JOURNAL OF AGRICULTURAL AND FOOD CHEMISTRY

Genotype, Location, and Year Influence Antioxidant Activity, Carotenoid Content, Phenolic Content, and Composition in Specialty Potatoes

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The influence of genotype, location, and year on antioxidant activity (AOA), total phenolics (TP), total carotenoids (TC), and phenolic composition was studied using specialty (colored) potatoes (*Solanum tuberosum* L.) from the Texas Potato Variety Development Program. Twenty-five potato genotypes were grown at two Texas locations (McCook and Dalhart) and in two years (2003 and 2004). The AOA, TP, and TC differed significantly with genotype (G), location (L), and year (Y). Phenolic composition differed significantly among genotypes and between locations. The AOA, TP, and chlorogenic acid content were significantly correlated with one another. Genotypic effects were significant for all parameters measured and were larger than location and year effects. Interaction effects (G × L and G × L × Y) were significant for most parameters, but were relatively smaller than genotypic effects. Lutein and violaxanthin were the major carotenoids identified, and genotypes differed significantly in their carotenoid content. Genotypes CO112F2–2P/P and ATTX98013–1R/R were stable between locations and years with high AOA and TP, suggesting that they could be used as parents in breeding varieties with improved health benefits.

KEYWORDS: Antioxidant capacity; phenolics; carotenoids; *Solanum tuberosum*

INTRODUCTION

Numerous epidemiological studies suggest that consumption of fruits and vegetables is associated with a reduced risk of various diseases (*1*–*3*). Bioactive compounds in fruits and vegetables that cause reduction in oxidative stress are responsible for these protective effects (*4*). Consumer awareness of the disease preventive role of antioxidants and their concerns about the safety of synthetic antioxidants promotes the preference for natural antioxidants from fruits and vegetables (*5*). In addition, synergistic effects of bioactive compounds in whole foods provide better protection against diseases than synthetic single-nutrient supplements (*3, 6*).

Potato (*Solanum tuberosum L.*) is the leading vegetable crop in the US, with a per capita consumption of about 137 pounds (*7*). Specialty (colored) potato tubers are high in antioxidant activity (AOA); total phenolics (TP), with content ranging from 530 to 1770 μg/g (*8*); and total carotenoids (TC), ranging from 97 to 536 μg/100 gfw (*9*). Major tuber polyphenols include chlorogenic acid (CGA), caffeic acid (CA), scopolin, ferulic acid (FA), and cryptochlorogenic acid, with the skin containing approximately double the amount of that in tuber flesh (*10*). Potato peel contains 50% chlorogenic acid and 41% gallic acid (*11*). Lutein, zeaxanthin, neoxanthin, violaxanthin, and lutein-5,6-epoxide are the major carotenoids identified in highly pigmented genotypes (*12*).

Varieties differ in their total phenolic content, with Russet Norkotah and Granola showing 2-fold higher concentration than Yukon Gold (*8*). Along with genotype, environment also influences total phenolic and carotenoid levels. Greater total phenolic content has been observed in higher, cooler, and more humid regions with less fertile sandy loams, as compared to lower, warmer, and drier regions with fertile loamy soils, with varietal influence much more pronounced than locality (*13*). Significant differences among environments and genotypes for carotenoids have been reported (*14, 15*). Earlier studies (*13*–*16*) reported the effects of environment on total phenolics and carotenoids, but no information has been found on the effect of location and year on individual potato phenolics (phenolic composition) and the percent contribution of genotype, location, year, and their interactions on AOA, TP, and phenolic composition.

Therefore, the objectives of this study were (1) to evaluate the effects of genotype, location, and year on AOA, TP, TC, and phenolic composition of 25 specialty potato genotypes from the Texas Potato Variety Development Program grown near McCook and Dalhart, Texas; (2) to identify the genotypic effects on carotenoid composition; and (3) to determine the relative

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10.1021/jf071543w CCC: $37.00
Published on Web 08/31/2007

