Figure legends

Fig. S1. The clustering analysis was performed using UPGMA, which is a type of hierarchical clustering method based on unweighted UniFrac distance metrics, and showed the relationship of the prokaryotic communities in the four samples (A0, at the beginning of aging; A1, after one month of aging; A2, after two months of aging; A3, after three months of aging).

Fig. S2. PCoA analysis of the prokaryotic communities in the four samples (A0, at the beginning of aging; A1, after one month of aging; A2, after two months of aging; A3, after three months of aging). The first two principal components (PC1 and PC2) can explain 80.96% of the data variance.

Fig. S3. The clustering analysis was performed using UPGMA, which is a type of hierarchical clustering method based on unweighted UniFrac distance metrics, and showed the relationship of the eukaryotic communities in the four samples (A0, at the beginning of aging; A1, after one month of aging; A2, after two months of aging; A3, after three months of aging).

Fig. S4. PCoA analysis of the eukaryotic communities in the four samples (A0, at the beginning of aging; A1, after one month of aging; A2, after two months of aging; A3, after three months of aging). The first two principal components (PC1 and PC2) can explain 74.88% of the data variance

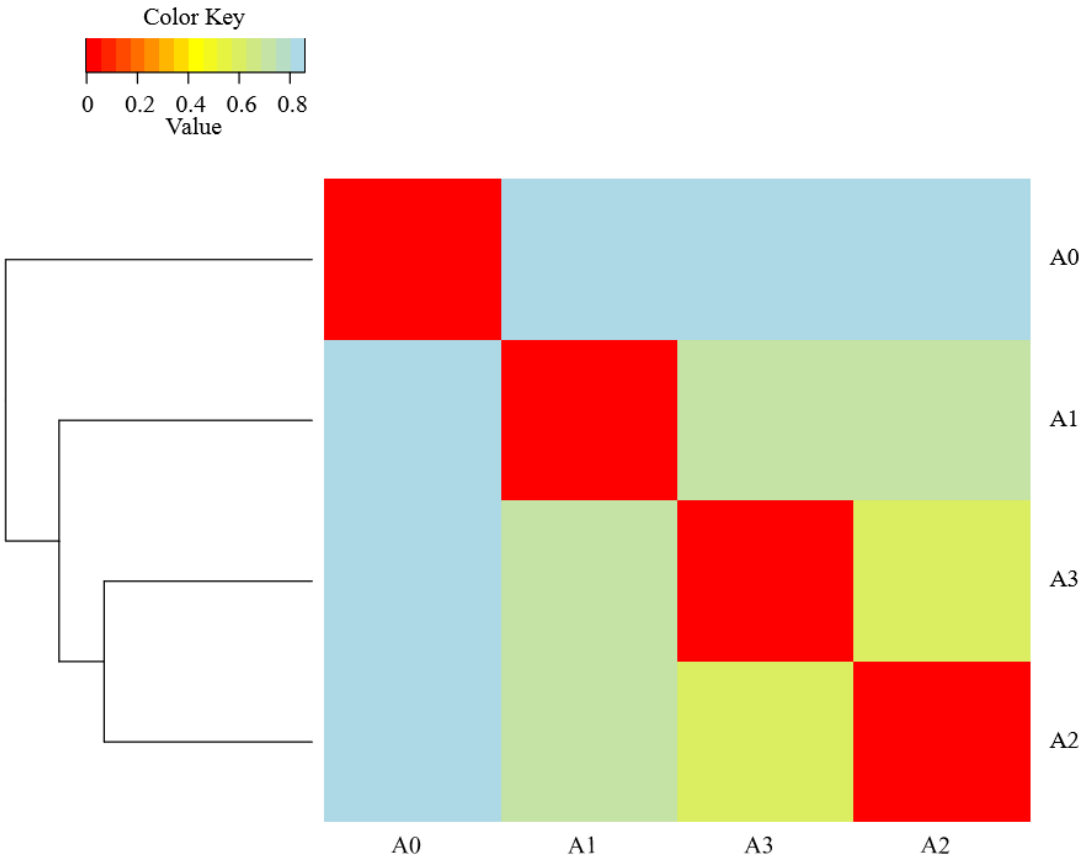

Fig. S1

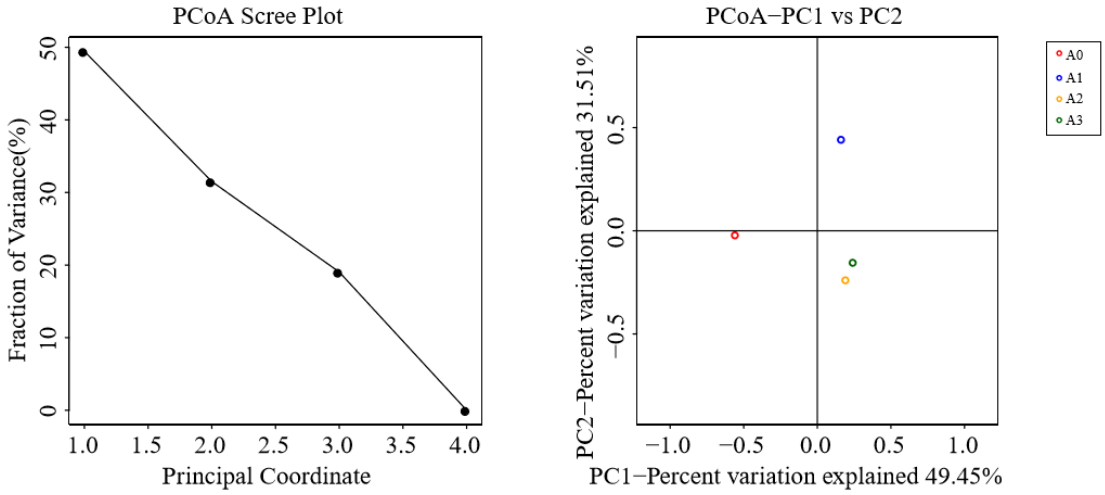
PCoA Scree Plot
Fraction of Variance(%)
0
10
20
30
40
50
1.0
1.5
2.0
2.5
3.0
3.5
4.0
Principal Coordinate
PCoA−PC1 vs PC2
PC2−Percent variation explained 31.51%
0.5
0.0
−0.5
−1.0
−0.5
0.0
0.5
1.0
PC1−Percent variation explained 49.45%
A0
A1
A2
A3

