Gelatinization and Retrogradation Traits of Starches from Argentinian Maize Inbred Lines: Patterns of Correlation Among Traits

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ABSTRACT

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Efforts are being made to identify sources of starches with unique end-use properties, such as thermal properties, within a wide array of maize germplasm. Because redundancy may exist when evaluating these traits, it would be useful to know the pattern of correlation among traits involved to focus the expensive stage of evaluation of germplasm on traits that do not provide redundant information. The objectives of this study were to analyze the pattern of correlations between starch gelatinization and retrogradation-associated traits in a group of 12 Argentine maize inbred lines and to develop predictive models among traits when possible. Traits measured by differential scanning calorimetry included gelatinization and retrogradation properties. Pearson correlation coefficients among starch thermal properties were determined from univariate analyses, and canonical correlations were determined from multivariate analyses. Canonical correlation analyses were more sensitive in detecting associations between starch gelatinization and retrogradation parameters than univariate analyses. Multiple regression equations to estimate the change in enthalpy of starch gelatinization and retrogradation traits, especially for change in enthalpy and percentage of retrogradation, were obtained and validated with an independent data set.

Efforts are being made to identify sources of unique starch properties within a wide array of maize germplasm (White et al 1990; Wang et al 1992, 1993a; Campbell et al 1995; Ng et al 1997; Pollak and White 1997; Seetharaman et al 2001; Ji et al 2004), which in turn would be related to the fine structure of the constituent polymers of starch (amylose and amylopectin) and the characteristics of the starch granules (size, crystallinity) (Banks and Greenwood 1975; Inouchi et al 1983; Zobel 1984; Yuan et al 1993; Shi and Seib 1995). Environment affects the expression of genes controlling thermal properties of starch (White et al 1991; Campbell et al 1994; Pollak and White 1997; Seetharaman et al 2001; Ji et al 2004; Eyhérabide et al 2006).

High correlation coefficients among starch thermal properties reported in the literature suggest that some level of redundancy may exist when evaluating these traits (Campbell et al 1994). Redundancy in traits might result from 1) genetic causes (pleiotropy and linkage disequilibrium), 2) similar responses to changes in environmental conditions, or 3) the way the traits are defined. The last cause, redundancy in the way the traits are defined, applies to gelatinization and retrogradation traits, which are defined as a function of other traits. For example, peak height index is a ratio between the enthalpy and the range of gelatinization temperature. In turn, gelatinization temperature is a function of onset and peak temperatures. The expression of any trait in an individual (phenotype) results from the effect of the genotype (array of genes that controls the trait), the effect of the environment, and the interaction between both effects. Contribution of each term to phenotype depends primarily on the trait. Genetic and phenotypic associations between the set of gelatinization traits as a whole and the set of retrogradation traits have not yet been reported. Considering that both groups of traits should depend on the composition and fine structure of the starch, which in turn affect the characteristics of starch granules, a strong association between both sets of traits is expected.

Breeders use field-plot techniques and statistical experimental designs to increase the correlation between phenotype and genotype. Mean phenotype across environments tends to be closer to the genotype because environmental effects tend to be cancelled out. When dealing with associations between two or more traits, their interpretations can also be made in terms of phenotypic and genotypic causes. Knowledge regarding correlations among traits is required in any breeding program because indirect responses to selection are present whenever genetic correlation exists. Indirect responses would be detrimental to the objectives of selection if positive genetic correlations occur between favorable and unfavorable traits. Nevertheless, a negative genetic correlation between favorable and unfavorable traits, or a positive correlation between favorable traits, implies a good scenario for selection. An indirect selection rather than a direct selection approach could be adopted advantageously depending on the magnitude of heritability and genetic correlation of traits. Furthermore, it would be useful to know the pattern of correlation of traits to focus the expensive stage of screening and evaluation of germplasm on those traits that do not provide redundant information and also to define more efficient selection indices to improve the aggregate genotype for starch thermal properties.

