Supplementary Information (SI) for Sustainable Energy & Fuels.

One-Pot Consolidated Bioprocessing of Waste Potatoes to L-Malic Acid by a Thermotolerant and Metabolically Versatile *Aspergillus terreus* BD Isolate

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Supplementary data

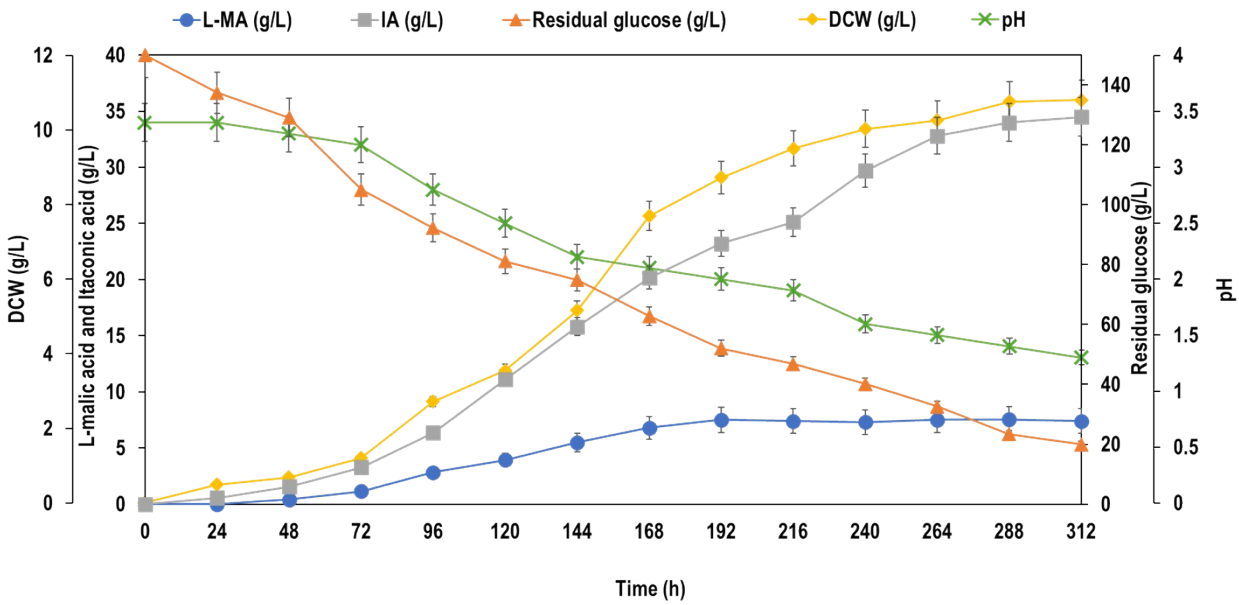


Figure S1: Time course fermentation profile of *A. terreus* BD cultivated in IA production medium showing produced L-MA (g/L), IA (g/L), residual glucose (g/L), DCW (g/L), and pH. Symbols: circle (L-MA), square (IA), triangle (residual glucose), rhombus (DCW), cross (pH).

