

2019 Sensory Quality and Composition – MARS Progress Report

Supplemental Analysis to USDA - Market Quality and Handling Research Unit

Introduction

This project was developed to evaluate sensory quality and composition of the germplasm seed bank collected by the North Carolina State University (NCSU) peanut breeding project. These data will be used in making decisions on which germplasm to utilize in future crossing programs for the development of breeding lines with superior flavor and sensory quality attributes.

To keep the sensory improvement objective moving forward, sensory panel and other chemical analysis data needs to be collected on germplasm from the NCSU peanut breeding project. Currently, there is a collection of ~740 plant introductions (PI) and/or accessions in the NCSU germplasm seed bank. A subset of these lines (210) were selected as samples to submit for flavor, sensory and other chemical evaluations. The samples were roasted to a common color, ground to a paste and submitted to the USDA Market-Quality and Handling Research Unit (MQHRU) in the Department of Food, Bioprocessing and Nutrition Sciences. Flavor score data was returned by the USDA-MQHRU for analysis by the NCSU peanut breeding project

Analysis & Results

Categorizing the multivariate data collected by the USDA-MQHRU into flavor profile groups would ultimately aid in parental selection due to the correlations among the sensory attributes (Figure 1). When selecting genotypes for crossing, a priority is placed on roasted peanut flavor or sweetness; however, these high priority traits are often negatively or positively associated with traits of interest or unwanted traits, respectively. Therefore, the efforts of this initial analysis from the data provided on 6 January 2020, was simply to cluster the genotypes (naïve approach i.e. not taking into consideration the color disparities in testa color during the roasting process) based on similar sensory values and to later separate these groups statistically based on rank of the various sensory attributes. First, the genotypes were reacquainted with their germplasm names. The USDA-MQHRU was not provided with the line identities or knowledge of replication within the dataset prior to the flavor panel evaluations. The sensory attributes were filtered/reduced based on the variance associated with the scores across all genotypes (Table 1). Those sensory attributes with a variance <0.01 were dropped prior to clustering into flavor segments. In order to group the genotypes, a cluster analysis was performed with an associated principal component analysis (PCA) to visualize the differences among groups (Figure 1). The sensory attributes influencing each principal component (PC) were determined to name the PC based on contributing attributes (Table 2). The mean values of each of the flavor segments (cluster groups) were analyzed statistically with a post-hoc means separation test (Tukey's HSD, $\alpha=0.05$) to determine differences among the groups and likely candidates for selection within the flavor segment showing the greatest overall performance for sensory attributes generally (Table 3). After the

analysis of the flavor segments, the roasting color groups were appended to the group data to determine the results correlated strongly with the roasting color profiles determined by the USDA-MQHRU (Table 4)

GitHub Repository for Data Analysis and Storage

A GitHub repository was developed to store the active, completed dataset used in the analysis and the Jupyter Notebook annotated for the analysis of the flavor segments. These values can be modified to reduce the flavor segment sizes, change the principal components visualized or to statistically analyze additional sensory attributes that were not included in the flavor segmentation (Table x).