Since 2004, research in our Pergamino Agriculture Experiment Station has focused on evaluating maize genotypes using differential scanning calorimetry (DSC) parameters of gelatinization and retrogradation, which are of particular interest for commercial applications of starch. The objectives of this study were to analyze the pattern of correlations between starch gelatinization- and retrogradation-associated traits in a group of Argentine maize inbred lines and to develop predictive models among traits when possible.

MATERIALS AND METHODS

Plant Materials

A group of 12 inbred lines developed by INTA from a wide array of germplasm sources was used for this study (Table I; Eyhérabide et al 2006). Seeds of lines were planted in the breeding nursery to increase seed for a maximum of five and a minimum of three cropping seasons. Seeds were collected by hand, dried at room temperature until reaching a grain moisture equilibrium of ≈10%, exact values for each sample depending on its kernel characteristics, and stored in cold storage (8ºC) inside sealed plastic bags. Seeds were identified by the inbred line name and the crop season of seed increase. Traits measured in each seed type were starch thermal properties of gelatinization and retrogradation, including onset temperature of gelatinization (T_{oG}), peak temperature of gelatinization (T_{pG}), range of gelatinization temperature (R_G), change in enthalpy of gelatinization (ΔH_G), peak height index of gelatinization (PHI$_G$) defined as the relation ($2\Delta H_G/R_G$), onset

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temperature of retrogradation (T_{oR}), peak temperature of retrogradation (T_{pR}), range of temperature (R_R), change in enthalpy of retrogradation (ΔH_R), and percentage of retrogradation (P_R).

An independent data set of means of starch thermal properties of gelatinization and retrogradation for a group of 48 hybrid cultivars in each of three growing environments and across growing environments was utilized to validate multiple regression equations that were significant. Aliquots of grain from each hybrid and location combination were obtained and manipulated in the same way as those from inbred lines.

Analytical Procedures

Starch was extracted for DSC analysis from five randomly selected seeds per corn line using procedures previously developed by White et al (1990) and modified by Krieger et al (1997). Thermal properties of starch samples were evaluated by differential scanning calorimetry (Pyris 6 DSC, Perkin Elmer). The system works under nitrogen atmosphere and is equipped with thermal analysis software (Pyris Software for Windows v.6.5.0.008, Perkin Elmer). Analyses were performed in duplicate and average values were reported as indicated in Eyhérabide et al (2006).

Statistical Methods

Pearson correlation coefficients among starch thermal properties were determined from univariate analyses, and canonical correlations were determined from multivariate analyses. The canonical correlation analysis maximizes the chance of finding linear combinations of variables (canonical variates) from two sets of variables. The minimum number of original variables included in any one set determines the maximum number of possible canonical variates. Pairs of canonical variates are chosen successively in such a way that they are uncorrelated with the previous one (Johnson and Wichern 1988). For this study, two sets of variables were chosen: those corresponding to starch gelatinization (T_{oG}, T_{pG}, ΔH_G, PHI$_G$), and those corresponding to retrogradation (T_{oR}, T_{pR}, ΔH_R, P_R).

Pearson correlation coefficient analyses were determined by using the CORR procedure, and canonical correlations were determined by using the CANCORR procedure (SAS Institute, Cary, NC). R_G and R_R were not included in the canonical correlation analyses to avoid problems of singularity of starch gelatinization and starch retrogradation matrices. Two matrices of data were submitted to canonical correlation analysis: one corresponding to the complete set of single observations (line and crop season combinations), named phenotypic matrix; and the other corresponding to the least squares means of lines across environments, named genotypic matrix. For breeding purposes, the genotypic matrix is more useful because its elements are less biased by growing season effects. To validate prediction models, coefficients of determination were computed between actual and predicted data sets.

