United States Department of Agriculture
Agricultural Research Service
National Plant Germplasm System

Morphometric Analysis of Cultivated Grape (*Vitis vinifera* L.)

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Introduction

To understand the genetic basis of phenotypes, especially economic phenotypes governed by polygenes, it is critical to accurately phenotype individuals. While currently massive amounts of genomic data are available, lack of accurate phenotypic data has become a serious impediment to develop genomics-assisted crop improvement programs, particularly in perennial and tree crop species. Accurate phenotyping of perennial crops is time consuming and resource intensive, especially when replicated, multi-year/location data are required to account for genotype-by-environment interactions. Knowledge of plant traits and their relationship with the economic traits and availability of high throughput capacity to phenotype are the essential for successful development of genomics-based breeding strategies.

We report here results of a numerical analysis on morphometric data collected in 2009 on a subset of cultivated grape germplasm collection representing wine, table and dual type cultivars. We analyze data to assess phenotypic variability, population structure, and to understand the genetic relationships among accessions.

Materials & Methods

A subset of 500 cultivated grape accessions representing the range of variability and geographic distribution of the cultivated grape (*V. vinifera*) from the germplasm collection maintained at the USDA Germplasm Repository, Davis, California is included in this study. A set of 25 nominal, ordinal, and metric traits (Table 1) from the 2009 evaluation of grape has been used to analyze phenotypic variability, population structure, and classify germplasm.

The nominal and ordinal data were coded as per Sneath and Sokal (1973) combined with the metric data, standardized, and analyzed to generate a pair-wise correlation matrix. A cluster analysis (CA) was performed on the correlation matrix using the neighbor-joining (NJ) algorithm to produce a phenogram depicting the phenotypic relationships among the cultivars (Fig. 1). Principal Components Analysis (PCA) along with 2D projection of accessions along the first principal axes (Fig. 2) accounting for 8 and 4.6 % of total variation, respectively, was used to further confirm the relationships and groups revealed in the CA.

The data were further analyzed for group-wise variability parameters such as mean, range, standard deviation, and coefficient of variation for different characters.

Table 1. List of descriptors used in the evaluation

Descriptor	Description
SKINCOLOR	Berry skin pigmentation - 1= yellow-green; 2=rose; 3=red; 4=red-gray; 5=dark red violet, 6=blue-black
FLESHCOLOR	Flesh color (yes/no)
FIRMNESS	Firmness of berry - 1=soft; 2=medium; 3=firm; 4=crisp
PETSINMALE	Petiolar sinus in mature leaf scored in 1-9 scale from wide open to very overlapping
SHOOTHABIT	Scored in 1-9 scale - 1=erect; 2=semi-erect; 5=horizontal; 7=semi-drooping; 9=drooping
LEAFLOBES	Number of leaf lobes - 1=entire; 2=three lobes; 3=five lobes; 4=seven lobes; 5=more than seven lobes
LEAFSHAPE	Leaf shape - 1=cordate; 2=wedge shaped; 3=pentagonal; 4=circular; 5=reniform; 6=other shapes
SHOOTCOLOR	color of upper surface 1=greeen, 2=green w/ bronze spots, 3=yellow, 4=yellow w/bronze spots, 5=copper yellow, 6=copper, 7=reddish, 9= other colors
SINUSTOOTH	has a tooth on side of petiolar sinus yes/no
NAKEDVEIN	has a naked vein on side of petiolar sinus yes/no
BERRYSHAPE	berrry shape 1=flat, 2=slightly flat, 3=roundish, 4=short elliptic, 5=ovate, 6=obtuse-ovate, 7=obovate, 8=cylindric, 9=long elliptic, 10=arched
BUDBURDATE	Days to bud burst expressed in Julian days
BLOOMDATE	Days to 50% bloom in Julian days
CLUSTLEN	Cluster length in cm.
CLUSTWID	Cluster width in cm.
PEDLENGTH	Pedicel length in cm.
CLUSTDEN	Cluster density scored in 1-9 scale from very loose to very dense
CLUSTWT	Average cluster weight in g.
BERRYWT	Average berry weight in g.
BERRYNO	Average number of berries/cluster
SEEDNUM	Average number of seeds/berry
SEEDWT	Average seed wieght in g.
BRIX	Brix reading using berry juice
ACIDITY	Titretable acidity
TIPANTHO	Anthocyanins of shoot tip scored 1-5 scale from very weak to very strong