GitHub Repository
<https://github.com/jcdunne/Flavor>

***Follow the instructions in the README.md to run the completed analysis

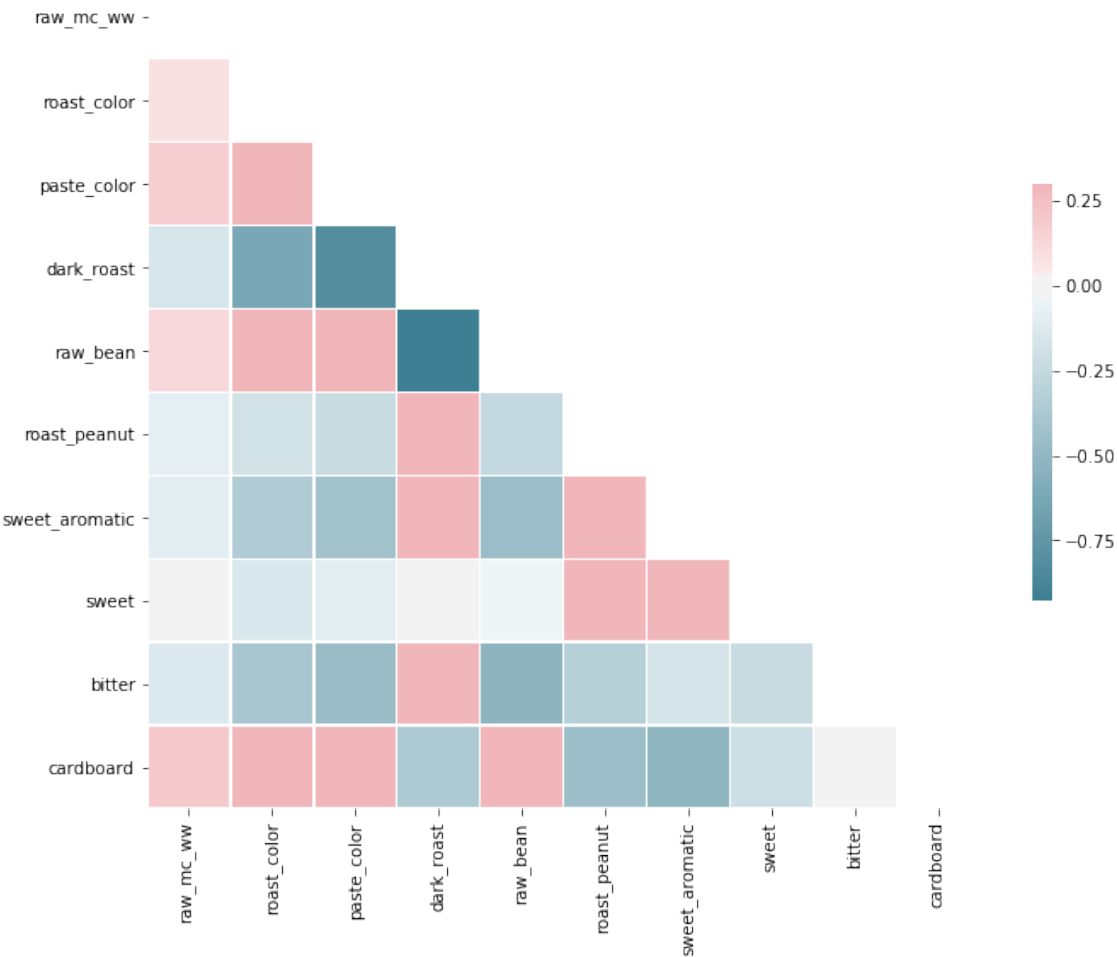


Figure 1. Correlation matrix for the sensory attributes used to determine the flavor segments in the cluster/principal component analysis.

Table 1. Variance associated with each of the sensory attributes provided by the USDA-MQHRU of the 210 lines screened in the USDA-MQHRU flavor panel.

Sensory Attribute	Variance
Paste Color	12.68
Roast Color	6.96
Mean Oil Content	4.10
Raw Moisture Content	0.32
Raw / Bean	0.26
Roast Peanut	0.25
Cardboard	0.24
Dark Roast	0.15
Sweetness	0.11
Sweet Aromatic	0.11
Bitterness	0.10
Spice	0.09
Wood Hulls Skins	0.04
Plastic / Chemical	0.04
Fruity Fermented	0.02
Tongue / Throat Burn	0.02
Painty	0.01
Metallic	0.01
Earthy	0.00
Astringent	0.00
Sour	0.00
Salty	0.00

*Sensory attributes with a variance <0.01 were not included in the flavor segmentation analysis

