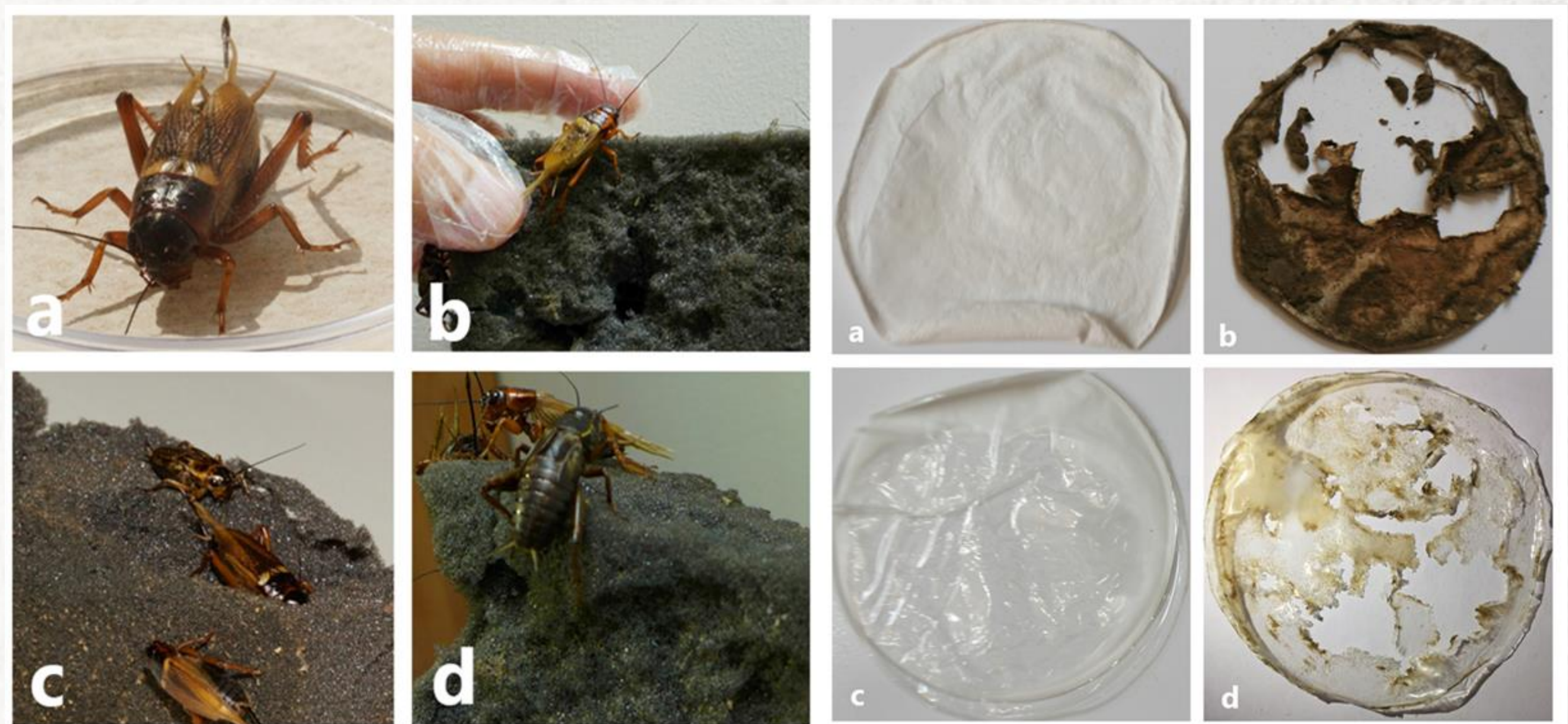


Genome and Transcriptome of *Aspergillus flavus* Reveal Its Polyurethane Biodegradation