RESULTS AND DISCUSSION

Pearson Correlation Analyses

Phenotypic data. Analyses of correlations among starch thermal properties obtained from the complete data set (phenotypic observations) revealed high and significant ($P < 0.01$) Pearson correlation coefficients (Table I) between some starch gelatinization traits: PHI$_G$ and R_G (–0.83), T_{oG} and T_{pG} (0.78), T_{oG} and R_G (–0.73). For starch retrogradation properties, significant ($P < 0.01$) correlations were detected such between ΔH_R and P_R (0.67) and T_{oR} and R_R (–0.63). Pearson correlation coefficients between gelatinization and retrogradation properties were, on average, smaller than those reported above. Thus, the highest correlation was found between ΔH_G and ΔH_R (0.54; $P < 0.01$), followed by that between PHI$_G$ and ΔH_R (0.51; $P < 0.01$). (Table I).

Genotypic data. Analyses of correlations among starch thermal properties obtained from the least squares means for lines across environments revealed several high and significant ($P < 0.01$) Pearson correlation coefficients between starch gelatinization traits (Table I): between PHI$_G$ and R_G (–0.96), T_{oG} and PHI$_G$ (0.92), T_{oG} and R_G (–0.88), T_{oG} and T_{pG} (0.87). Wang et al (1992) found few correlation coefficients higher than 0.5 between gelatinization traits, but a high correlation between ΔH_G and T_{oG} in single mutant inbred lines. Our results revealed a different pattern of correlations, possibly as a result of differences in genetic background (Sanders et al 1990). For starch retrogradation properties, significant correlations were detected between several traits: ΔH_R and P_R (0.86; $P < 0.01$), R_R and P_R (–0.69; $P < 0.05$), T_{oR} and P_R (0.67; $P < 0.05$). As for the phenotypic data, Pearson correlation coefficients between gelatinization and retrogradation properties were, on average, less than those reported above. The greatest correlation was found between T_{pG} and ΔH_R (0.64; $P < 0.05$), followed by those between ΔH_G and ΔH_R (0.53; $P < 0.10$), T_{oG} and ΔH_R (0.51; $P < 0.10$), and T_{oG} and T_{pR} (0.50; $P < 0.10$).

The pattern of correlation suggests that lines with greater T_{oG} tended to have greater T_{pG} and PHI$_G$. This last association could be explained by the negative association between T_{oG} and R_G. Inbred lines with greater T_{pG} tended to have greater ΔH_G and smaller R_G. This fact could explain the negative association with PHI$_G$. Similar to lines with higher T_{oG}, lines with greater T_{pG} would present greater ΔH_R. PHI$_G$ was defined as the ratio $2\Delta H_G/R_G$. Lines with the greatest PHI$_G$ mean values would be those with the smallest R_G mean values because both terms of that ratio would not be correlated (–0.20ns), and R_G is the denominator of PHI$_G$. Lines with greater ΔH_G also tended to have greater ΔH_R.

Lines with greater T_{oR} tended to have greater T_{pR} and P_R, but lesser R_R. Lines with greater T_{pR} tended to have greater T_{oR}, whereas lines with greater R_R had lesser P_R. Lines with greater ΔH_R tended to have greater P_R. The R_G was not correlated with any retrogradation traits.

TABLE I

Correlations Among Observed Values of a Group of Inbred Lines Cultivated in Different Crop Seasons for Starch Thermal Properties Based on Phenotypic Data (Above Diagonal) and Least Squares Means for Lines Across Environments (Below Diagonal)[a–c]

