

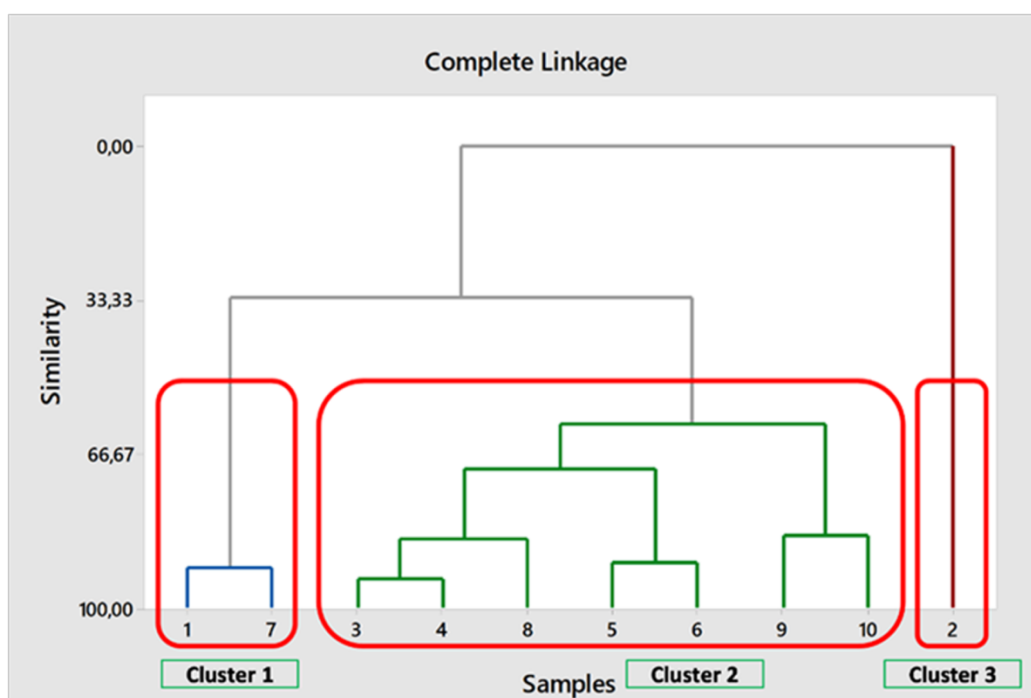


Figure S1. Dendrogram for hierarchical clustering analysis regarding phenolic contents. Samples S1 and S7 form the first cluster, with 91.11% similarity. In the second cluster, S3 and S4 had the highest similarity (93.48%) and then S8 joins them with 85.11% similarity. Moreover, S5 and S6 were linked together with 90.09% similarity and then they join the group consisting of S3, S4 and S8, with 69.84% similarity. Finally, S9 and S10 were linked together with 84.39% similarity and then joined the previous group with 60.09% similarity. S2 dissociates from all other samples and forms a distinct cluster alone.