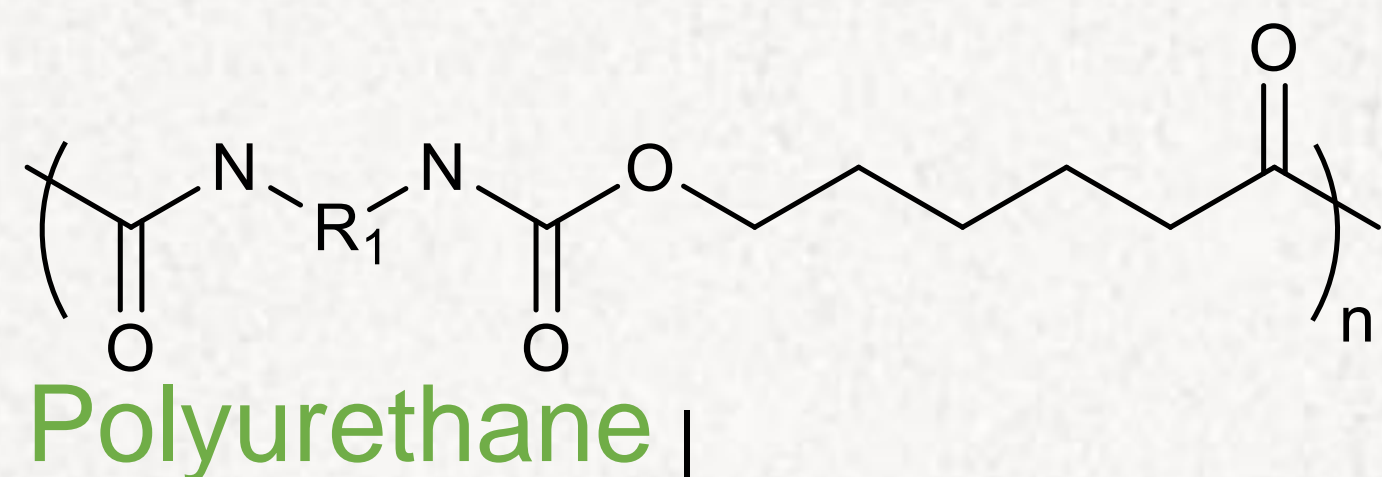
Shijie Zhang, Kunming Institute of Botany, Chinese Academy of Sciences

● Isolation and Biodegradation Test for *Aspergillus flavus* G10

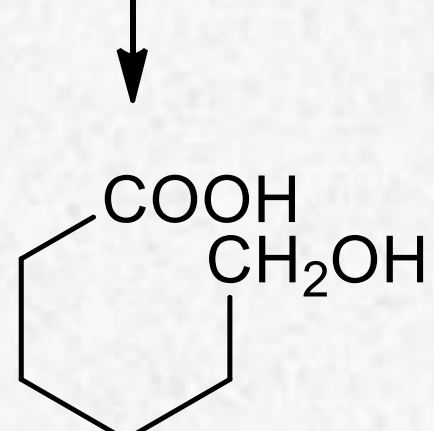
Aspergillus flavus G10, isolating from the guts of plastic-eating crickets, can effectively degrade polyester polyurethane.