Trait	T_{oG}	T_{pG}	R$_G$	ΔH_G	PHI$_G$	T_{oR}	T_{pR}	R_R	ΔH_R	P_R
T_{oG}		0.78***	–0.73***	–0.04ns	0.58***	0.15ns	0.31**	0.11ns	0.28**	0.34***
T_{pG}	0.87***		–0.14ns	–0.12ns	0.09ns	0.22*	0.38***	0.09ns	0.12ns	0.23*
R_G	–0.88***	–0.54*		–0.08ns	–0.83***	–0.00ns	–0.08ns	–0.07ns	–0.32**	–0.29**
ΔH_G	0.46ns	0.60**	–0.20ns		0.58***	–0.05ns	0.03ns	0.07ns	0.54***	–0.26*
PHI$_G$	0.92***	0.66**	–0.96***	0.40ns		–0.06ns	0.09ns	0.14ns	0.51***	0.06ns
T_{oR}	0.34ns	0.35ns	–0.24ns	–0.20ns	0.13ns		0.51***	–0.63***	0.30**	0.39***
T_{pR}	0.50*	0.44ns	–0.45ns	0.13ns	0.40ns	0.59**		0.33**	0.20ns	0.20ns
R_R	0.12ns	0.04ns	–0.18ns	0.37ns	0.26ns	–0.56*	0.34ns		–0.15ns	–0.25*
ΔH_R	0.51*	0.64**	–0.26ns	0.53*	0.29ns	0.48ns	0.15ns	–0.40ns		0.67***
P_R	0.32ns	0.39ns	–0.18ns	0.03ns	0.09ns	0.67**	0.09ns	–0.69**	0.86***	

[a] Gelatinization properties: onset temperature, T_{oG}; peak temperature, T$_{pG}$; range of temperature, R_G; peak height index, PHI$_G$; change in enthalpy, ΔH_G.

[b] Retrogradation properties: onset temperature, T$_{oR}$; peak temperature, T_{pR}; range of temperature, R_R; change in enthalpy, ΔH_R; % of retrogradation, P$_R$.

[c] ***,**,* Indicate significance at $P < 0.01$, $P < 0.05$, and $P < 0.10$; ns indicates not significant.

Patterns of phenotypic and genotypic correlations from univariate analyses. General patterns of correlations among gelatinization traits and retrogradation traits revealed by univariate analyses from the phenotypic data were similar to those obtained from the genotypic data. However, absolute values for the Pearson correlation coefficients between T_{oG} with T_{pG}, R_G, or PHI_G were greater when least squares means of lines across environments were considered. There was a strong association between T_{oG} and T_{pG}. Lines that had higher T_{oG} exhibited narrower R_G and taller thermograms. Lines with higher T_{pG} also had narrower R_G, taller thermograms, and greater ΔH_G. Analyses of correlation from the matrix of genotypic data detected significant correlations between traits that were declared nonsignificant using the matrix of phenotypic data. Possibly this finding could be a result of the contribution of environment to the total phenotypic correlation.

Univariate analyses of the pattern of correlations among gelatinization traits with retrogradation traits from phenotypic and genotypic data showed very few cases with correlation coefficients of ≈0.5. In general, higher Pearson correlation coefficients were found when using genotypic data than when using phenotypic data, but just a few of them were declared significant: T_{oG} and T_{pR} (0.50; $P < 0.05$), T_{oG} and ΔH_R (0.51; $P < 0.05$), ΔH_G and ΔH_R (0.53; $P < 0.05$), and T_{oG} and ΔH_R (0.64; $P < 0.01$).

Canonical Correlation Analyses

Phenotypic data. Univariate multiple regression analyses for predicting gelatinization variables indicated that ΔH_G and PHI_G could be predicted (adjusted-R^2 0.99 and 0.37, respectively) from the retrogradation variables, especially ΔH_R and P_R. Multiple regression equations are

$$\Delta H_G = 0.02\ T_{oR} - 0.02\ T_{pR} + 1.29\ \Delta H_R - 1.13\ P_R$$

$$\text{and } PHI_G = -0.19\ T_{oR} + 0.11\ T_{pR} + 0.84\ \Delta H_R - 0.45\ P_R$$

Multiple regression coefficients for ΔH_G and PHI_G on ΔH_R and P_R were all significant ($P < 0.01$). Coefficients of determination between predicted and actual data obtained from the validation data set were 0.99 for ΔH_R and 0.21 for P_R.

