, while disrupted by an independent repeat-element insertion in its closest relatives, including five other *Aspergillus tubingensis* strains. The burnettiene A cytotoxic polyketide pathway shows a genuine intraspecific split, present in S23 and only two of five reference conspecific strains. This supported by maximum-likelihood phylogenetic testing as vertical inheritance with differential loss rather than horizontal transfer. Three additional pharmaceutical important BGCs (kojic acid, nidulanin A, TAN-1612) were investigated in comparable depth, revealing patterns ranging from lineage-specific gene loss to broad ancestral conservation. These findings demonstrate that even within a single, well-characterized fungal species, biosynthetic gene cluster content can vary meaningfully at the strain level, underscoring the value of comparative, reference-panel-based genome mining for prioritizing pharmaceutically promising isolates.