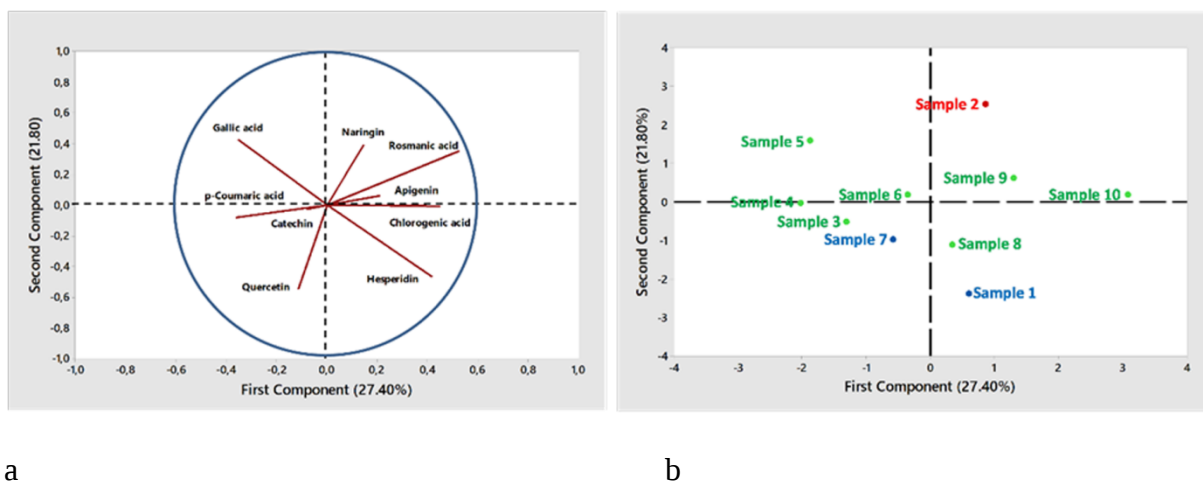


Figure S2. Phenolics map (a) and score plot of samples (b) for PC1 and PC2. Considering eigenvalues greater than 1, five principal components were significant (these PCs represent approx. 87.6% of the total variance). The PC1 with 2.4673 eigenvalue explains 27.40% of the total variance while PC2 with 1.9661 eigenvalue explains 21.80%. The positive part of PC1 was related to naringin, rosmanic acid, apigenin, chlorogenic acid and hesperidin, whereas the positive part of PC2 was related to p-coumaric acid, gallic acid, naringin, rosmanic acid and apigenin. For both PCs, the negative parts are related with except these phenolic contents. S2 significantly dissociates from all other samples in terms of phenolic contents, parallel to the clustering analysis results.

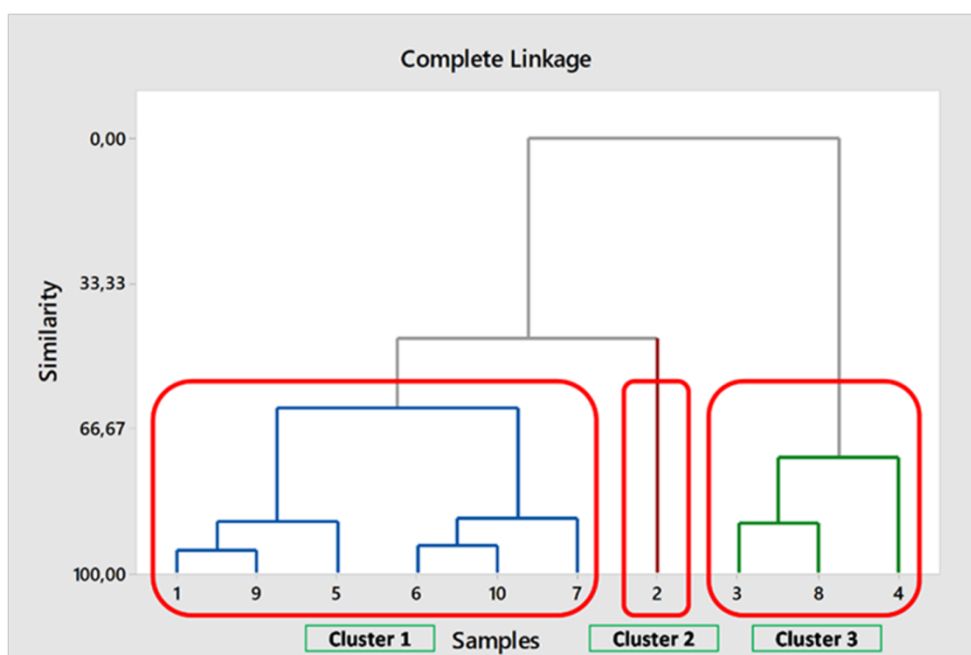
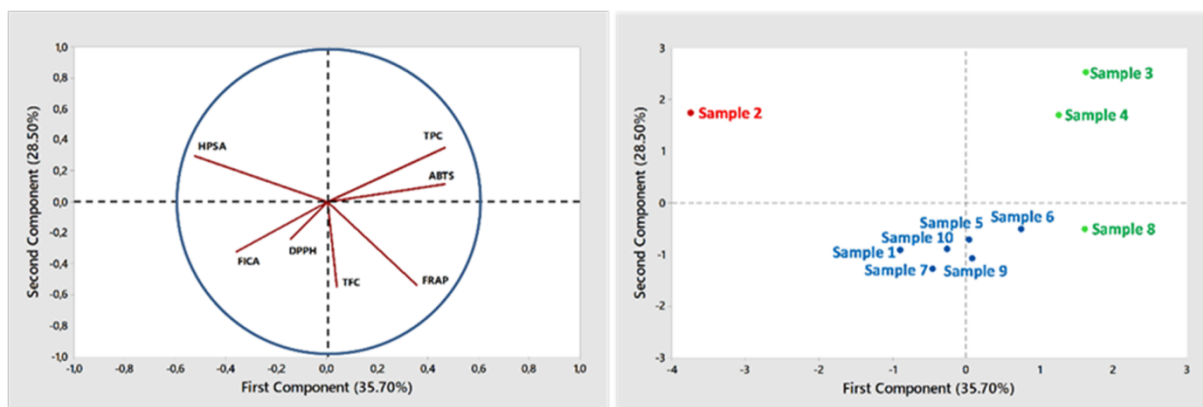