● Transcriptomic Analysis

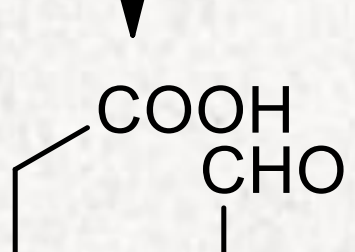


a Esterase



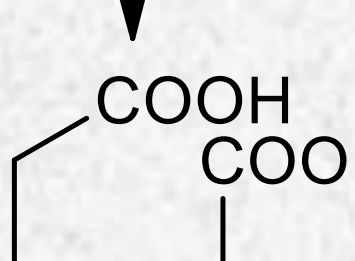
6-Hydroxyhexanoic acid

b ChnD



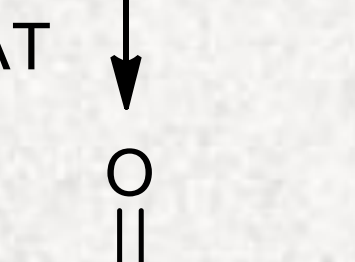
6-Oxohexanoic acid

c ChnE



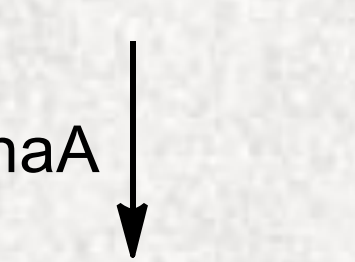
Adipic

d ACoAL

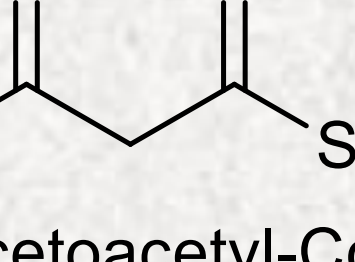


