

Supplementary Material

Morphological characteristics and phylogenetic analysis of strain HG18

Morphological observations indicated that when cultured on PDA plates at 28 °C for 5–7 days, strain HG18 produced colonies with cottony aerial mycelia that transitioned from white to pale yellow and finally to earth yellow. Lactophenol cotton blue staining of spore suspensions revealed fusiform, sickle-shaped macroconidia with distinctly swollen central cells, narrow and tapered apical cells, and 2–6 septa, consistent with the morphological characteristics of *Fusarium*.

ITS sequence alignment showed that HG18 shared >99% homology with *Fusarium longifundum*, *F. equiseti*, and *F. hainanense*. Phylogenetic analysis placed HG18 within the same clade as these species, confirming its assignment to the genus *Fusarium*. However, due to the high conservation of ITS sequences within *Fusarium*, accurate species-level discrimination was not possible. Because TEF-1 α exhibits higher sequence polymorphism in *Fusarium* and is the recommended molecular marker for species-level identification, it was used for further resolution. Based on the combined ITS and TEF-1 α analysis, strain HG18 was classified as *Fusarium equiseti* and designated *F. equiseti* HG18.

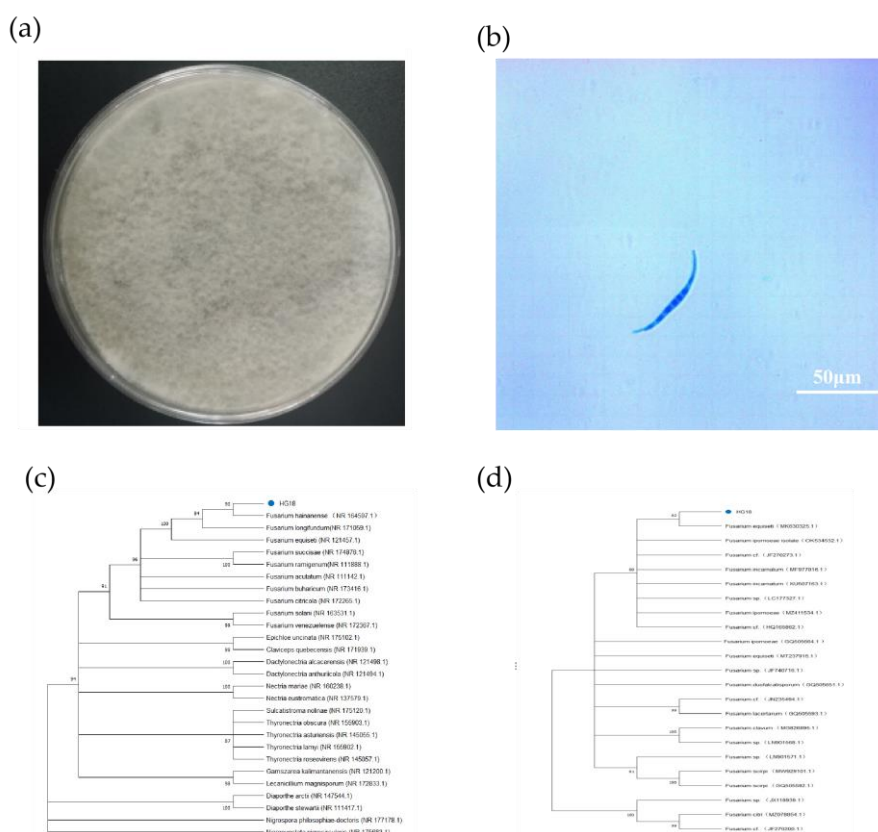


Figure S1. Morphological characteristics and phylogenetic analysis of strain HG18. **(a)** Colonial and spore morphology of strain HG18; **(b)** spore morphology of strain HG18; **(c)** phylogenetic tree based on ITS sequences; **(d)** phylogenetic tree based on TEF-1 α sequences.

Table S1. Primers used in this study.

Primer Name	Sequence (5'→3')
ITS-F	TCCGTAGGTGAACCTGCGG
ITS-R	TCCTCCGCTTATTGATATGC
TEF1 α F	ATGGGTAAGGARGACAAGAC
TEF1 α R	GGARGTACCAGTSATCATGTT

Structural characterization data of the purified product

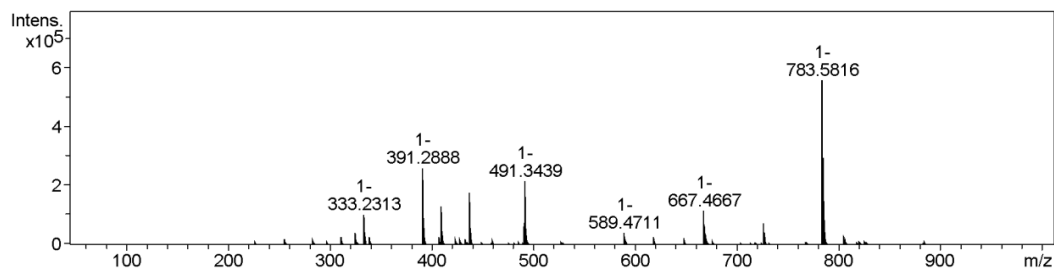


Figure S2. HRMS spectrum of purified UDCA, showing ions at m/z 391.2888 $[M-H]^-$ and 783.5816 $[2M-H]^-$.