Univariate multiple regression analyses for predicting retrogradation variables indicated that ΔH_R and P_R could be predicted (adjusted-R^2 0.37 and 0.16, respectively) from the gelatinization variables. Multiple regression equations are

$$\Delta H_R = 1.16\ T_{oG} - 0.63\ T_{pG} + 0.87\ \Delta H_G - 0.63\ PHI_G$$

$$\text{and } P_R = 1.19\ T_{oG} + 0.76\ T_{pG} + 0.14\ \Delta H_G - 0.77\ P_G$$

Multiple regression coefficients for ΔH_R with T_{oG} and ΔH_G were significant ($P < 0.10$ and $P < 0.01$, respectively), whereas the multiple regression coefficient for P_R with T_{oG} was significant ($P < 0.10$).

Values for the first canonical variates for starch gelatinization (G_1) were highly dependent on ΔH_G (0.98; Table II). High values of ΔH_G determined high values for G_1. On the other hand, the first canonical variate for starch retrogradation (R_1) was mostly affected by ΔH_R and P_R. High values for R_1 resulted from high values for ΔH_R and small values for P_R. Coefficients for the second canonical variate for starch gelatinization (G_2) suggested a contrast between both T_{oG} and ΔH_G with T_{pG} and PHI_G. Coefficients for the second canonical variate for starch retrogradation (R_2) showed a positive association with T_{pR} and P_R. The association of starch gelatinization and starch retrogradation with their respective canonical variates also is reflected in the correlation coefficients (Table III). Canonical correlations between G_1 and R_1, and between G_2 and R_2 were 0.99 and 0.45, respectively.

The canonical correlation between G_1 and R_1 was higher than any simple correlation coefficient between pairs of gelatinization and retrogradation original traits. The first two canonical variates for starch gelatinization explain 80% (34 + 46%) of the total standardized variance for starch gelatinization, whereas the first two canonical variates for retrogradation traits accumulate only 54% (9 + 45%) of the total standardized variance for starch retrogradation. On the other hand, the first two canonical variates for starch gelatinization explain 43% (34 + 9%) of the total standardized variance for starch retrogradation, and the first two canonical variates for retrogradation traits explain only 18% (9 + 9%) of the total standardized variance for starch gelatinization.

Genotypic data. Univariate multiple regression analyses for predicting gelatinization variables indicated that ΔH_G and T_{pG} could be predicted (adjusted-R^2 0.99 and 0.40, respectively) from the retrogradation variables, especially ΔH_R and P_R. Multiple regression equations are

$$\Delta H_G = -0.09\ T_{oR} + 0.04\ T_{pR} + 1.92\ \Delta H_R - 1.56\ P_R$$

$$\text{and } T_{pG} = 0.15\ T_{oR} + 0.24\ T_{pR} + 1.18\ \Delta H_R - 0.75\ P_R$$

Regression coefficients for ΔH_G with ΔH_R and P_R were both significant ($P < 0.01$), and regression coefficients for T_{pG} with ΔH_R was significant ($P < 0.10$). The coefficient of determination between predicted and actual data obtained from the validation data set was 0.98 for ΔH_G.

Univariate multiple regression analyses for predicting retrogradation variables indicated that ΔH_R and T_{oR} could be predicted (adjusted-R^2 0.42 and 0.30, respectively) from the gelatinization variables. Multiple regression equations are

$$\Delta H_R = 3.35\ T_{oG} - 1.16\ T_{pG} + 0.62\ \Delta H_G - 2.29\ PHI_G$$

$$\text{and } T_{oR} = 3.14\ T_{oG} - 0.83\ T_{pG} - 0.29\ \Delta H_G - 2.11\ PHI_G$$

The multiple regression coefficient for ΔH_R with PHI_G was significant ($P < 0.10$). Other multiple regression coefficients for T_{oR} with gelatinization variables were not significant.