Acetyl-CoA

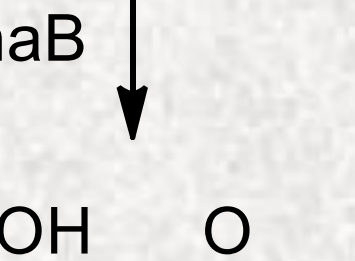
e ACoAT



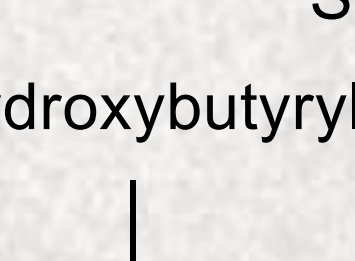
PhaA



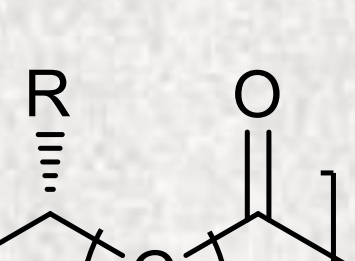
PhaB



PhaC

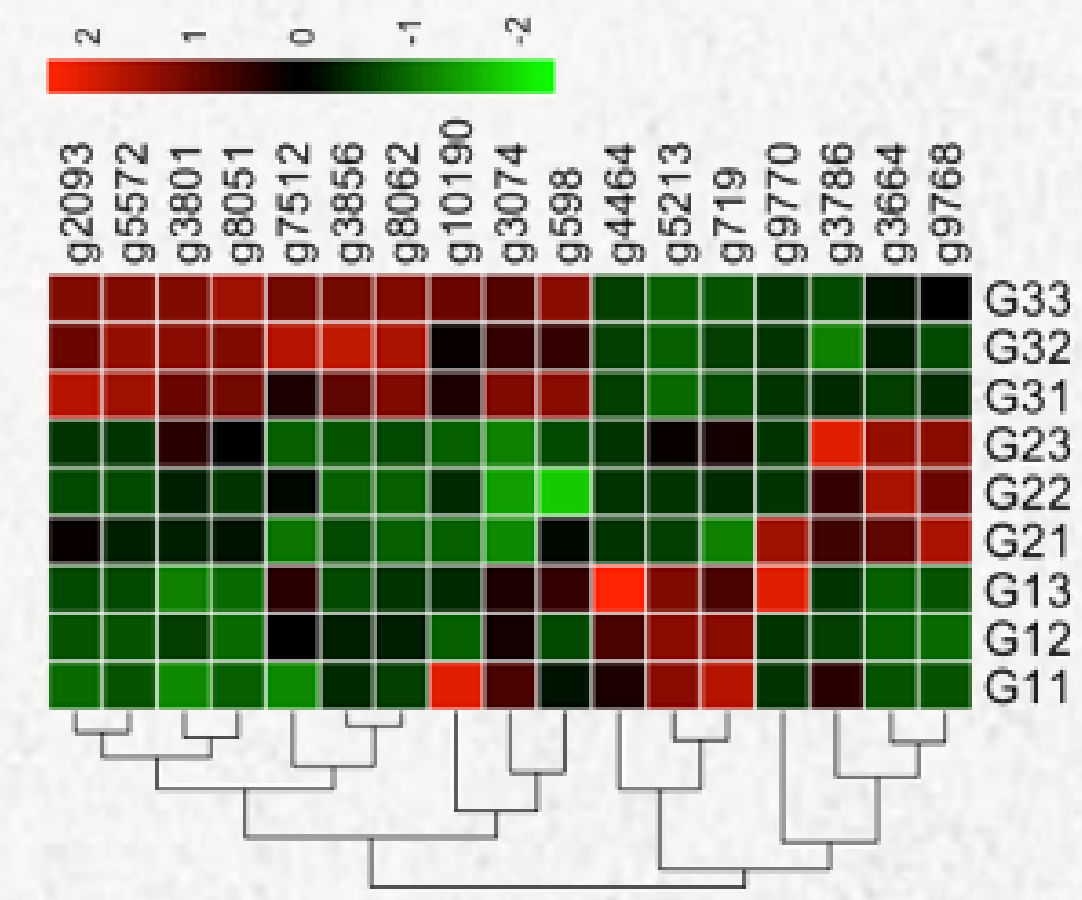


PHA

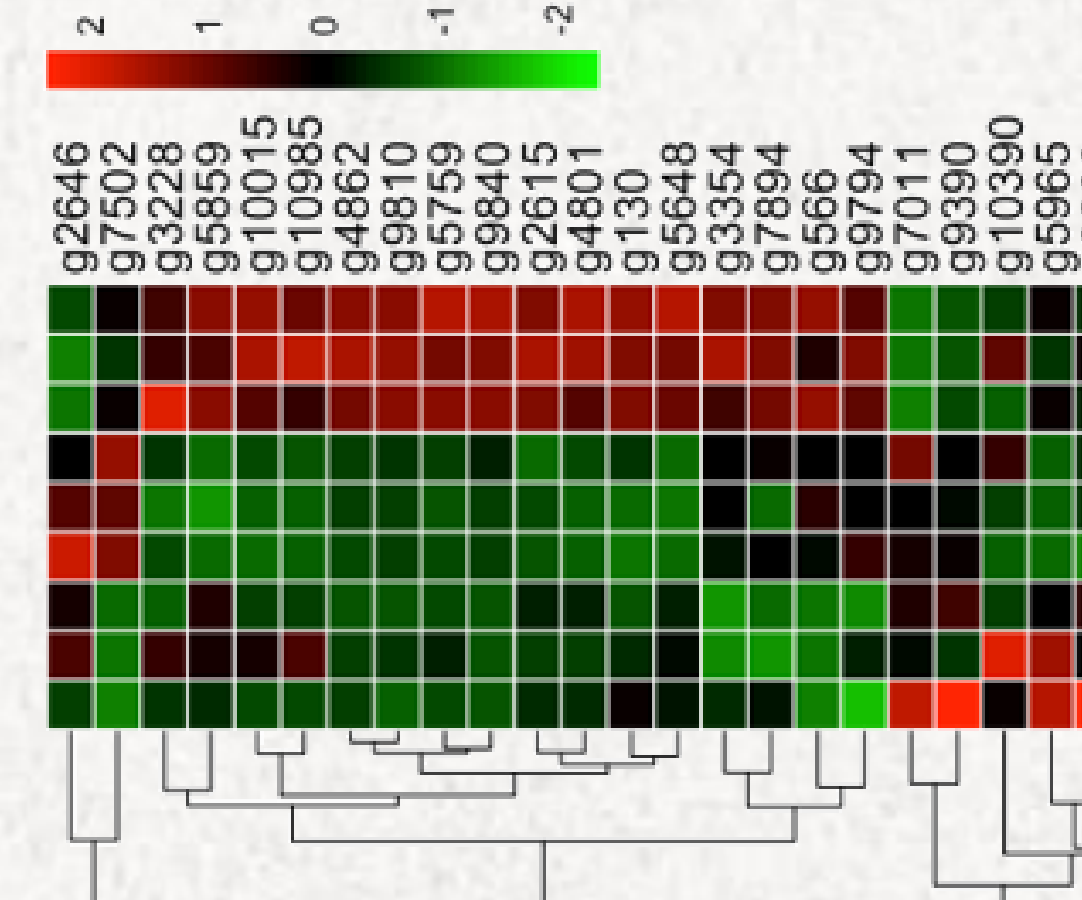


Succinic Acid

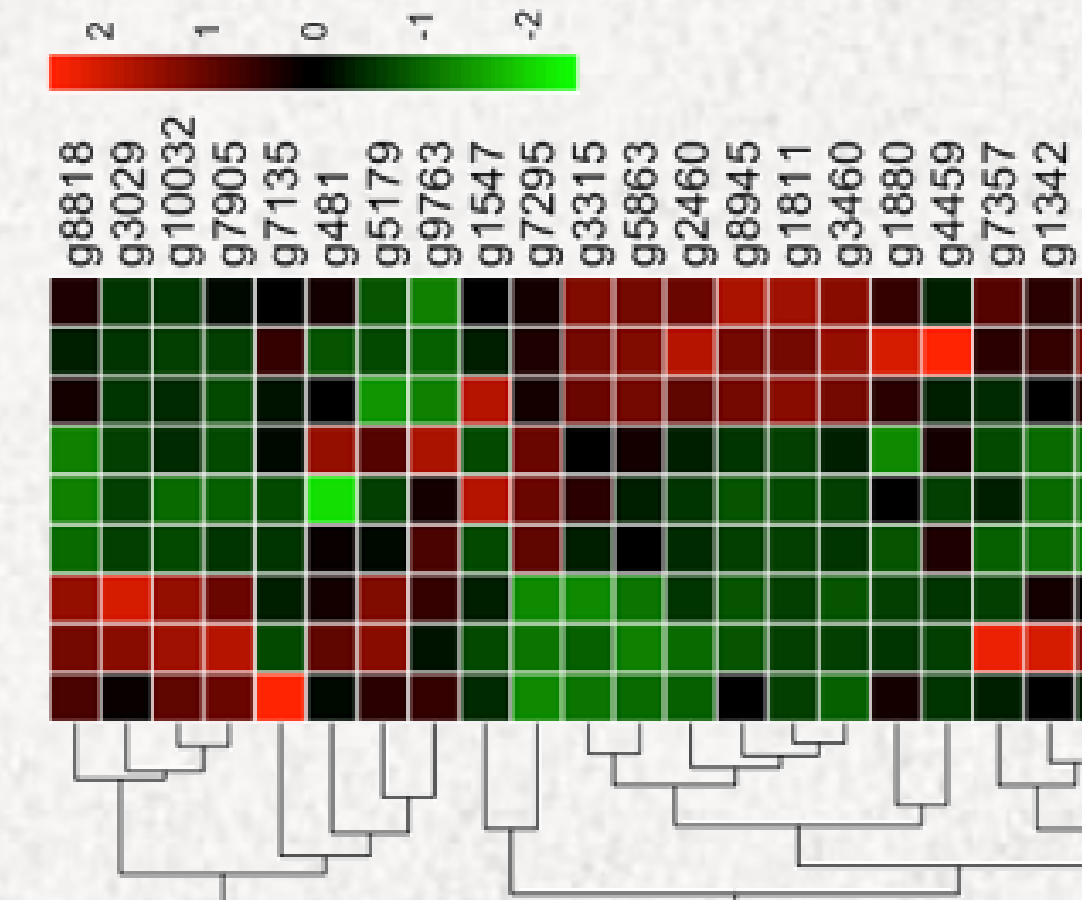
