Supplementary Material for

Valorizing plastic wastes by insect consumption

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Supplemental Results

Molecular identification and phylogenetic classification of *A. flavus* G10

The strain *A. Flavus* G10 was submitted to Herbarium of Kunming Institute of Botany (KIB), Chinese Academy of Sciences (CAS), Kunming, Yunnan, China and HKAS No. was 101889. A phylogenetic study (Fig. S1) based on a combined data sets of loci (LSU, RPB2, ITS, BTUB and CAM) was conducted to determine the relationship among *Aspergillus* section *Flavi* members. The final dataset included 3271 total characters, of which 2168 characters are constant, 777 characters are parsimony-informative (23.75%), while 326 variable characters are parsimony-uninformative in the maximum parsimony analysis (TL = 2435, CI = 0.644, RI = 0.793, RC = 0.511, HI = 0.356). In the phylogram, ML and MP values equal to or greater than 70 % and BYPP values greater than 0.95 are given above each node (Fig. S1). The ML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of -16016.105263. The matrix had 1036 distinct alignment patterns, with 20.83 % being undetermined characters or gaps. Parameters for the combined dataset was as follows: Estimated base frequencies; A = 0.232666, C = 0.252689, G = 0.268734, T = 0.245911; substitution rates AC = 1.198516, AG = 3.642609, AT = 1.139202, CG = 0.716346, CT = 6.351285, GT =

1.000; proportion of invariable sites I = 0.430234; gamma distribution shape parameter α = 0.954354.

Similarly, the number of one greenish-brown fungus colonies in the treated fecula (per one fecula unit, Fig. 3b, c) was higher by three fold than the untreated (Fig. 3a). This fungus was cultured on MEA culture plate (Fig. 3b) and was identified by microscopic (Fig. 3 c, d, e, f, g, and h), molecular and phylogenetic techniques to be *A. flavus* G10.