Values for the first canonical variates for starch gelatinization (G_1) were highly dependent on ΔH_G (Table IV). High values of ΔH_G determine high values for G_1. The first canonical variate for starch retrogradation (R_1) was mostly affected by ΔH_R and P_R. The greatest values for R_1 result from high values for ΔH_R and low values for P_R. Coefficients for the second canonical variate for starch gelatinization suggest a contrast between both T_{oG} and ΔH_G with T_{pG} and PHI_G. Coefficients for the second canonical variate for starch retrogradation (R_2) showed a positive association with T_{pR} and P_R. The canonical correlations between G_1 and R_1 and between G_2 and R_2 were 0.99 and 0.77, respectively (Table V), which were greater than any coefficient of correlation between pairs of original retrogradation and gelatinization traits.

Square roots of canonical correlation coefficients indicated a large shared variance between both sets of traits. The first two canonical variates for starch gelatinization explain 64% (43 + 21%) of the total standardized variance for starch gelatinization, whereas the first two canonical variates for retrogradation traits explain 65% (8 + 57%) of the total standardized variance for starch retrogradation. On the other hand, the first two canonical variates for starch gelatinization explain 57% (43 + 14%) of the total standardized variance for starch retrogradation, and the first two canonical variates for retrogradation traits explain 48% (8 + 40%) of the total standardized variance for starch gelatinization.

Patterns of phenotypic and genotypic correlations from multivariate analyses. Canonical correlation analyses from phenotypic and genotypic data allowed the determination of two pairs of variates that explained a high percentage of the variance for traits and revealed a high correlation of gelatinization traits with retrogradation traits that was not revealed by the magnitude of the Pearson correlation coefficient. The estimated correlation coefficients between G_1 with R_1 and G_2 with R_2 were greater than the single correlation coefficients between any gelatinization trait with any retrogradation trait (Table I). Canonical variates obtained from both phenotypic and genotypic data sets had similar relative

TABLE II
Standardized Canonical Coefficients for Starch Gelatinization and Starch Retrogradation Variables Associated with the First Two Gelatinization (G_1 and G_2) and Retrogradation (R_1 and R_2) Canonical Variates, Considering Thermal Starch Properties[a]

		Canonical Variates			
Process	**Traits**	G_1	G_2	R_1	R_2
Gelatinization	T_{oG}	–0.04	2.03		
	T_{pG}	0.04	–0.61		
	ΔH_G	0.98	0.56		
	PHI_G	0.04	–0.98		
Retrogradation	T_{oR}			0.01	–0.17
	T_{pR}			–0.01	0.66
	ΔH_R			1.30	0.22
	P_R			–1.13	0.57

[a] Abbreviations defined in Table I.

TABLE III
Correlations Between T_{oG}, T_{pG}, ΔH_G, PHI_G, T_{oR}, T_{pR}, ΔH_R, and P_R with Gelatinization (G_1 and G_2) and Retrogradation (R_1 and R_2) Canonical Variates and Their Canonical Correlation Obtained from Phenotypic Correlation Matrix[a]

	Gelatinization Canonical Variables		Retrogradation Canonical Variables	
Variables	G_1	G_2	R_1	R_2
T_{oG}	–0.02	0.97		
T_{pG}	–0.11	0.82		
ΔH_G	0.99	–0.01		
PHI_G	0.59	0.48		
T_{oR}			–0.05	0.46
T_{pR}			0.03	0.73
ΔH_R			0.55	0.68
P_R			–0.26	0.78
R_1	0.99	0.00		
R_2	0.00	0.45		

[a] Abbreviations defined in Table I.

TABLE IV
Standardized Canonical Coefficients for Starch Gelatinization and Starch Retrogradation Variables Associated with the First Two Gelatinization (G_1 and G_2) and Retrogradation (R_1 and R_2) Canonical Variates, Considering the Thermal Starch Properties (Least Squares Means for Lines Across Environments[a]

		Gelatinization Canonical Variables		Retrogradation Canonical Variables	
Process	**Traits**	G_1	G_2	R_1	R_2
Gelatinization	T_{oG}	–0.09	5.63		
	T_{pG}	0.02	–2.06		
	ΔH_G	1.00	0.11		
	PHI_G	0.07	–3.55		
Retrogradation	T_{oR}			–0.10	–0.15
	T_{pR}			0.03	0.66
	ΔH_R			1.92	–0.25
	P_R			–1.58	1.08

[a] Abbreviations defined in Table I.