Table 1. Parentage and Tuber Characteristics of 25 Specialty Potato Genotypes

genotype[a]	skin color	flesh color	tuber shape	parentage
ATTX98013–1	red	red	oblong	A83360 × MAZAMA
ATTX961014–1	red	yellow	oblong	A90601–2R × MAZAMA
ATTX96750–1	white	yellow	round	A90601–2R × CO86218–2R
ATTX98012–5	red	yellow	round	A95053–55 × A93156–3
ATTX98444–16	red	yellow	oblong	A83360–9R × T48YF
ATTX98444–4	yellow	yellow	oblong	A83360–9R × T48YF
ATTX98462–3	reddish yellow	reddish yellow	oblong	ATD251–5RY × BO811–13RY
ATTX98491–3	yellowish red	yellow	round	P94A2–3Y × A92657–1R
ATTX98493–1	red	yellowish red	round	P94A2–3Y × BO811–13RY
ATTX98500–2	purple	yellow	oblong	P94A2–4Y × Granola
ATTX98500–4	purple	yellow	oblong	P94A2–4Y × Granola
ATTX99325–1	red	yellow	oblong	AGRIA × W1100R
CO111F2–1	purple	purple	oblong	ND2008–2 × All Blue
CO112F2–2	purple	purple	oblong	ND2008–2 × All Blue
CO141F2–1	purple	purple	oblong	ND2008–2 × All Blue
CO142F2–1	red	red	oblong	ND2008–2 × ND3574–5R
COTX00104–2	purple	yellow	round	ND3574–5R × CO86218–2
COTX00104–4	red	yellow	round	ND3574–5R × CO86218–2
COTX99086–4	yellowish red	yellow	oblong	AC91848–2 × CO89097–2
COTX99338–1	yellowish red	yellow	long	Russet Nugget × Crispin
NDTX4528–3	purple	purplish white	long	3581–3 × 3276–1
NDTX4528–4	purple	purplish white	long	3581–3 × 3276–1
NDTX4528–4B	purple	purplish white	long	3581–3 × 3276–1
PATX99P32–2	reddish yellow	yellowish red	round	PA96RR01–220 × All Red
PATX99P41–1	reddish yellow	yellowish red	round	PA96RR01–120 × N40–1

[a] ATTX, cross made in Aberdeen, ID, and selected in Texas; CO, cross made and selected in Colorado; COTX, cross made in Colorado and selected in Texas; NDTX, cross made in North Dakota and selected in Texas; PATX, cross made in Prosser, WA, and selected in Texas.

Table 2. Climatic Conditions and Physical and Chemical Characteristics of Soils at Two Texas Locations (McCook and Dalhart)[a]

	temp (°C)[b]								Kg/ha			
location	min	max	rain fall (mm)[b]	Soil type	CEC	pH	EC (mmho/cm)	OM (%)	N	P	K	plant/harvest
McCook	10.7	23.6	1.5	McAllen sandy loam	15.0	6.5	0.1	0.3	11.7	50.7	98.7	Dec/April
Dalhart	14.4	30.2	2.5	Tivoli fine sand	5.5	7.1	0.1	1.1	13.4	35.2	282.4	May/Oct

[a] CEC = cation exchange capacity, EC = electrical conductivity (soluble salts), OM = organic matter, N = nitrate nitrogen, P = total phosphorus, K = total potassium, Plant/harvest = planting and harvesting. [b] Average per location per year from planting to harvest. Crops were produced under center pivot irrigation as required.

contributions of genotype, location, year, and their interactions on these parameters in specialty potatoes.

MATERIALS AND METHODS

Materials. Three-hundred-twenty specialty potato genotypes from the Texas Potato Variety Development Program were screened for their antioxidant activity, phenolic content, and carotenoid content. The top 25 genotypes (**Table 1**) with different skin/flesh colors (R = red, P = purple, Y = yellow, and W = white) were grown at two Texas locations, McCook (near the Mexican border) and Dalhart (in the northwest corner of the Panhandle), in two different years, 2003 (Year 1) and 2004 (Year 2). These locations represent the two climatic extremes of potato production in Texas, including altitude, latitude, mean annual temperature, light intensity, and production season, and are located nearly 1000 miles apart. Environmental conditions of these locations and planting and harvest dates are presented in **Table 2**. A randomized complete block design with three replications was used. Tubers were harvested and transported at ambient temperature (25 °C) to Texas A&M University, College Station, TX, for analysis.

The 2, 2-diphenyl-1-picrylhydrazyl (DPPH) radical and Folin–Ciocalteu reagents were obtained from Fisher Scientific (Pittsburg, PA). Phenolic acid standard compounds were purchased from Sigma (St. Louis, MO). Solvents for extraction and HPLC were obtained from VWR International (Bristol, CT).

Sample Preparation. Six uniformly sized tubers from each replication were selected, washed, and diced into 0.5 cm cubes. Three 5 g samples and three 10 g samples were stored in falcon tubes at −80 °C until analysis. For AOA, TP, and PC analysis, 5 g tuber samples were homogenized with 15 mL of ethanol using a tissumizer (Ultra Turrax), and stored at −20 °C overnight. The supernatant was collected by centrifugation. For carotenoid content and composition analyses, 10 g tuber samples were homogenized with 15 mL of methanol plus butylated hydroxy toluene (BHT) (1 g/L). Five milliliters of methanol with BHT and 10 mL of hexane were added to the homogenized tissue and kept at −20 °C. Ethanol and hexane layers were collected separately after centrifugation. A second extraction was made by adding 5 mL of methanol and 10 mL of hexane to the previous extracts.