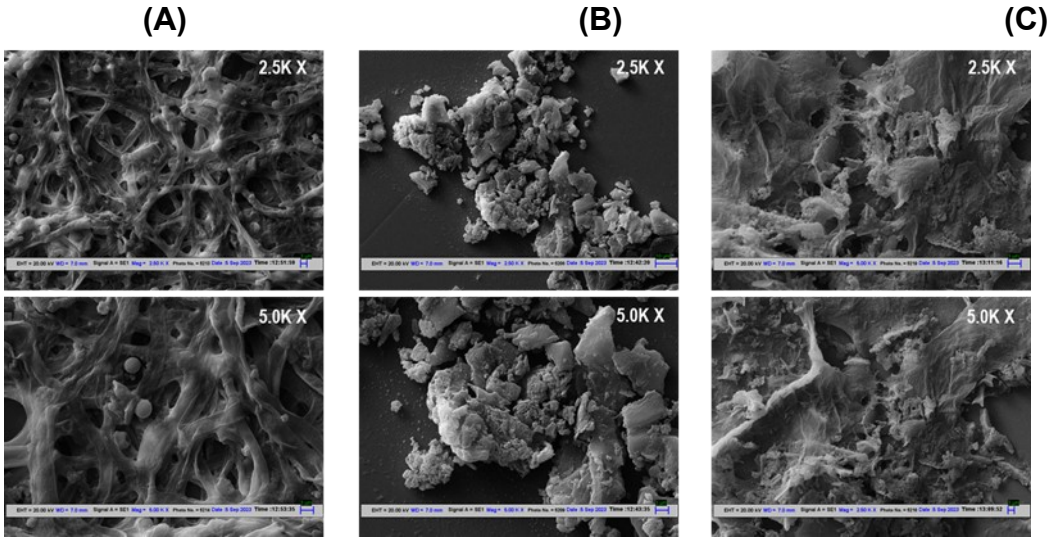
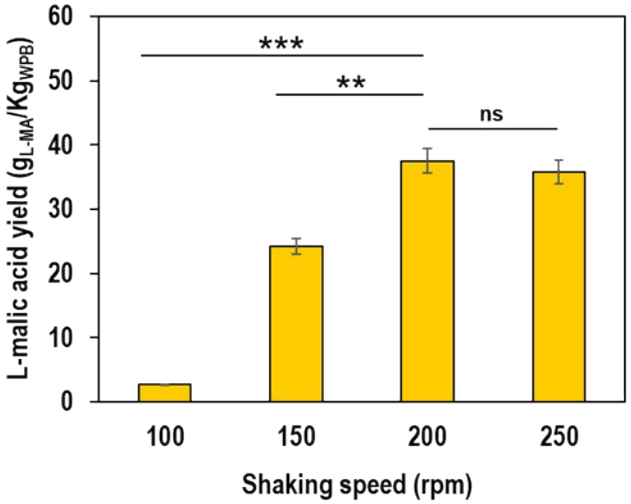


Figure S2. Scanning electron micrographs showing morphology of (A) *A. terreus* BD cultured in EHWP medium after 48 h; (B) starch granules in unfermented WPB slurry; and (C) *A. terreus* BD growth around the degraded starch granules in the SSF culture after 48 h

(A)



(B)

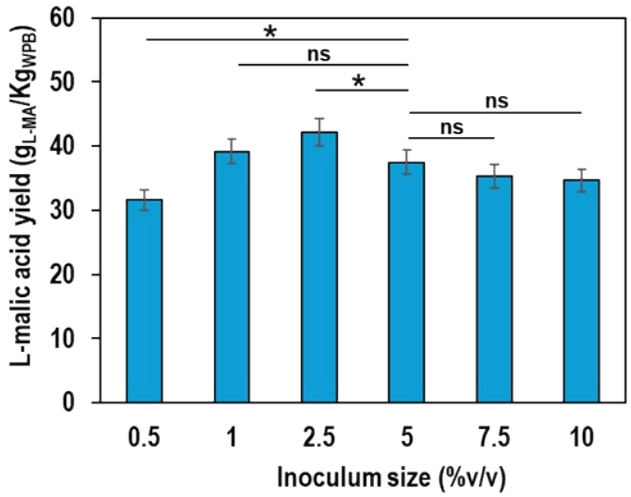


Figure S3: Effect of (A) shaking speed, and (B) inoculum size on L-MA yield

Table S1: Primers used for the qRT-PCR of key IA and L-MA pathway genes.

Gene	Primer sequence (5'-3')
Cis-aconitate decarboxylase (*cad*) ATEG_09971	FP-ATGACCAAGCAATCTGCGGAC RP-GCTTGCGTGCACGCGATT
Malate dehydrogenase (*mdh*) ATEG_05653	FP-CCTTTCTCTAGCTAATCATCGTTCCCACCA RP-AGCCTCATATTTGTCGGCAGGGATCTG
Fumarase (*fum*) ATEG_07205	FP-ATGTTGACCTCTGCCAACTCC RP-CTTGGTGCCCATGGTGCCAC
Malate synthase (*mls*) ATEG_07126	FP-ATGAGCCAAGTCGACGTGCAG RP-GGAGGTAGAAGTACGGGCCGA
Internal Transcriber Spacer (*its*) Reference gene	FP-TCCGTAGGTGAACCTGCGG RP-TCCTCCGCTTATTGATATGC

Table S2: WPB and H_2O calculation for different solid loadings in a 100 mL reaction volume

Solid Loading (% w/v)	**5%**	**10%**	**15%**	**20%**	**25%**	**30%**
Total WPB (g)	20	40	60	80	100	120
Solid content in WPB (g)	5	10	15	20	25	30
Water content in WPB (mL)	15	30	45	60	75	90
Additional H_2O (mL)	85	70	55	40	25	10
Starch content (g)	3.7	7.4	11.1	14.8	18.5	22.2
Glucose content (g)	4.1	8.2	12.3	16.4	20.5	24.6