Results and Discussion

- The cultivated grape collection possess significant amount of variability for all characters included in the study.
- Cluster and berry traits exhibited coefficient of variation ranging from 30 to well over 60 percent reflecting breeding value and scope for genetic improvement of grape for these traits.
- The CA revealed four major groups within the cultivated grape included in the analysis (Fig. 1) – Group 1 is mainly made up of table grapes along with some Southern European wine grapes often used in breeding of table grapes mostly from West and South Asia and Asia Minor, but some from Eastern and Southern Europe; Group 2 is mostly composed of European wine grapes; Group 3 is similar to Group 1 containing table grapes from Eastern Europe and East and West Asia along with some less known wine types from Southern and Eastern Europe; and Group 4 is predominantly wine grapes from Europe and occasionally a few table grapes and hybrids.
- The PCA elucidated groups more or less similar to the CA with groups 1 and 3 somewhat overlapping in both analyses.
- The four groups revealed in the cluster analysis differed for mean and coefficient of variation for all metric traits (Table 2).
- The plant traits used in the study did not clearly distinguish between table and wine grapes. However, both CA and PCA brought out some specific differences among groups with respect to the frequency and composition of wine, table and dual use type grapes.

Overall, the cultivated grape germplasm collection evaluated possess considerable phenotypic variability as suggested by the variability measures computed, which translates into the breeding value of the collection and the scope for genetic improvement of both wine and table grapes. The population structure based on the phenotypic traits may be somewhat different from the molecular traits and should not be neglected while developing genomics-based selection strategies.