TABLE V
Correlations Between T_{oG}, T_{pG}, ΔH_G, PHI_G, T_{oR}, T_{pR}, ΔH_R, and P_R with Gelatinization (G_1 and G_2) and Retrogradation (R_1 and R_2) Canonical Variates, and Their Canonical Correlation, Obtained from the Genotypic Correlation Matrix (Least Squares Means for Lines Across Environments)[a]

	Gelatinization Canonical Variables		Retrogradation Canonical Variables	
Variables	G_1	G_2	R_1	R_2
T_{oG}	0.45	0.60		
T_{pG}	0.66	0.59		
ΔH_G	1.00	0.02		
PHI_G	0.40	0.33		
T_{oR}			–0.21	0.84
T_{pR}			0.13	0.63
ΔH_R			0.52	0.71
P_R			0.01	0.82
R_1	0.99	0.00		
R_2	0.00	0.77		

[a] Abbreviations defined in Table I.

weights for the original gelatinization and retrogradation traits. Scores for the first canonical variates were dominated by ΔH_G (gelatinization) and ΔH_R and P_R (retrogradation) (Tables II and IV). Scores for the second canonical variates would be greater for lines with greater T_{oG} and ΔH_G and lesser T_{pG} and PHI_G (gelatinization), and for lines with greater T_{pR} and P_R (retrogradation). Considering genotypic data, the first gelatinization variate (G_1) that explained a high percentage of the variance accounted for all the gelatinization traits (43%) was highly correlated (0.99) with the first retrogradation variate (R_1) that explained a low percentage of the variance accounted for the retrogradation traits taken as a whole (8%). In turn, the second gelatinization variate (G_2) that explained a low percentage of the standardized variance accounted for all the gelatinization traits (21%) was highly correlated (0.77) with the first retrogradation variate (R_1) that explained a greater percentage of the standardized variance accounted for the retrogradation traits taken as a whole (57%). It could be speculated that this different pattern of explained variance between the two pairs of variates might reflect the presence of two sets of genes, both affecting gelatinization and retrogradation of starch, but each set of genes has a stronger effect on starch gelatinization or on starch retrogradation.

CONCLUSIONS

Canonical correlation analysis was more informative than univariate analysis for detecting associations between starch gelatinization and retrogradation processes. Results obtained from the canonical correlation analysis also suggested that genetic and environmental factors that influence gelatinization parameters also affect retrogradation parameters. A hierarchical order of gelatinization and retrogradation traits might be inferred from data, indicating their significance to the first canonical variates. For example, ΔH_G seems to be of paramount importance because this variable was the major contributor to G_1, which explained almost half (43%) of the standardized variance for starch gelatinization. Similarly, both T_{pR} and P_R made an important contribution to R_2, which in turn explained almost 45% of the standardized variance for retrogradation. Predicting starch gelatinization-associated traits from retrogradation-associated traits reached high enough determination coefficients for practical use only for ΔH_G. The validation using an independent data set confirmed the feasibility of predicting ΔH_G from retrogradation traits, mainly ΔH_R and P_R. Unfortunately, the data did not provide a screening advantage regarding DSC analytical procedures. For practical purposes, a prediction of retrogradation traits from gelatinization traits would have been the most helpful because the gelatinization process must be accomplished first, before retrogradation can be measured; thus, time spent on retrogradation tests could be eliminated and substituted by a correlation formula.

Because maize is the most important raw material for starch manufacturing, much effort is given to improving its quantity and quality through breeding. Although detailed information about the relationship between the structural and functional properties of starches is needed to provide direction for genetic modifications, the results reported here will streamline data analyses by identifying redundant DSC parameters. Similarly, information on the hierarchical order of contribution of each parameter demonstrates which DSC parameters are the most important contributors to G_1 and R_2.

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