Figure S3. Dendrogram for hierarchical clustering analysis from the point of antioxidant contents. This dendrogram clearly shows that the pollen samples can be split up 3 main clusters (Fig. 3S). The first cluster, with 61.81% similarity, consists of six samples as S1, S5, S6, S7, S9 and S10. The formation process of this cluster demonstrates that S1 and S9 have the highest similarity (94.80%) and then S5 join them with 87.94% similarity level. Moreover, S6 and S10 are linked together with 93.76% similarity level and then S7 joins them with 87.32% similarity level. Finally, these clusters join each-other. The other cluster contains three samples (S3, S4 and S8) with 73.27% similarity. Examination of this cluster components indicates that S3 and S8 (88.49% similarity) forms a cluster and then S4 joins them. S2 dissociates from all other samples and forms another cluster alone in terms of antioxidant contents, just like the case in terms of phenolic contents.



a)

b)

Figure S4. Antioxidants map (a) and score plot of samples (b) for PC1 and PC2. Considering eigenvalues greater than 1, three principal components were significant, and these PCs represent approximately 82.90% of the total variance. PC1 with 2.4959 eigenvalues explains 35.70% of the total variance, while PC2 with 1.9975 eigenvalues explains 28.50%. And the last PC (PC3) with 1.3097 eigenvalue represents the 18.70% of the total variance. The positive part of PC1 is related with TPC, ABTS, FRAP and TFC, while the positive part of PC2 is related with HPSA, TPC and ABTS. In part b) S2 significantly dissociates from all other samples in terms of antioxidant contents, parallel to the clustering analysis results. Besides, for PC1 and PC2, the proximity of the positions of S1, S5, S6, S7, S9 and S10 on the plot indicates that these samples had a fairly similar structure in terms of their antioxidant content, which supports the results obtained from clustering analysis. Similar comments and evaluations can be made for other samples. These findings demonstrate that the antioxidant contents can be used to classify these pollen samples.