Fig. S2

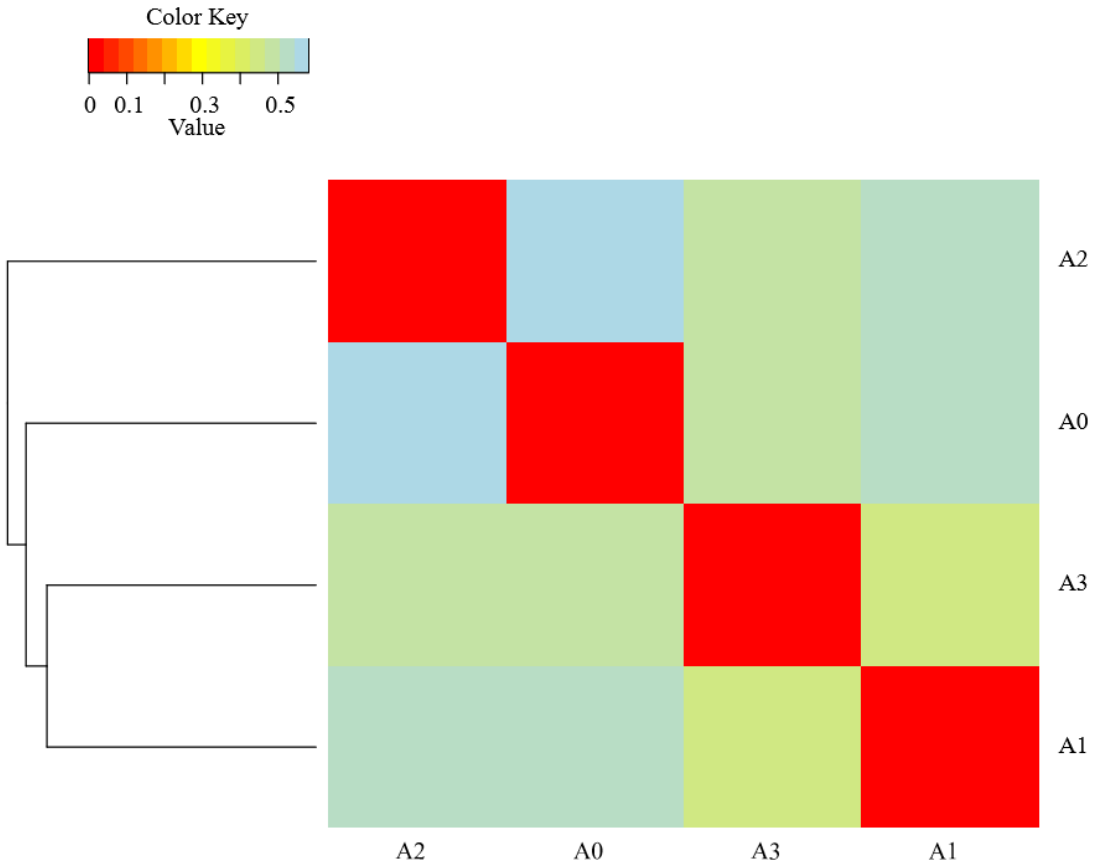

Fig. S3

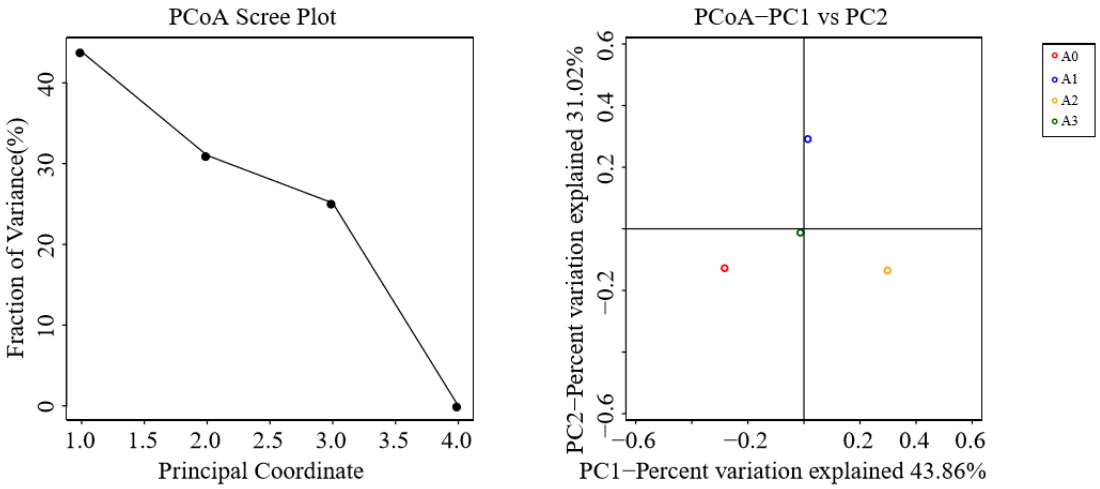
PCoA Scree Plot
Fraction of Variance(%)
0
10
20
30
40
1.0
1.5
2.0
2.5
3.0
3.5
4.0
Principal Coordinate
PCoA−PC1 vs PC2
PC2−Percent variation explained 31.02%
0.6
0.4
0.2
−0.2
−0.6
−0.6
−0.2
0.2
0.4
0.6
PC1−Percent variation explained 43.86%
A0
A1
A2
A3

Fig. S4