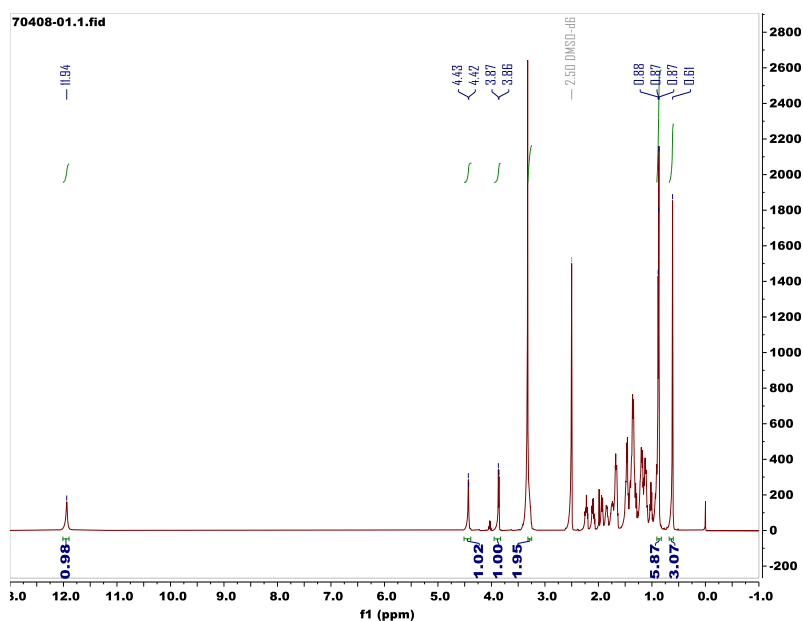


Figure S3. ^1H NMR spectrum of purified UDCA. ^1H NMR (600 MHz, $\text{DMSO}-d_6$) δ 11.94 (s, 1H), 4.43 (d, $J = 4.6$ Hz, 1H), 3.86 (d, $J = 6.9$ Hz, 1H), 3.33–3.24 (m, 2H), 0.91–0.77 (m, 6H), and 0.61 (s, 3H).

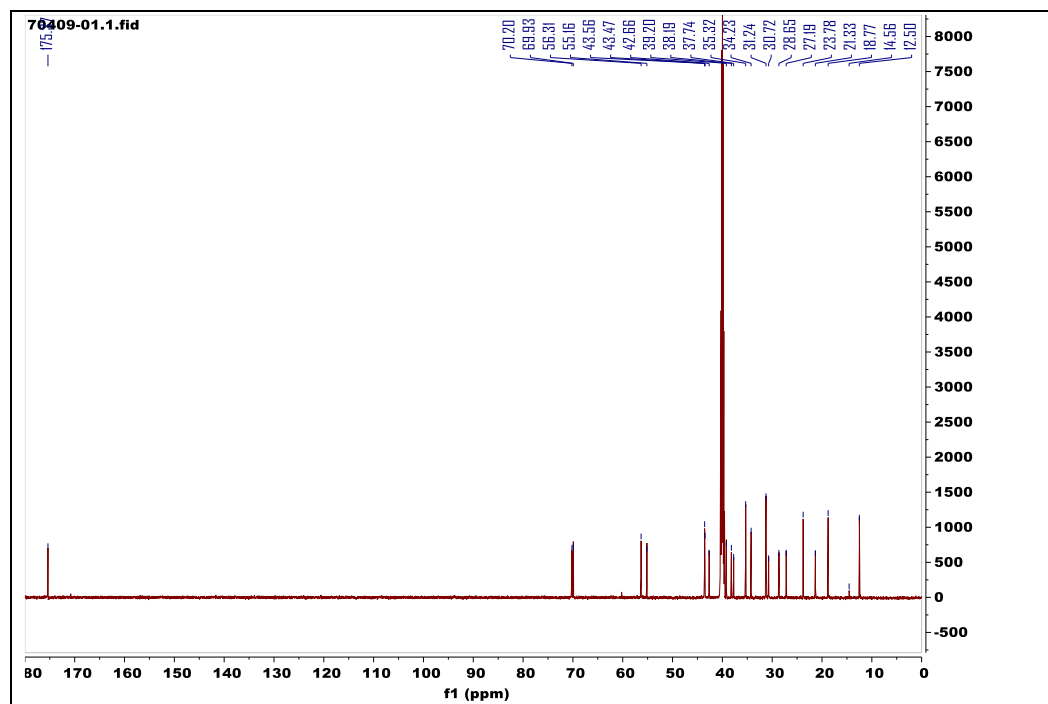


Figure S4. ^{13}C NMR spectrum of purified UDCA. ^{13}C NMR (151 MHz, $\text{DMSO}-d_6$) δ 175.37, 70.20, 69.93, 56.31, 55.16, 43.56, 43.47, 42.66, 39.20, 38.19, 37.74, 35.32, 34.23, 31.24, 30.72, 28.65, 27.19, 23.78, 21.33, 18.77, 14.56, and 12.50.

Statistical analysis of the Plackett–Burman screening design.

Table S2. ANOVA analysis of the Plackett–Burman screening model.

Factor	Sum of Squares	df	Mean Square	F-value	p-value	Sig.
Model	0.016	8	0.002	12.20	0.0320	Significance
pH	3.01E-03	1	2.00E-03	12.203	0.0234	*
KCl	9.08E-03	1	3.01E-03	18.356	0.0050	**
Temperature	8.33E-06	1	9.08E-03	55.373	0.8361	
Inoculum volume	6.75E-04	1	8.33E-06	0.051	0.1354	
Yeast extract	2.41E-03	1	6.75E-04	4.119	0.0313	*
Peptone	2.08E-04	1	2.41E-03	14.695	0.3416	
Dextrin	4.08E-04	1	2.08E-04	1.271	0.2126	
Fermentation time	2.08E-04	1	4.08E-04	2.492	0.3416	
Residual	4.92E-04	3	2.08E-04			
Total	0.016	11				

Note: $R^2=0.9702$; Adj $R^2=0.8907$; * $p < 0.05$; ** $p < 0.01$.