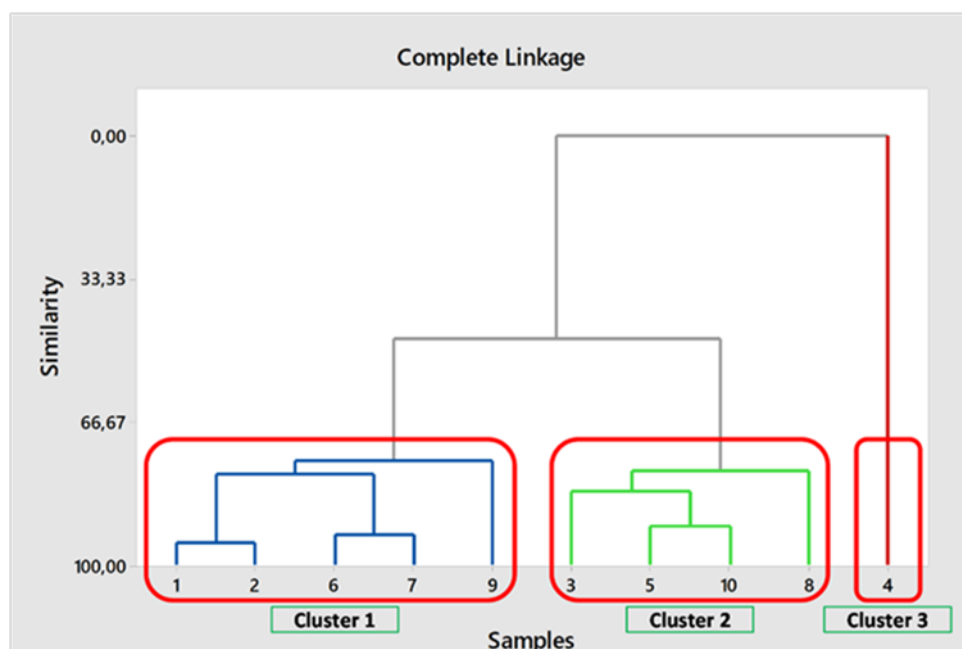


Figure S5. Dendrogram for hierarchical clustering analysis from the point of element concentrations. The y-axis of the dendrogram presents the similarity measure for clusters join. The pollen samples can be split 3 main clusters. The first cluster, with 75.60% similarity, consists of five samples (S1, S2, S6, S7 and S9). S1 and S2 had the highest similarity (94.63%). S6 and S7 were linked together with 92.94% similarity and then these clusters joined each-other with 78.73% similarity. The second cluster contains four samples (S3, S5, S8, and S10, with 77.91% similarity). S5 and S10 (91.01% similarity) form a cluster and then S3 joins them with 82.82% similarity. Finally, S8 joins the group of three samples. S4 dissociates from all other samples and forms the third cluster alone.

