Pulse Diversity for Polyphenolic Secondary Metabolites

J.B. Morris, USDA, ARS, PGRCU, Griffin, GA, 30223, USA
Brad.Morris@ars.usda.gov

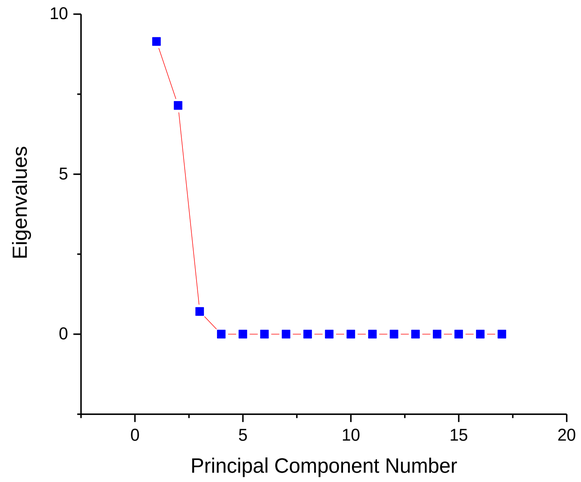
Abstract

The pulse species including guar (*Cyamopsis tetragonoloba* L. Taub.), *Lablab purpureus* L. Sweet, *Macrotyloma uniflorum* (Lam.) Verdc., *Teramnus labialis* (L.f.) Spreng, alfalfa Medicago *sativa* (L.) ssp. *sativa*], green beans (*Phaseolus vulgaris* L.), fava beans (*Vicia faba* L.), blackeye pea [*Vigna unguiculata* (L.) Walp. ssp. *unguiculata* group *unguiculata*], mung bean [*V. radiata* (L.) R. Wilczek], soybean [*Glycine max* (L.) Merr.], common bean (*Phaseolus vulgaris* L. cv. *Zolfino*), red kidney bean (*P. vulgaris* L.), pinto bean (*P. vulgaris* L.), white bean (*P. vulgaris* L.), green peas (*Pisum sativum* L.), and black cowpea [*V. unguiculata* (L.) Walp. ssp. *sinensis*] were subjected to a meta-analysis for specific polyphenolic flavonoids. Flavonoids have been shown to have anti-cancer potential. The flavonoid data from all species were subjected to a cluster and principal component meta-analysis. The cluster analysis showed 11 distinct clusters for flavonoid content in the 17 species. The guar accessions showed 4 clusters with the highest flavonoid concentrations (ranging from 71 to 181 mg/100g). The *Teramnus labialis* accessions showed 3 clusters with the next highest flavonoid concentrations (ranging from 21 to 50 mg/100g). All other species produced very low flavonoid concentrations (ranging from 0.26 to 6.43 mg/100g. The principal component analysis showed that the first, second, and third components accounted for 30, 54, and 74% of the total variation. The guar and *T. labialis* accessions produced numerically higher flavonoid concentrations relative to the other 15 species.

Materials & Methods

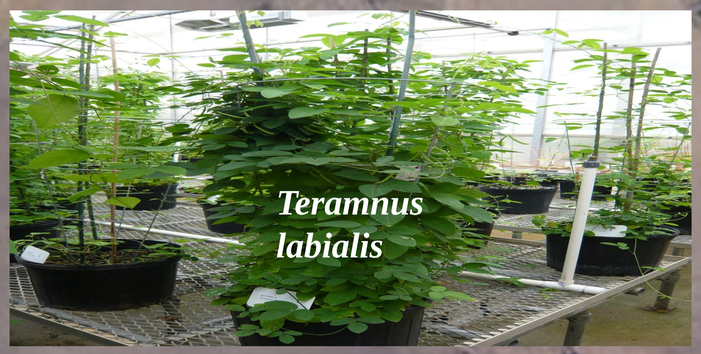
Flavonoid (myricetin, quercetin, kaempferol, isorhamnetin) data from 64 samples including 19 guar, 15 *Teramnus labialis*, 7 horsegram, and 10 *Lablab purpureus* accessions from field or greenhouse-grown plants plus 1 each of raw common bean, black cowpea, mature red kidney bean, raw cowpea, raw white bean, raw pinto bean, raw broadbean, raw soybean, mature broadbean, raw mungbean, unprepared green peas, raw snap beans, and raw alfalfa seed samples reported in the USDA flavonoid database were combined in a meta-analysis using principal component analysis (PCA) and cluster analysis (CA) to determine flavonoid variability among samples and which taxon(s) produced higher flavonoid content.

