# Isolation, characterization and toxicological potential of Alternaria-mycotoxins (TeA, AOH and AOH) in different Alternaria species from various regions of India

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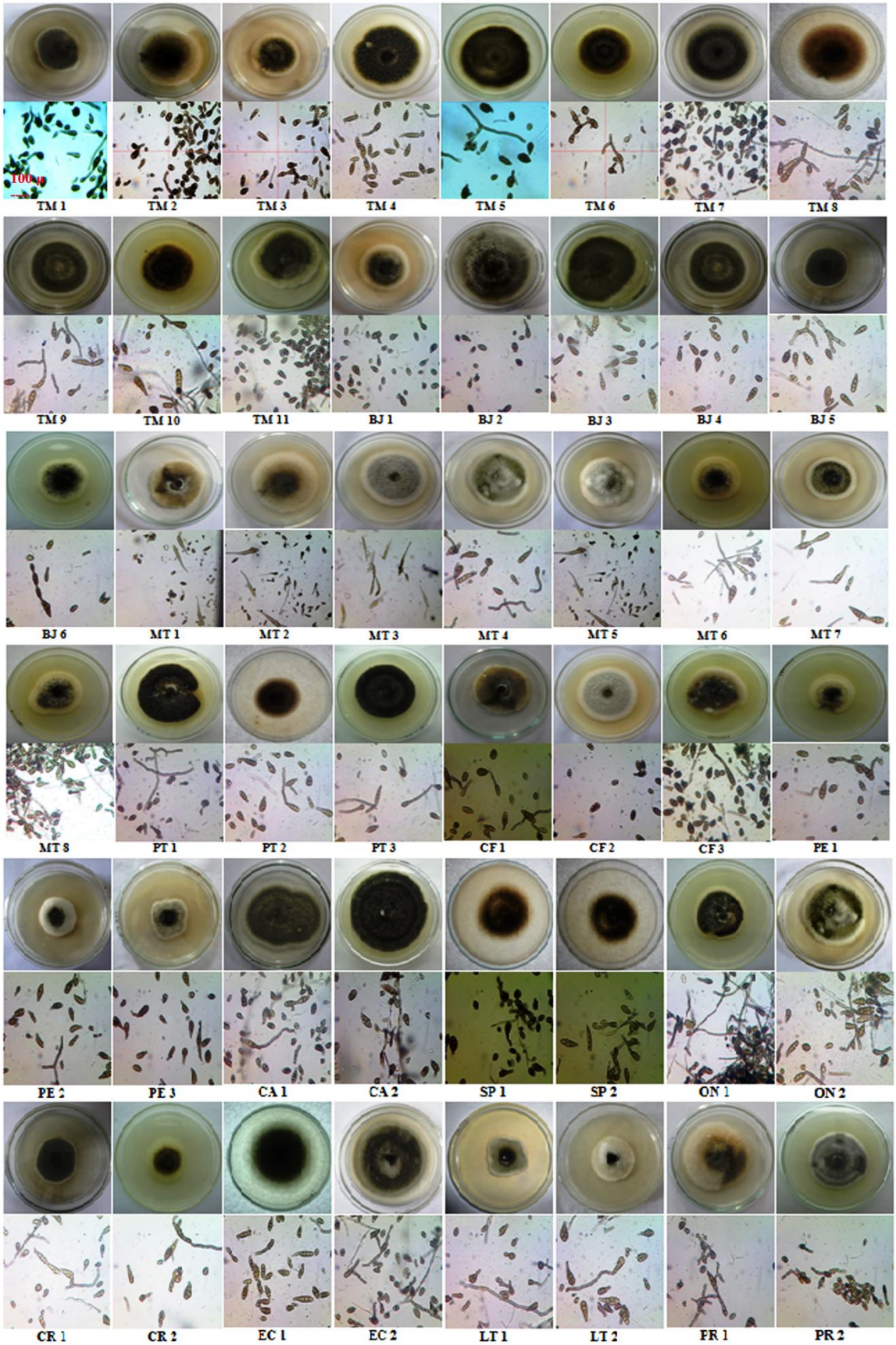
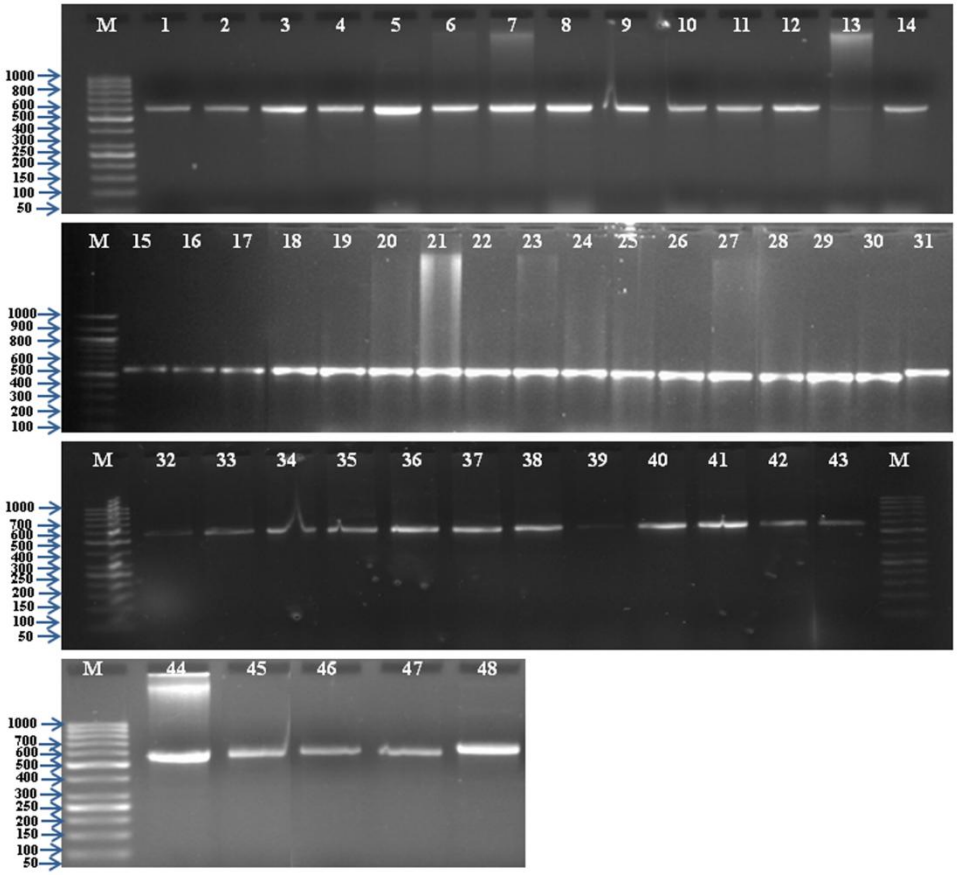