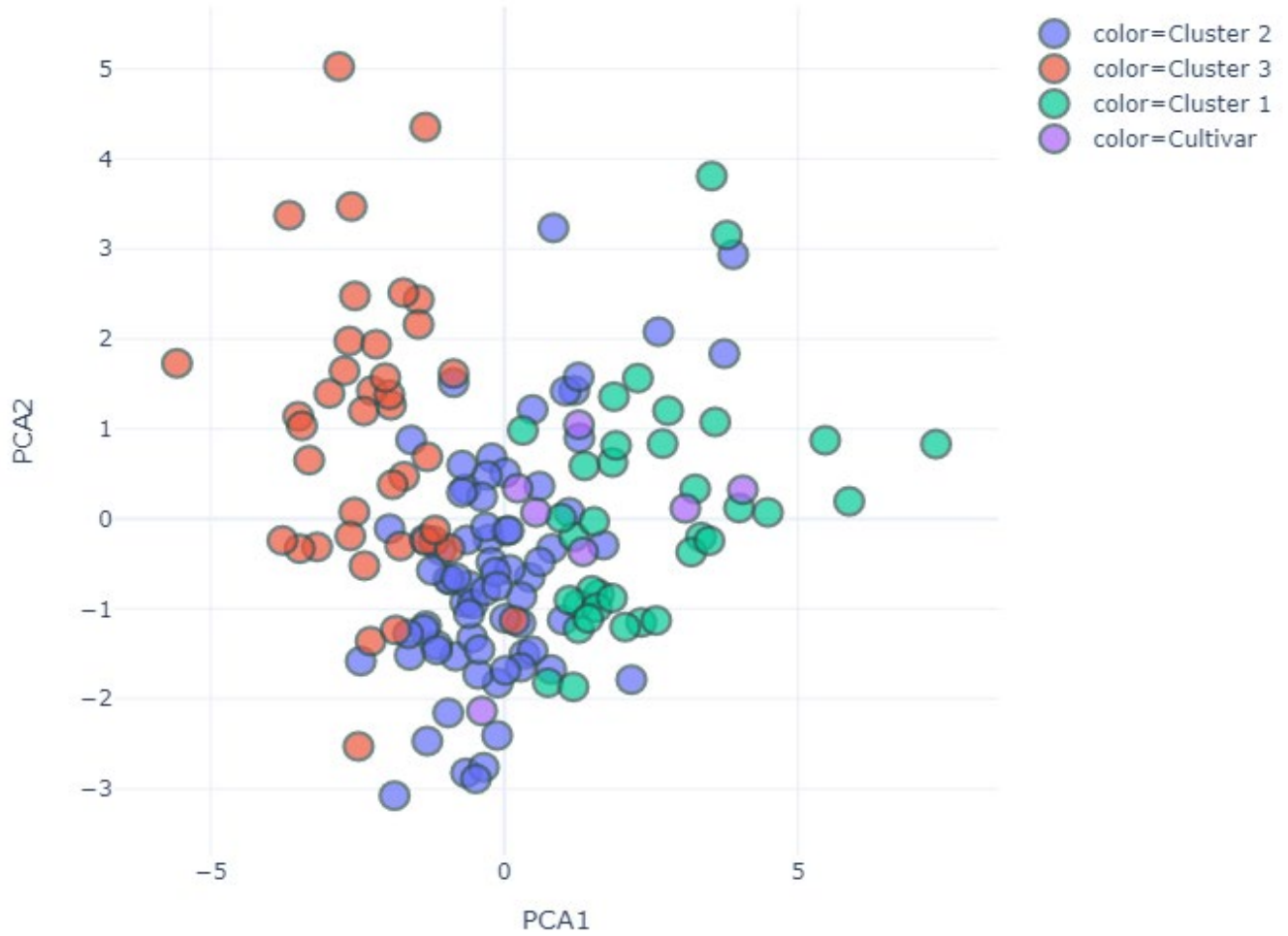


Figure 2. Principal Components (PCA1 & 2) separated based on flavor segmentation groupings of the 210-germplasm lines submitted to the USDA-MQHRU flavor panel.

Table 2. Percentage contributions of each sensory attribute to the named principal components used in the development of flavor segmentation grouping

Principal Components	Mean Oil	Raw Moisture	Roast Color	Paste Color	Dark Roast	Raw Bean	Roast Peanut	Sweet Aromatic	Sweetness	Bitterness	Cardboard	Variance Explained
Color (PCA1)	4.50%	10.40%	38.40%	43.40%	42.80%	42.10%	22.90%	31.70%	10.80%	19.60%	29.80%	40.00%
Flavor (PCA2)	13.20%	6.40%	12.90%	14.50%	14.80%	18.00%	48.60%	41.10%	39.30%	52.20%	23.40%	19.60%
Pre-roast (PCA3)	69.40%	66.60%	5.90%	2.80%	0.40%	2.50%	1.80%	9.40%	21.60%	6.50%	9.90%	13.70%
Sweet (PCA4)	11.40%	30.70%	25.20%	8.80%	22.90%	17.00%	37.00%	16.60%	73.70%	16.10%	8.00%	7.10%
Cardboard (PCA5)	2.30%	19.10%	33.70%	11.00%	25.60%	26.80%	11.10%	18.40%	33.50%	15.60%	71.90%	6.20%
Total												86.70%

Table 3. Mean separation testing among sensory attributes between the flavor segments and the check cultivars

Flavor Segment	Mean Oil	Raw Moisture	Roast Color	Paste Color	Dark Roast	Raw Bean	Roast Peanut	Sweet Aromatic	Sweetness	Bitterness	Cardboard
Cluster 1	50.40 AB*	4.91 B	47.72 c	53.28 A	3.41 A	1.49 B	3.54 A	3.05 A	2.99 AB	2.76 A	0.58 B
Cluster 2	51.40 A	4.89 B	52.76 A	49.95 B	2.79 c	2.28 A	3.27 B	2.79 B	2.87 B	2.45 B	1.04 A
Cluster 3	51.50 A	4.81 B	49.93 B	46.07 c	3.10 B	1.93 A	3.63 A	3.02 A	3.02 A	2.48 B	0.73 AB
Cultivar	48.90 B	6.67 A	50.86 B	51.79 B	2.98 BC	2.11 A	3.51 AB	2.92 AB	2.86 B	2.36 B	0.95 A

*Letters that differ are significantly different according to Tukey's HSD multiple comparison test ($\alpha = 0.05$)