Figure 1. Cluster analysis depicting the relationships among grape accessions

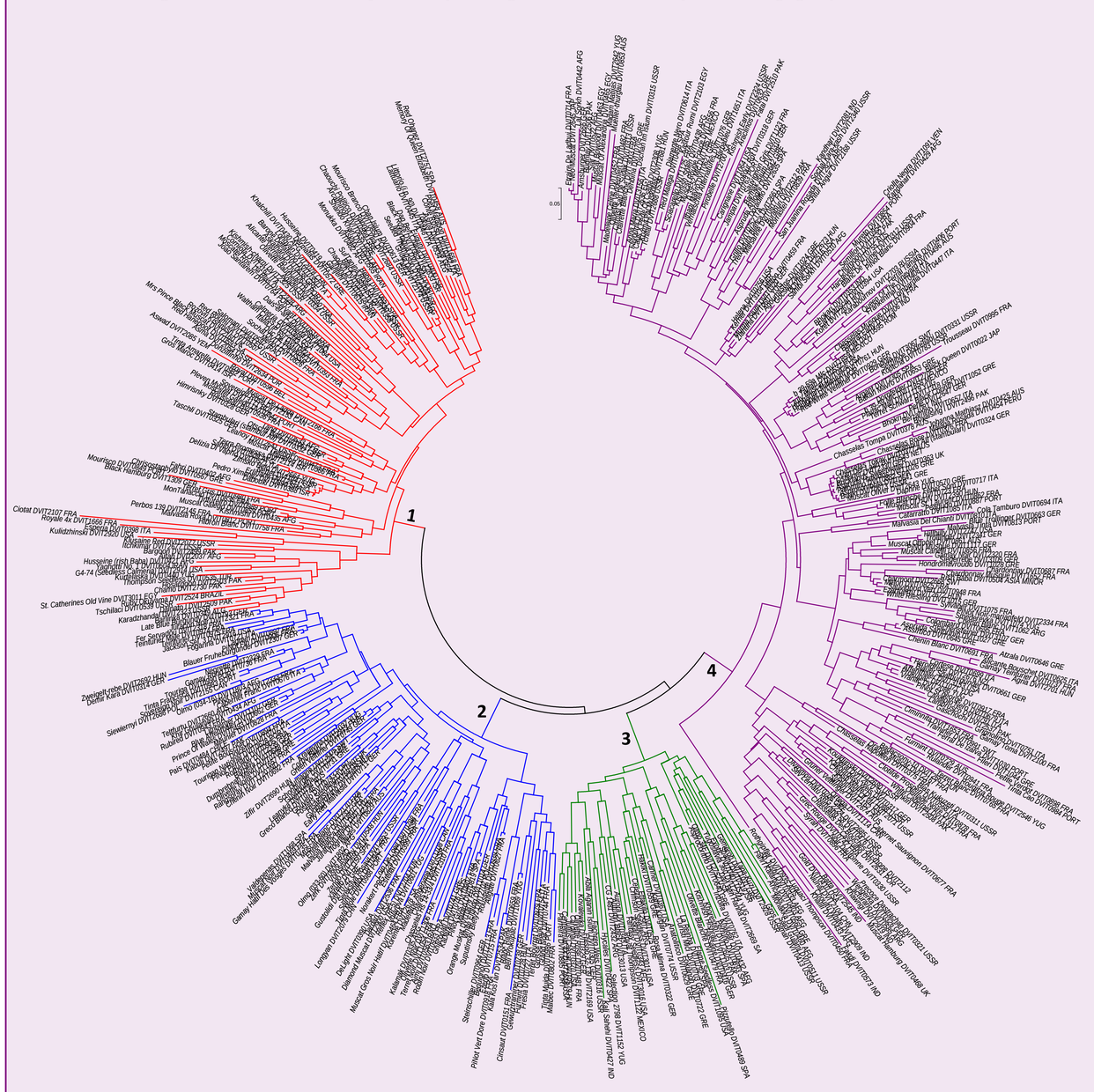

Figure 2. Principal components analysis
2D Projection of Grape Accessions
(Numbers in the Plot Refer to Clusters on NJ Tree in Fig. 1)

