Supplementary Figure 3

Genetic clusters according to STRUCTURE of six global populations of *Teratosphaeria destructans*

Teratosphaeria destructans individuals were assigned to clusters (K) according to their allele frequency. Twenty independent iterations of K = 1–10 were performed using the admixture model, with 50 000 burn-in iterations followed by 500 000 Markov Chain Monte Carlo (MCMC) iterations using the program STRUCTURE 2.3.4 (Falush et al., 2003).

Calculating L(K) and ΔK using the online CLUMPAK (Clustering Markov Packager Across K) platform (Kopelman et al., 2015) with best K function revealed the optimal number of clusters was three. Individuals were separated into an Indonesian cluster (1), a South Africa-Thailand-Vietnam cluster (2) and a Chinese cluster (3) (Fig. S4).
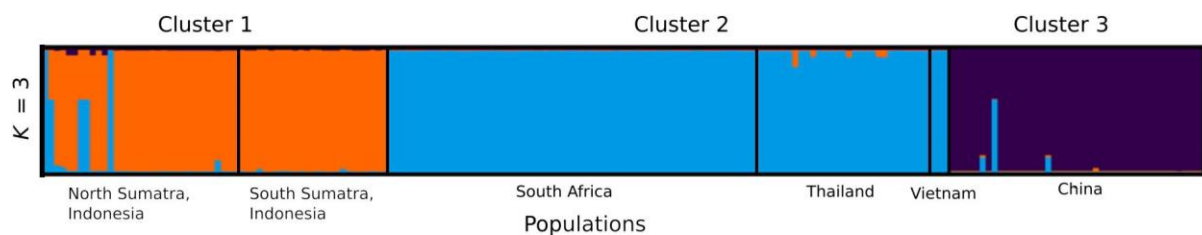

Figure S3. STRUCTURE plot for *Teratosphaeria destructans* isolates from six geographic populations. The optimal number of genetic clusters (ΔK) = 3. Each vertical bar represents one individual.