Table 4. Percentage breakdown of color group separation as determined by the USDA-MQHRU among the flavor segments analyzed from data collected from the USDA-MQHRU flavor panel

Color Group	Flavor Segment			
	Cluster 1	Cluster 2	Cluster 3	Cultivar
Group 1	20.8%	0.0%	15.5%	0.0%
Group 2	18.8%	0.0%	14.7%	0.0%
Group 3	27.1%	4.9%	12.9%	0.0%
Group 4	31.3%	24.4%	35.3%	71.4%
Group 5	0.0%	17.1%	7.8%	14.3%
Group 6	2.1%	17.1%	10.3%	0.0%
Group 7	0.0%	36.6%	3.4%	14.3%

*Percentage reflects the 'Hi-Rep' color group determined by the USDA-MQHRU based on the Hunter colorimeter scores; Red denotes optimal color range (49.6-50.7)

Conclusions

Based on the initial results contained within this report, selections among each of the flavor segments must be made since there is not a clear difference among the top performing lines within each segment. The initial screen was primarily needed to subset the germplasm into 'good', 'moderate' and 'poor' flavor segments in which to conduct a more thorough sensory panel screen and to collect chemical and proteomic data. Although the flavor segment #1 & #3 show the highest overall quality among the sensory attributes used in the analysis, selections among the remaining flavor segment will be made to capture the best quality lines. The future directions of this research, above the aforementioned panel screen, would be to increase the seed source of each line selected (Table 5); employ a graduate student to begin making crosses to elite agronomic and disease resistant, Virginia- and runner-type lines for the development of a flavor specific cultivar development program (1. Population development for mapping and 2. Cultivar release for use in MARS candy production); and lastly to begin sequencing some of these lines for QTL-seq analysis of flavor-related markers for marker-assisted selection among the flavor improvement cultivar development program.

Line Information from Flavor Selections

NC Accession	Color Group	Mean Oil	Raw Moisture	Roast Color	Paste Color	Dark Roast	Raw Bean	Roast Peanut	Sweet Aromatic	Sweetness	Bitterness	Cardboard	Flavor Segment
Chimera	4	49.50	4.92	49.35	47.99	3.17	1.88	4.50	3.40	3.47	2.30	0.50	Cluster 1
NC Bunch	4	51.31	4.78	48.26	47.46	3.36	1.66	4.03	3.28	3.13	2.46	0.38	Cluster 1
PI 393641	4	49.77	4.47	48.00	46.72	3.33	1.26	3.85	3.33	3.57	3.10	0.40	Cluster 1
Tatu	4	48.40	4.79	50.83	53.85	2.73	2.20	3.84	2.90	2.97	2.33	1.15	Cluster 2
Spanish	4	48.24	5.28	51.27	52.82	2.77	2.19	3.70	3.04	3.36	2.27	0.65	Cluster 2
Sunbelt Runner	4	53.45	5.08	50.50	51.22	3.14	1.90	4.14	3.16	2.74	2.42	0.90	Cluster 3
Lupinus-Gigas	4	50.73	4.69	49.88	50.54	3.14	1.86	4.09	3.14	3.00	2.41	0.71	Cluster 3
PI 229553	4	50.42	5.06	50.54	51.32	3.04	1.99	4.03	3.41	3.47	2.27	0.60	Cluster 3
Short Valencia Ex Ec. 1	4	48.75	4.27	49.47	49.80	3.08	1.90	4.01	3.24	2.92	2.41	0.27	Cluster 3
Florunner component	4	52.61	5.11	49.81	51.03	3.12	1.85	3.98	3.27	3.39	2.13	0.42	Cluster 3
Tifton 8	4	51.61	4.29	49.27	48.65	3.12	1.90	3.98	3.28	3.37	2.24	0.40	Cluster 3
Normal Seg. DMC	4	51.13	5.12	49.75	48.19	3.21	1.77	3.94	3.23	3.10	2.50	0.51	Cluster 3
Ilex-Hedera	4	52.43	4.80	49.68	48.89	3.29	1.79	3.94	3.13	3.23	2.42	0.60	Cluster 3
Normal	4	50.56	4.74	50.04	49.57	3.14	1.96	3.88	3.18	2.96	2.48	0.71	Cluster 3
GK 7	4	55.19	4.43	50.37	48.90	2.99	2.03	3.86	3.03	3.12	2.25	0.50	Cluster 3
Florispán component	4	53.77	5.02	50.43	51.09	2.95	2.13	3.85	3.11	2.99	2.37	0.70	Cluster 3
PI 341839	4	52.06	4.37	49.91	50.17	3.12	1.80	3.83	3.27	3.10	2.94	0.75	Cluster 3