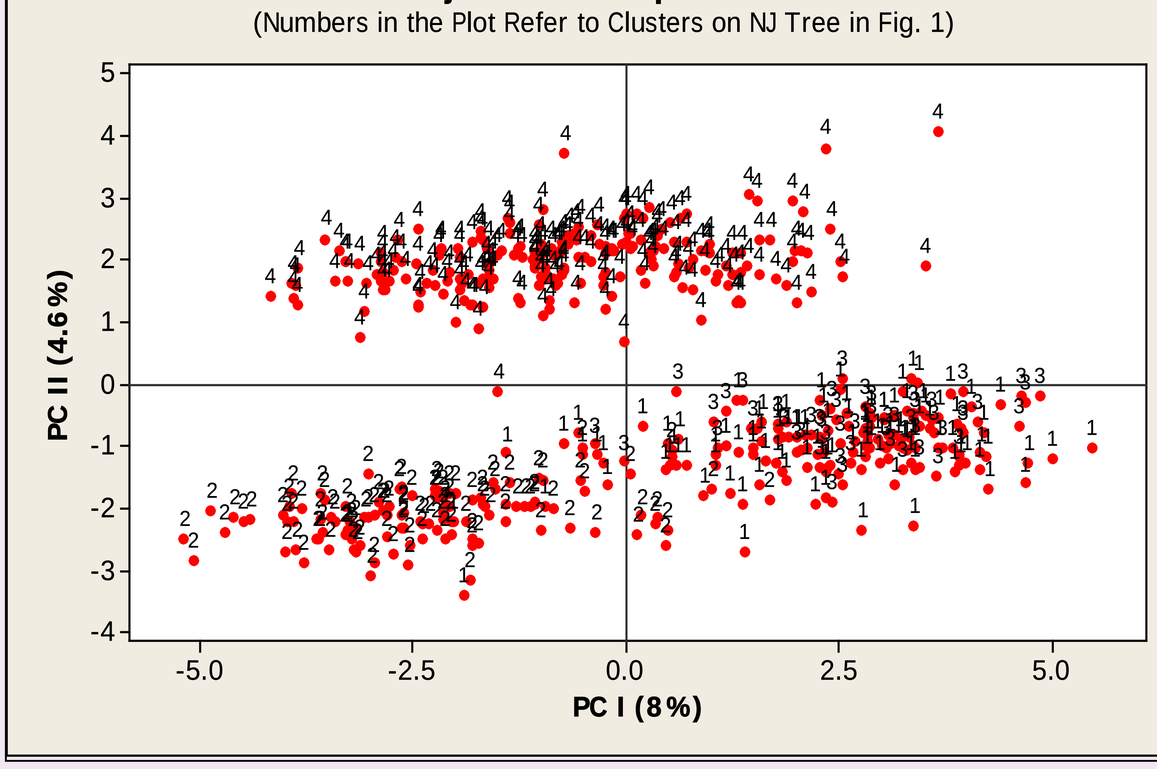

Table. 2 Variability parameters

Variable	GROUP	N	Range	Mean	SD	CV (%)
BUDBURST	G1	116	29	92.405±0.522	5.618	6.08
	G2	117	29	89.752±0.465	5.026	5.6
	G3	52	26	91.288±0.656	4.733	5.19
	G4	215	30	90.563±0.398	5.832	6.44
BLOOMDATE	G1	116	21	135.68±0.269	2.9	2.14
	G2	117	22	132.85±0.266	2.87	2.16
	G3	52	20	135.83±0.465	3.35	2.47
	G4	215	27	133.75±0.224	3.29	2.46
CLUSTLEN	G1	116	370	223.58±6.03	64.9	29.03
	G2	117	295.6	164.35±3.95	42.72	25.99
	G3	52	773	235.2±15	108.1	45.95
	G4	215	1217.41	195.88±7.21	105.66	53.94
CLUSTWDTH	G1	116	262.63	145.11±4.09	44.06	30.36
	G2	117	201.76	112.56±3.69	39.94	35.49
	G3	52	160	146.61±4.89	35.29	24.07
	G4	215	319.13	124.05±2.73	40.06	32.29
PEDLEN	G1	116	95	32.87±1.47	15.84	48.19
	G2	117	119	23.08±1.42	15.39	66.71
	G3	52	93	30.54±2.62	18.93	61.97
	G4	215	87	27.12±1.01	14.78	54.5
CLUSTDEN	G1	116	8	3.897±0.207	2.228	57.17
	G2	117	8	6.094±0.221	2.385	39.14
	G3	52	6	3.25±0.284	2.047	62.99
	G4	215	8	5.074±0.167	2.443	48.14
CLUSTWT	G1	116	2116.8	761.9±37.8	407.3	53.46
	G2	117	1412.4	455.5±24.9	269.2	59.1
	G3	52	1658.7	829.5±56.5	407.7	49.16
	G4	215	1693	558.8±22.6	331	59.23
BERRYWT	G1	116	16.138	6.842±0.303	3.264	47.71
	G2	117	10.72	3.454±0.167	1.81	52.4
	G3	52	15.878	8.253±0.534	3.851	46.67
	G4	215	15.282	4.601±0.164	2.406	52.31
BERRY#	G1	116	323.74	124.23±6.23	67.11	54.02
	G2	117	27678	378±236	2549	675.22
	G3	52	320.58	112.77±9.22	66.46	58.93
	G4	215	1967.9	142.6±10.4	151.8	106.48
SEED#	G1	116	3.3	1.8802±0.0722	0.7774	41.35
	G2	117	3.3	2.1923±0.0556	0.6017	27.45
	G3	52	3.3	1.573±0.121	0.872	55.45
	G4	215	3.7	2.1209±0.0383	0.5609	26.45
SEEDWT	G1	116	2	0.9103±0.0402	0.4325	47.51
	G2	117	533.8	5.46±4.56	49.27	902.06
	G3	52	1.7	0.8769±0.0643	0.4638	52.89
	G4	215	11.1	0.9349±0.0515	0.7548	80.74
BRIX	G1	116	26.2	19.698±0.252	2.717	13.79
	G2	117	13.8	20.568±0.205	2.215	10.77
	G3	52	11.7	19.788±0.337	2.429	12.28
	G4	215	15.1	20.389±0.148	2.164	10.62
ACIDITY	G1	116	1.017	0.499±0.0173	0.1862	37.32
	G2	117	1.077	0.6306±0.0189	0.2042	32.38
	G3	52	0.51	0.445±0.0169	0.1218	27.38
	G4	215	1.197	0.5666±0.0139	0.2045	36.09
TIPANTHO	G1	116	6	3.147±0.176	1.894	60.19
	G2	117	6	3.291±0.175	1.894	57.56
	G3	52	6	3.135±0.305	2.197	70.07
	G4	215	6	3.274±0.134	1.961	59.88

Reference

Sneath, P.H.A. and Sokal, R.R. 1973. Numerical Taxonomy – The Principles and Practice of Numerical Classification. W.H. Freeman & Co., San Francisco