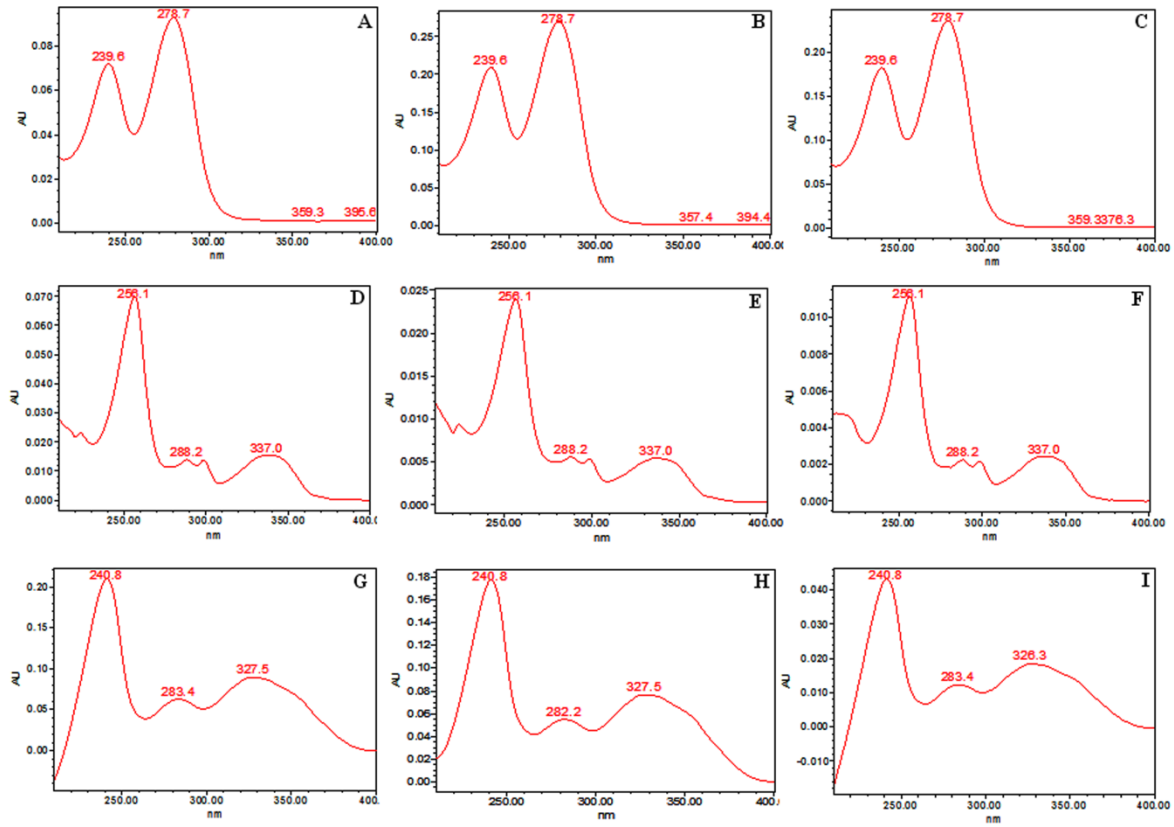

**Supplementary Figure S1.** Different isolates of *Alternaria* pathogen grown on PDA plate and its conidial morphology isolated from vegetables, crops, and weeds from different regions of India; Scale bar represents 100 μ.



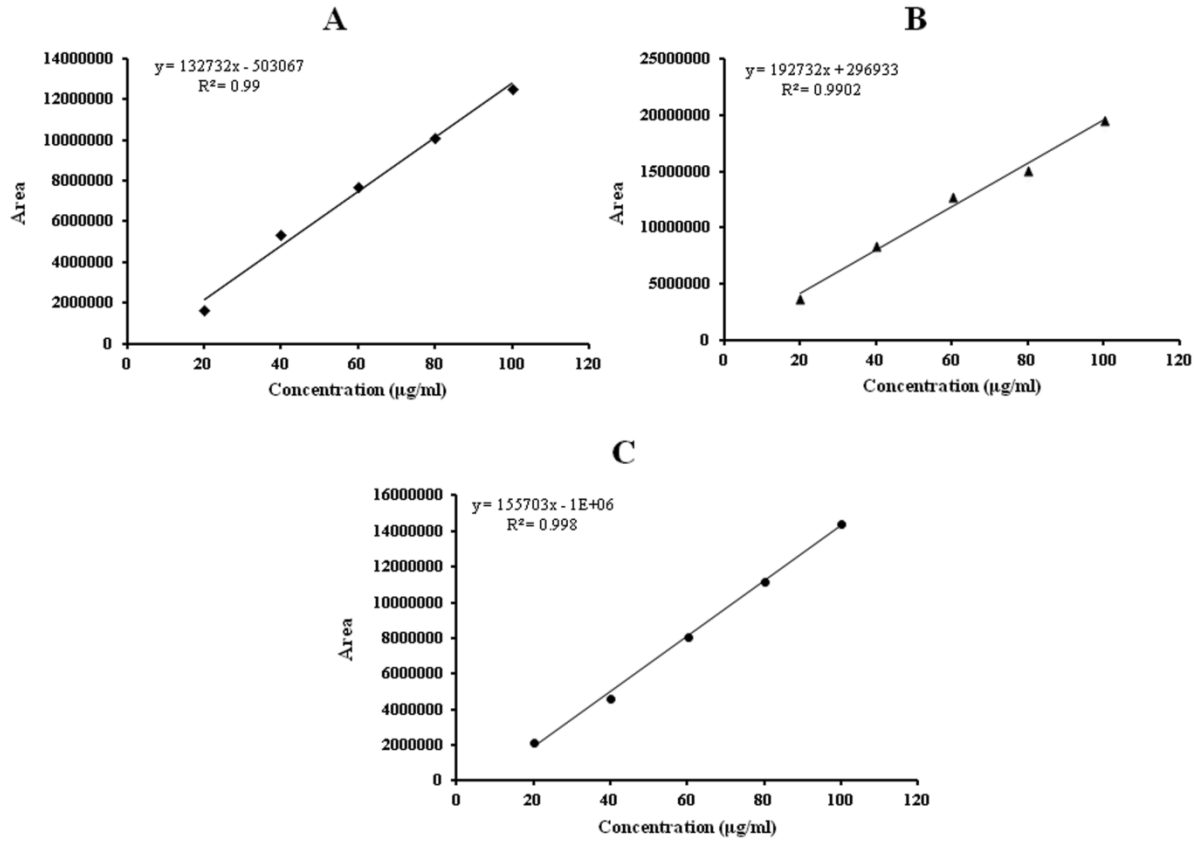

**Supplementary Figure S2.** Gel electrophoresis of PCR products with primers forward and reverse (ITS1/ITS4) of DNA from fungal isolates. Picture shows the amplified product of all 48 isolates of *Alternaria* species. The amplified products were found between 500-600 bp.