a Esterase



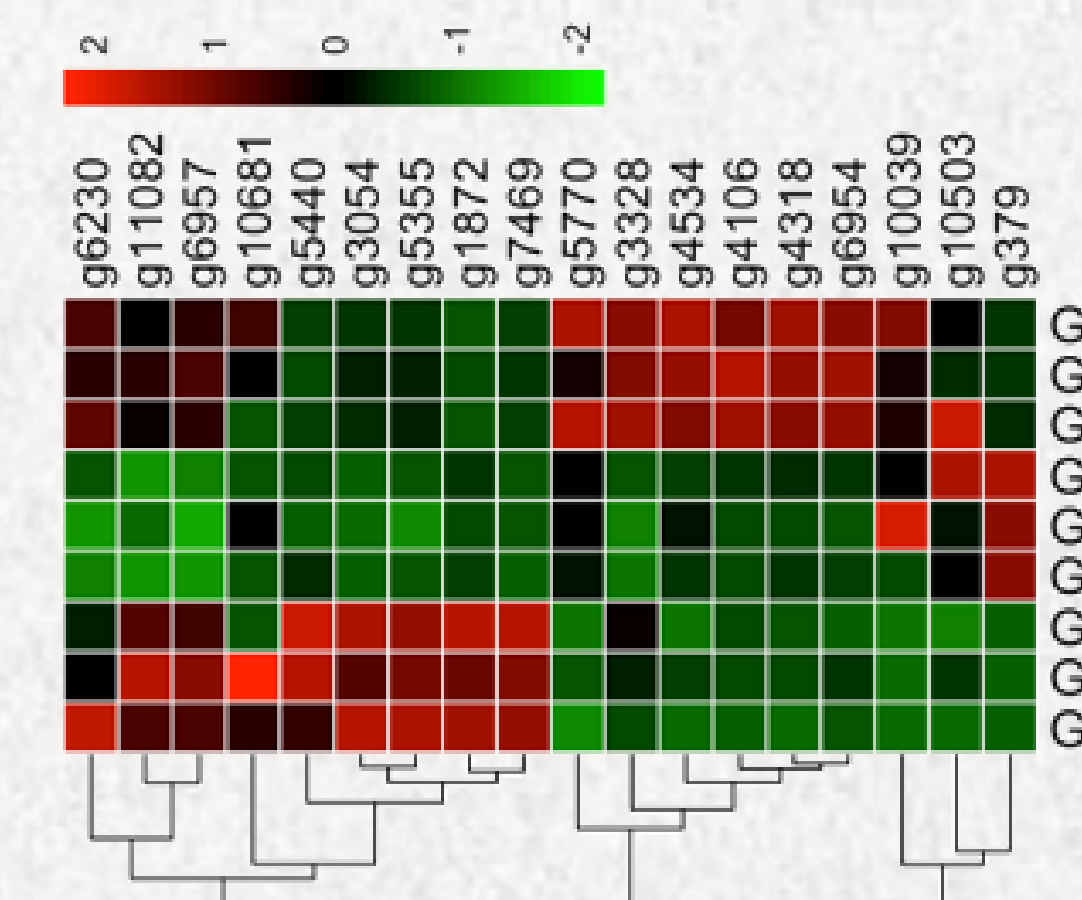
b ChnD



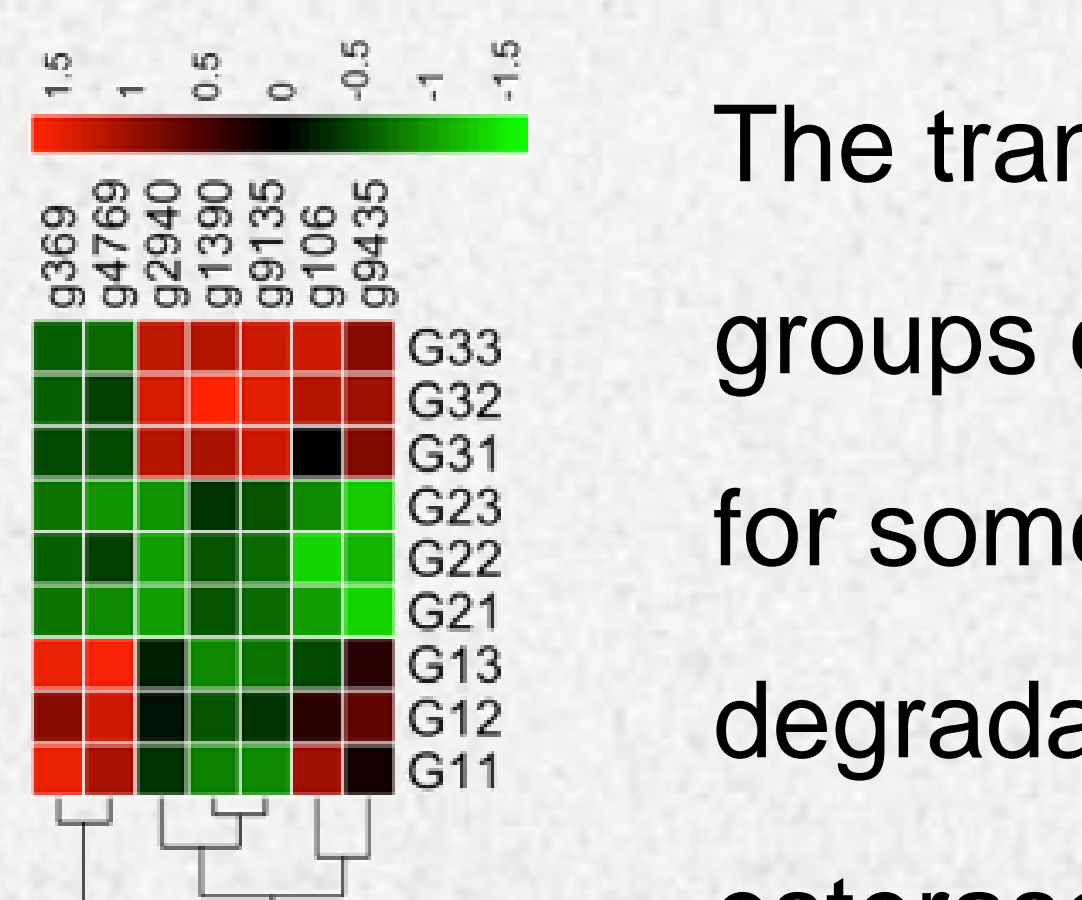
c ChnE



d ACoAL



e ACoAT



The transcriptional profiling of different groups of this strain showed that the genes for some crucial enzymes related to PU degradation were upregulated, including esterase and so on.

G11 (12, 13): Control group; G21 (22, 23): PU-nondegradable *A. flavus* G10; G31 (32, 33): PU-degradable *A. flavus* G10

● Genomic Analysis

The genome of this fungus is about 37 Mb in size and phylogenetic analysis confirmed that *A. flavus* G10 and *A. oryzae* are closely related species.

