

including 68 from Shanting District, 9 from Yicheng District, 4 from Shizhong District, and 19 from Tengzhou City.

Using the method for estimating the optimal K value, Structure clustering analysis based on microsatellite data showed that ΔK reached its maximum at $K=3$; therefore, the optimal K value was 3. The studied populations were divided into three genetic clusters rather than being grouped according to sampling regions. This indicates the presence of gene flow among different regions, which is consistent with the results of the UPGMA clustering analysis.

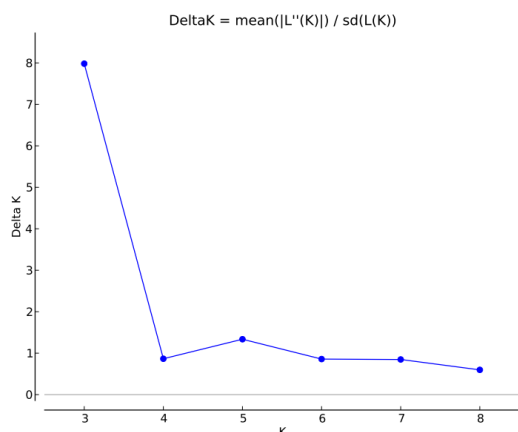


Figure 1 The deltaK (ΔK) values of structure output

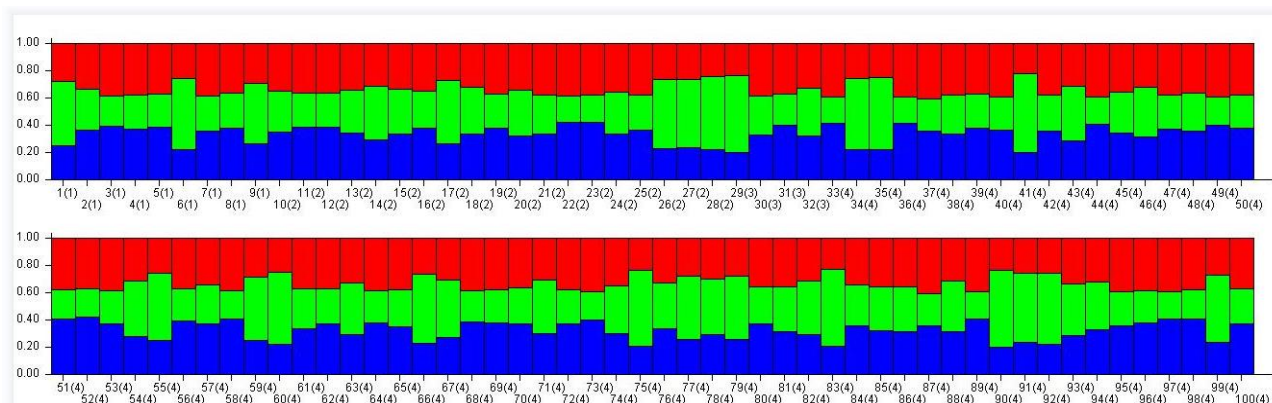


Figure 2 The structure output at $K=3$

Table 4 Distribution of *P. orientalis* germplasm subpopulations when $K=3$

Sub-population	Shanting	Yicheng	Shizhong	Tengzhou	Total	Q-Value
Sub-population 1	27	3	2	7	39	0.619
Sub-population 2	18	5	0	5	28	0.476
Sub-population 3	23	1	2	7	33	0.461
Total	68	9	4	19	100	0.5187

Using PowerMarker software, UPGMA clustering based on Nei's genetic distance was performed on 100 samples from four populations. The clustering results showed both similarities and differences compared with the three clusters identified by STRUCTURE. The main difference was that the proportions of samples from each provenance differed among the clusters. The similarity was that germplasm from the Shanting provenance was distributed across all three clusters. Based on the clustering outcomes from both methods, further analyses of kinship relationships among germplasm accessions can be conducted. To some extent, the clustering results indicate that genetic relatedness among populations is associated with geographic distribution; however, most samples did not cluster strictly according to their sampling regions, suggesting that there is a certain level of gene flow among different regions.