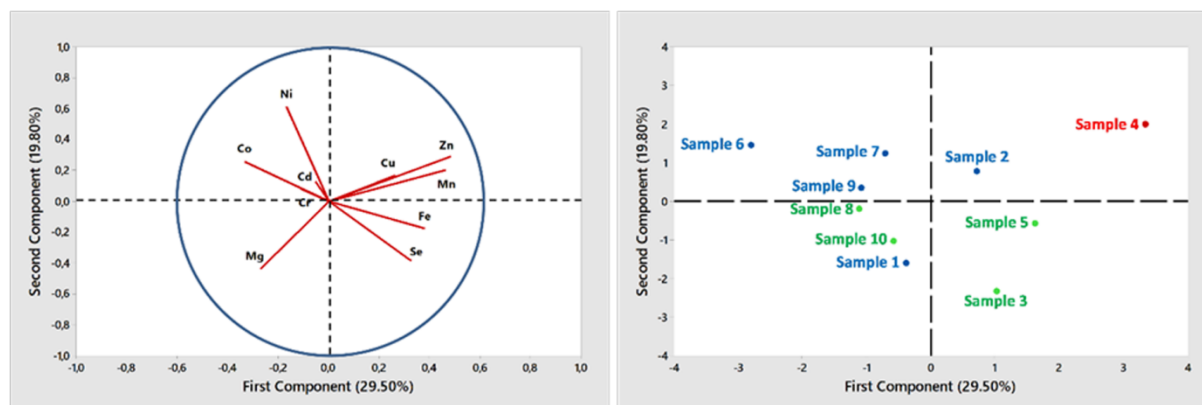


Figure S6. Element map (a) and score plot of samples (b) or PC1 and PC2. To determine the number of main principal components, two statistical approaches can be chosen. The first one is to select components with an eigenvalue greater than 1 and the second one is to select components whose ratio to explain the total variance is greater than a pre-determined value. When the first way is chosen, there were four principal components with an eigenvalue greater than 1 and these first four components represented approx... 78.60% of the total variance. PC1 with 2.9506 eigenvalue explained 29.50% of the total variance while the PC2 with 1.9783 eigenvalue explained 19.80%. Next two components (PC3, PC4) with 1.5050 and 1.4234 eigenvalues represented the 15.10% and 14.20% of the total variance, respectively. The positive part of PC1 is related to Cu, Zn, Mn, Fe, and Se, while the positive part of PC2 is related to Co, Cr, Ni, Cd, Cu, Zn, Mn. For each PC, the negative parts are related with except these elements. S4 significantly dissociated from all other samples in terms of element concentrations, parallel to the clustering analysis results. Besides, for PC1 and PC2, the proximity of the positions of S6, S7 and S9 on the plot indicates that these samples had a fairly similar structure in terms of heavy metals concentrations, which supports the results obtained from clustering analysis. Similar comments and evaluations can be made for other samples. These findings demonstrate that the given variables can be used to classify these pollen samples.

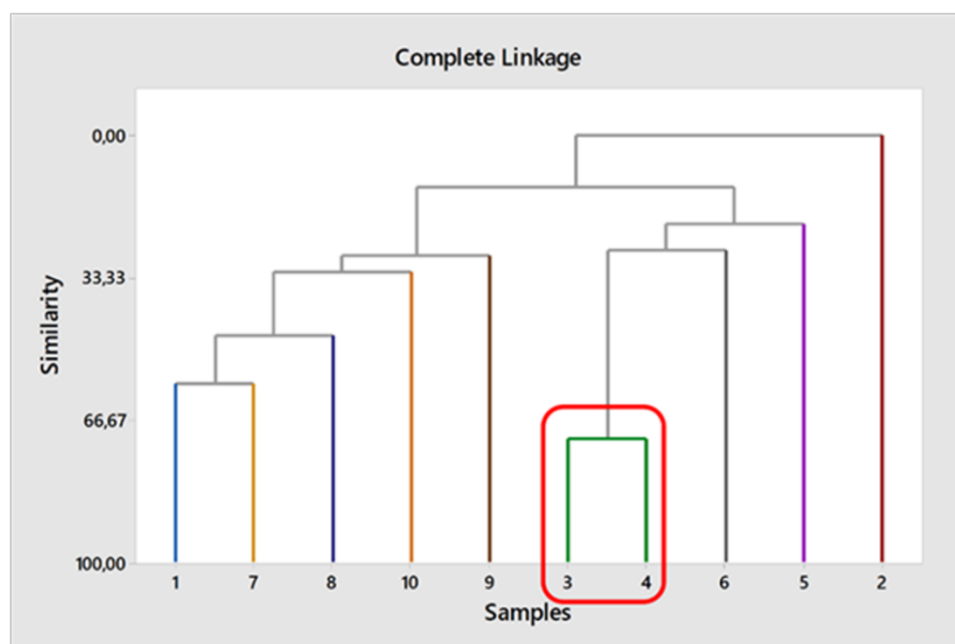


Figure S7. Dendrogram for hierarchical clustering analysis regarding phenolic and antioxidant contents. Samples 3 and 4 form a cluster, with 70.97% similarity. Since each of the other samples were not similar to each other, they formed separate clusters.