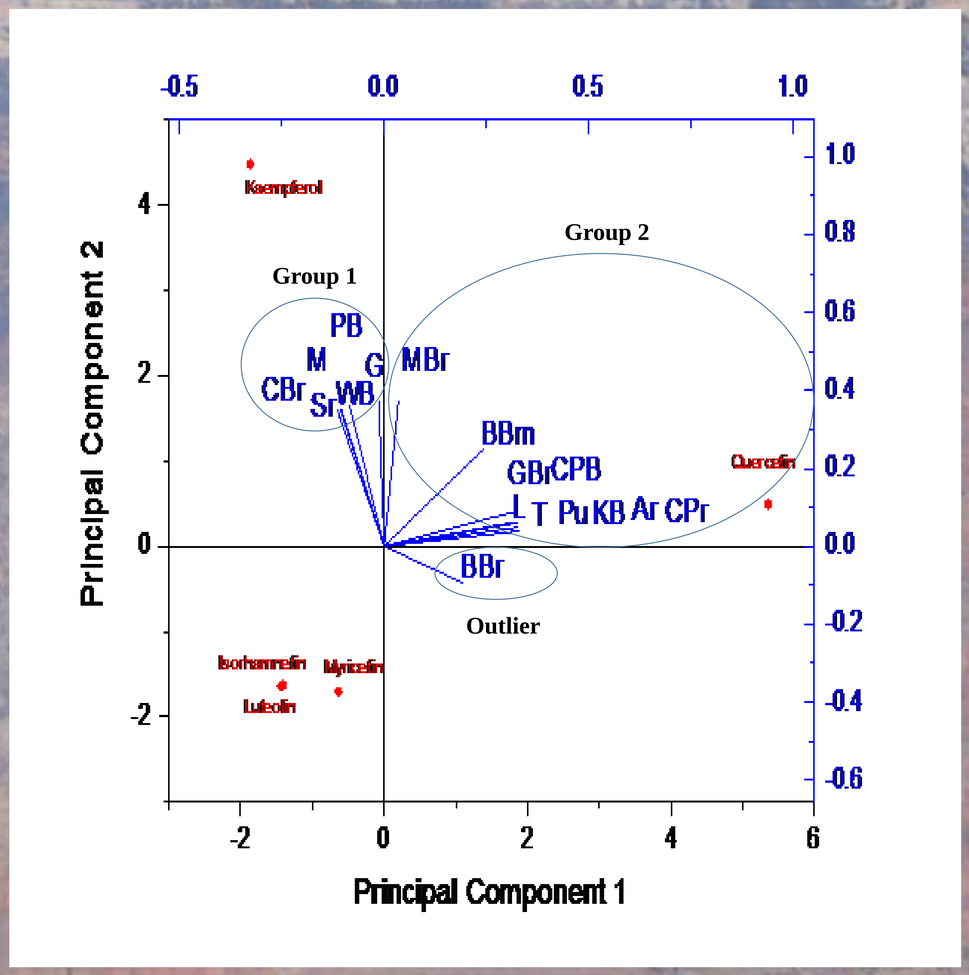
Results and Discussion



Scree plot of the 17 accession characteristics

PCA helps to identify the most suitable variables among accessions. The scree plot based PCA shows that detecting principal components with an Eigenvalue greater than an arbitrary value K = 1.

