

Figure S1. Ordination diagrams based on similarity matrix calculated from DGGE patterns of (A) total bacteria (B) total fungi (C) *Oxalobacteraceae* (D) *Actinobacteria* communities in unamended and chitin-amended soils. Unamended soil samples Dec-09, June-10, Nov-10, March-11, April-12 referred as D, J, N, M and A. Chitin-amended soil samples Dec-09, June-10, Nov-10, March-11, April-12 referred as D+, J+, N+, M+ and A+. Position of circles represent the mean positions of three replicates. Sampling points assigned with “\*” were significantly different ( $P < 0.05$ ). Values on the axes indicate the percentage of total variation explained by each axis.

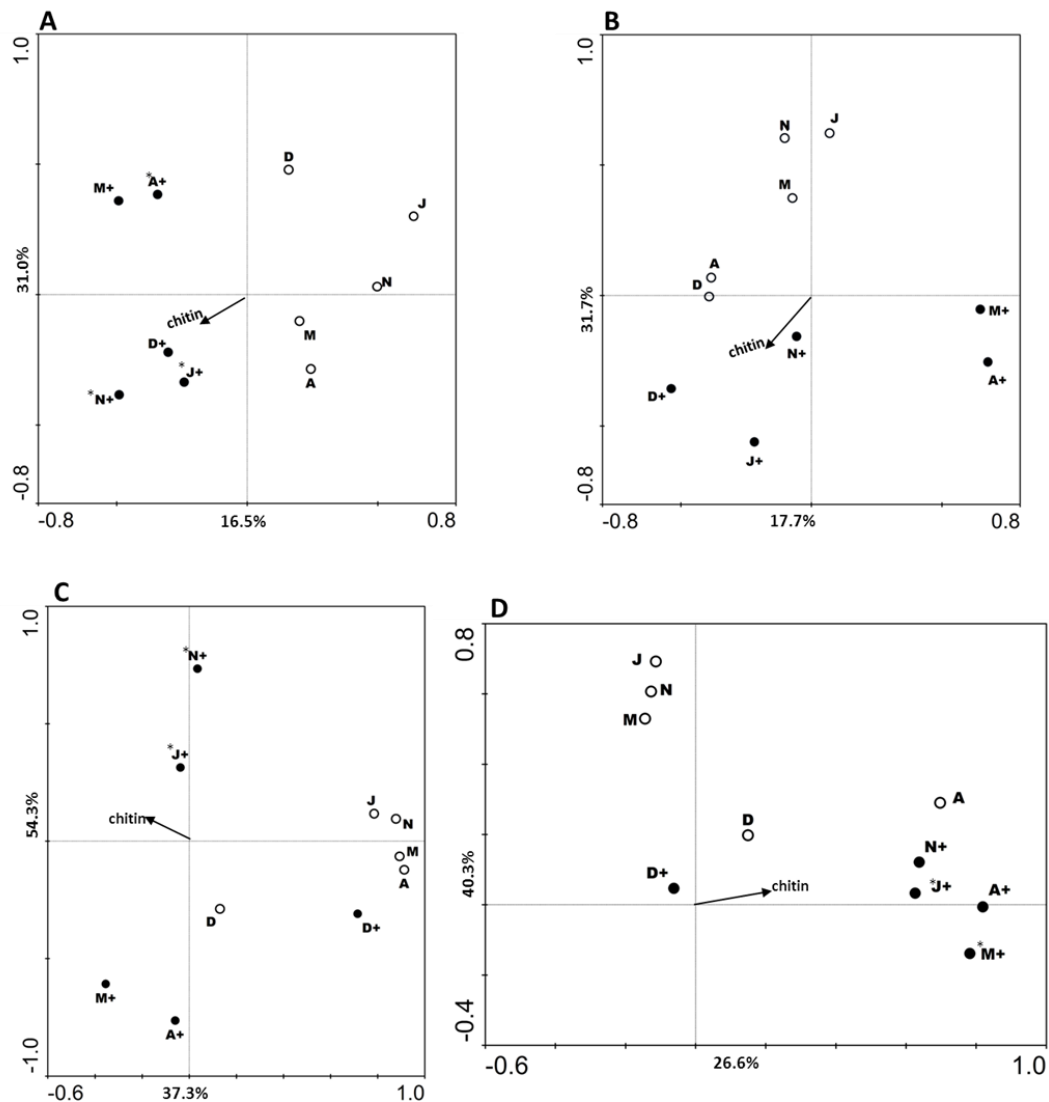


Figure S2. DGGE profiles (A) total bacteria (B) total fungi (C) *Oxalobacteraceae* (D) *Actinobacteria* (E) chitinolytic (chiA) communities in unamended and chitin-amended (assigned with "+") soils.