**Supplementary Figure S3.** Multiple sequence alignment of all the *Alternaria* spp. isolates showing conservation of residues as revealed through CLC Sequence Viewer 6.8.2.

(Supplementary Figure S3 given in separate PDF Image)




**Supplementary Figure S4.** Comparison of UV spectra of standard metabolites and isolated fungal metabolites from HPLC connected with diode array detector. **(A)** absorption peaks of standard TeA at 239.6 nm and 278.7 nm **(D)** absorption peaks of standard AOH at 256.1 nm, 288.2 nm and 337.0 nm **(G)** absorption peaks of standard AME at 240.8 nm, 283.4 nm and 327.5 nm **(B)** absorbance peaks of TeA (maximum conc.) as recorded form isolate TM 4 **(C)** absorbance peaks of TeA (minimum conc.) as recorded form isolate PE 1 **(E)** absorbance peaks of AOH (maximum conc.) form isolate TM 4 **(F)** absorbance peaks of AOH (minimum conc.) from isolate ON 1 **(H)** absorbance peaks of AME (maximum conc.) from isolate TM 4 **(I)** absorbance peaks of AME (minimum conc.) from BJ 6




**Supplementary Figure S5.** Calibration curve of (A) tenuazonic acid, (B) alternariol, and (C) alternariol monomethyl ether standards.

**Supplementary Table S1.** LOD, LOQ, coefficient $r^2$ and calibration curve equation of each toxin (TeA, AOH, and AME) of *Alternaria*.

| **Toxins** | **LOD (µg/ml)** | **LOQ (µg/ml)** | **coefficient $r^2$** | **equation** |
|---|---|---|---|---|
| TeA | 28.42 | 86.13 | 0.99 | Y=132732x-503067 |
| AOH | 28.03 | 84.94 | 0.9902 | Y=192732x+296933 |
| AME | 12.66 | 38.36 | 0.998 | Y=155703x-1E+06 |

**Supplementary Table S2.** Ion source setting on Accucore RP-MS 100 X 3, 2.6 µm, ACQ-TQD-QBB1152 instrument.

| **Settings** | **ES+** | | **ES-** | |
|---|---|---|---|---|
| Source temperature (°C) | 120 | 118 | 120 | 118 |
| Desolvation temperature (°C) | 350 | 346 | 350 | 346 |
| Cone gas flow (L/Hr) | 30 | 30 | 30 | 30 |
| Desolvation gas flow (L/Hr) | 650 | 650 | 650 | 650 |
| Capillary voltage (KV) | 3.50 | 3.49 | 3.50 | 3.49 |
| Collision gas flow (mL/Min) | 0.18 | 0.14 | 0.10 | 0.14 |
| Ion energy 1 | 1.00 | | 1.00 | |
| Ion energy 2 | 3.00 | | 1.00 | |
| MS mode entrance | 50.00 | | 50.00 | |
| MS mode collision energy | 5.00 | | 3.00 | |
| MS mode exit | 50.00 | | 50.00 | |
| MS/MS mode entrance | 2.00 | | 2.00 | |
| MS/MS mode collision energy | 15.00 | | 25.00 | |
| MS/MS mode exit | 2.00 | | 2.00 | |
| HM RF Lens (V) | (+) 0.0 | | (-) 0.0 | |
| LM 1 resolution | 12.00 | | 12.00 | |
| HM 1 resolution | 12.00 | | 12.00 | |
| LM 2 resolution | 15.00 | | 15.00 | |
| HM 2 resolution | 15.00 | | 15.00 | |
| Multiplier | -504.50 | | -504.50 | |

Note: Ion mode: ESI; Ion polarity: Positive and negative
(MS method: C:\MassLynx\INTERNAL2011.pro\ACQUDB\SAIF9086.EXP)