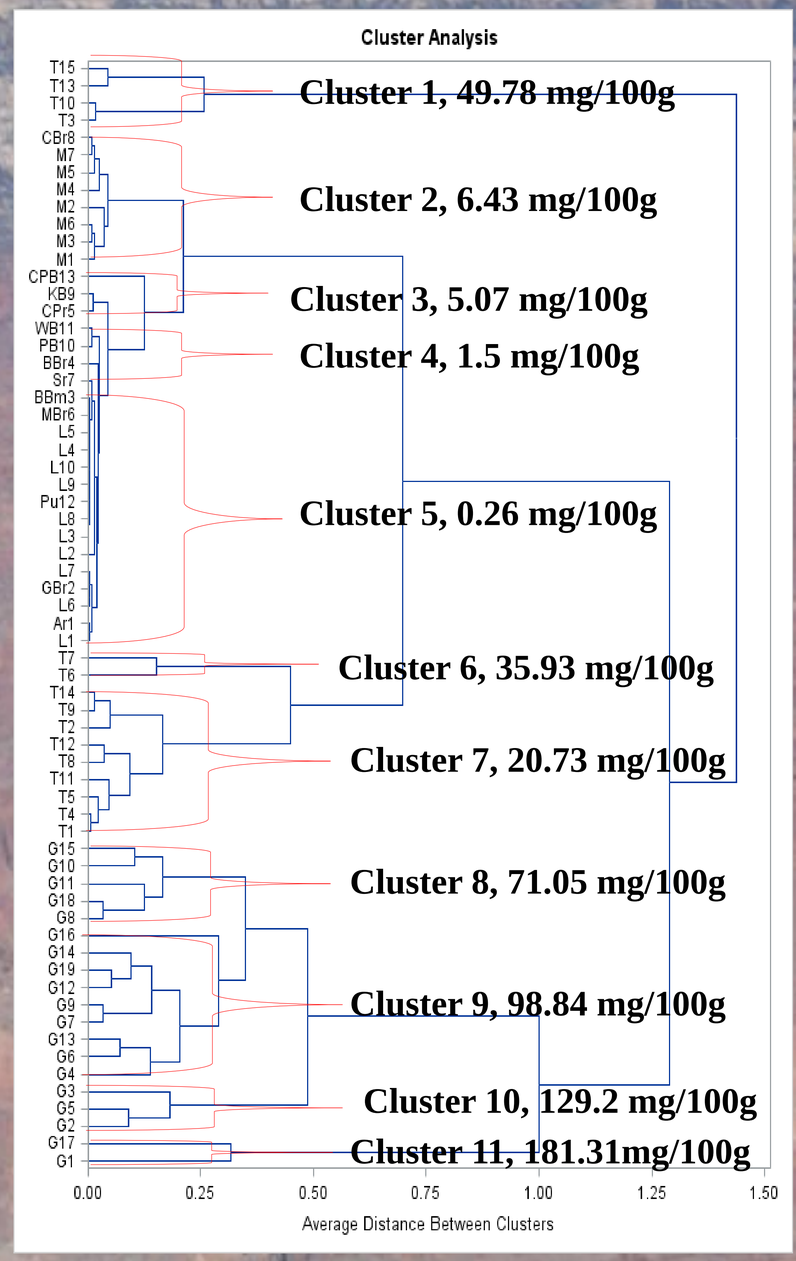




Biplot of the 17 accession characteristics

G – immature guar pods
T – mature *Teramnus labialis* seeds
M – mature horsegram seeds
CBr – raw common bean
CPB – black cowpea
KB – mature red kidney bean
CPr – raw cowpea
WB – raw white bean
PB – raw pinto bean
BBr – raw broadbean
Sr – raw soybean
BBm – mature broadbean
MBr – raw mungbean
Pu – unprepared green peas
GBr – raw snap beans
L – mature lablab beans
Ar – raw alfalfa seeds

PC1 and PC2 together explained about 96% variation in the 64 species. In PC1, mature *T. labialis*, raw alfalfa, raw cowpeas, mature red kidney bean, and unprepared green peas with eigenvalues of 9.14 and 7.14 caused 53.8 and 95.8% of the total variation for flavonoids. Immature guar pods and raw mungbean were the most variable in PC2. The biplot showed that the distribution of the species was focused on 3 groups and 1 outlier. Group 1 included raw pinto bean, mature horsegram, raw common bean, raw soybean, raw white bean, and immature guar pods. They were closely grouped on the negative end of PC1. Group 2 included raw mungbean, mature broadbean, raw snap bean, black cowpea, mature lablab beans, mature *Teramnus labialis* seeds, unprepared green pea, mature red kidney bean, raw alfalfa seed, and raw cowpea. The species in the 2nd group were distributed on the positive sides of PC1 and PC2. Kaempferol and quercetin were located on the positive side of PC1 and PC2. However, isorhamnetin, luteolin, and myricetin were located on the negative side of PC1 and PC2. Proximity of the species to kaempferol and quercetin were strongly influenced on the closest species.



The average distance cluster analysis grouped the original 64 species into well defined phenotypes with 11 distinct flavonoid producing species. Clusters 1 and 6 represent 6 medium flavonoid producing *T. labialis* accessions (averaging 42.85 mg/100g). Clusters 2, 3, 4, and 5 represent very low flavonoid producing species including 7 horsegram, 1 each of common bean, black cowpea, red kidney bean, cowpea, white bean, pinto bean, broadbean, mungbean, green peas, snap beans, alfalfa seeds, soybean, and 10 lablab beans (averaging 3.31 mg/100 g), while cluster 7 shows 9 low flavonoid producing *T. labialis* accessions (20.73 mg/100g). Clusters 8, 9, and 10 represent 17 high flavonoid producing guar accessions (averaging 99.69 mg/100 g), but 2 guar accessions produced higher flavonoid concentration (averaging 181.31 mg/100 g).