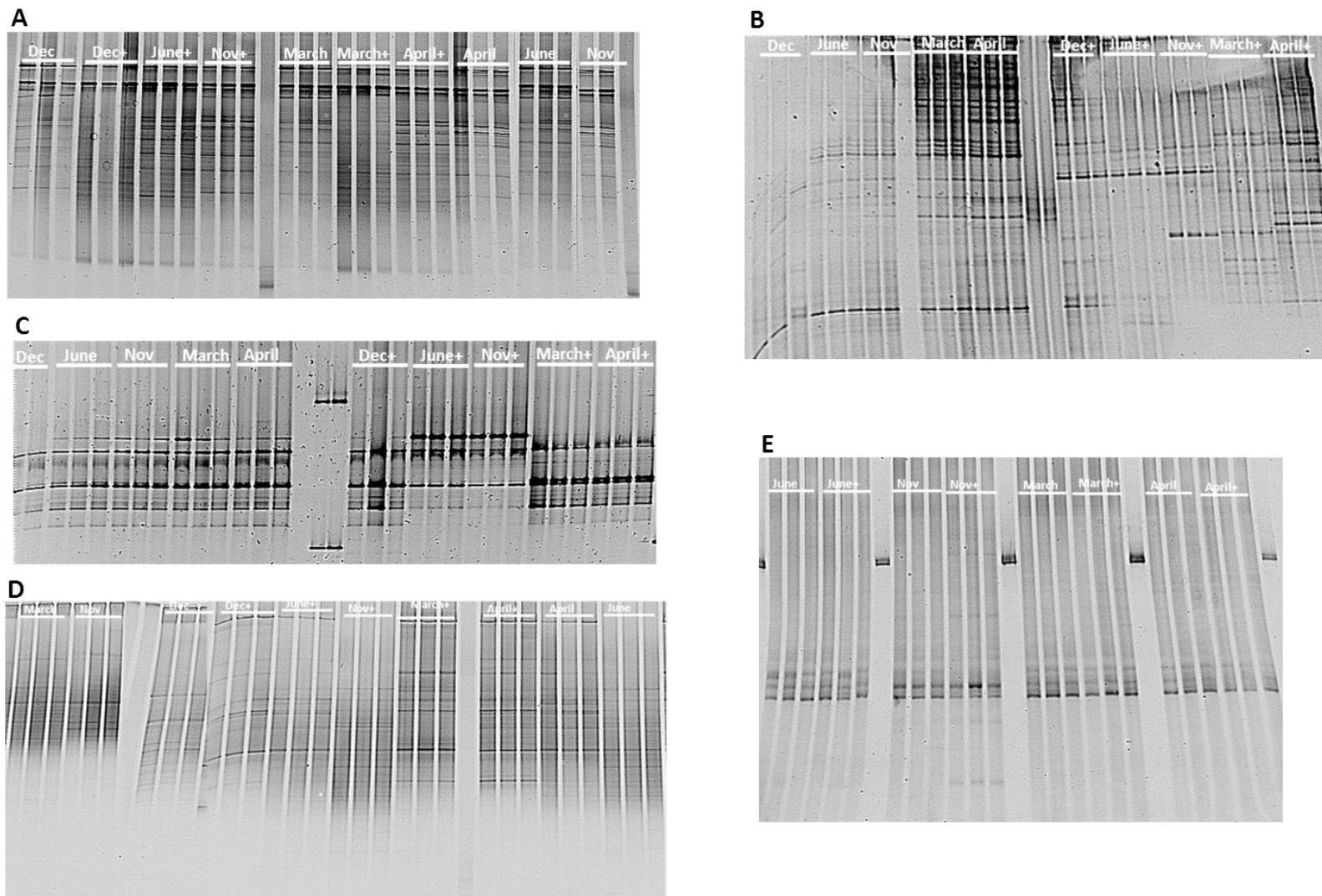


Figure S3. Structure of bacterial chitinolytic community. Clustering of unamended and chitin-amended soils DGGE profiles based on UPGMA and Jaccard correlation coefficient. Unamended soil samples Dec-09, June-10, Nov-10, March-11, April-12 referred as Dec, June, Nov, March and April. Chitin-amended soil samples Dec-09, June-10, Nov-10, March-11, April-12 referred as Dec+, June+, Nov+, March+ and April+. Sampling points assigned with "\*" were significantly different ( $P < 0.05$ ).