Antioxidant Activity. Total antioxidant activity (AOA) of the specialty potatoes was determined via a modified 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay (*17*). The sample solution (150 μL) was allowed to react with the DPPH radical in an ethanol solution, at a concentration of 50 μM. The absorbance was measured at 515 nm against the blank (pure ethanol) using a spectrophotometer. The difference in absorbance is proportional to the AOA of the sample and was expressed as micrograms of trolox equivalents per gram of fresh weight (μg of TE/gfw).

Total Phenolic Content. The Folin–Ciocalteu colorimetric method (*18*) was used to measure total phenolic content of the samples. Nanopure (2400 μL) water was added to 150 μL of the clear supernatant sample, followed by the addition of 150 μL of 0.25N Folin–Ciocalteu reagent and 300 μL of 1N Na_2CO_3. The absorbance reading was recorded every 30 min and compared to a prepared blank at 725 nm until no significant change in absorbance was observed. The results were expressed as milligrams chlorogenic acid equivalents per 100 g of tissue (mg of CGAE/100 gfw).

Phenolic Composition. Samples were concentrated by drying 7 mL to completion in a heated speed vacuum and resuspending in 1 mL of ethanol for HPLC analysis. The HPLC system equipped with a binary pump (Waters 515), an autoinjector (Waters 717 plus), and a photodiode array (PDA) detector (Waters 996) was used with a 4.6 × 150 mm, 5 μm, Atlantis C-18 reverse-phase column at 40 °C. A 20 μL sample

Table 3. Antioxidant Activity (AOA), Total Phenolics (TP) and Total Carotenoids (TC) of 25 Specialty Potato Genotypes Grown at Two Texas Locations and for Two Years (2003 and 2004)

	AOA (μg of TE/gfw)[c]					TP (mg of CGAE/100 gfw)[c]					TC (μg of LE/100 gfw)[c]				
	Dalhart		McCook			Dalhart		McCook			Dalhart		McCook		
genotype[a]	Y1	Y2	Y1	Y2	mean (G)[d]	Y1	Y2	Y1	Y2	mean (G)[d]	Y1	Y2	Y1	Y2	mean (G)[d]
ATTX98013–1R/R	654b	579b	754a	656b	660	131a	91c	111b	96c	107	286ab	345a	267b	320ab	304
ATTX961014–1R/Y	127c	113c	210b	449a	225	59c	58c	103a	88b	77	367a	305a	344a	224a	307
ATTX96750–1W/Y	159b	128b	352a	84b	181	63b	55bc	85a	41c	61	261c	484a	273c	352b	343
ATTX98012–5R/Y	167b	140b	543a	232b	270	84a	69ab	82ab	66b	75	257ab	266a	160b	157c	211
ATTX98444–16R/Y	223b	333a	336a	114c	252	87b	56c	95a	60c	75	354b	512a	270b	161b	413
ATTX98444–4Y/Y	75b	47b	444a	162b	182	88a	60b	88a	65b	75	345a	591a	378a	448a	446
ATTX98462–3RY/RY	186b	202b	380a	254b	256	62b	56bc	85a	48c	63	530a	276bc	422ab	516a	346
ATTX98491–3YR/Y	293c	361b	309c	446a	352	87a	69b	77ab	67b	75	502c	662b	387c	888a	610
ATTX98493–1R/YR	356b	202c	494a	314b	341	92a	77b	98a	64c	83	525b	887a	385c	930a	682
ATTX98500–2P/Y	326c	549ab	489b	620a	496	71b	78ab	90a	67b	77	437a	436a	396a	344a	403
ATTX98500–4P/Y	151c	246b	345a	330a	268	76a	69a	83a	72a	75	191b	655a	320b	533a	425
ATTX99325–1R/Y	196ab	146b	270a	153b	191	60a	67a	63a	57a	62	273a	339a	210a	328a	288
CO111F2–1P/P	543b	592b	707a	592b	608	102a	108a	117a	103a	108	377a	363a	332a	372a	361
CO112F2–2P/P	783a	586b	763a	730a	716	112b	114b	155a	111b	123	611a	569a	587a	554a	577
CO141F2–1P/P	272b	202b	365a	411a	316	74b	77b	119a	77b	87	173b	291a	166b	271a	225
CO142F2–1R/R	496b	661a	448b	717a	580	72a	94a	102a	89a	91	226b	381a	207b	373a	297
COTX00104–2P/Y	342b	484a	335b	204c	341	86a	53b	78a	52b	67	125b	536a	101b	421a	296
COTX00104–4R/Y	251bc	167c	425ab	468a	319	78a	61b	72ab	65ab	69	482a	187b	469a	186b	331
COTX99086–4YR/Y	741a	586b	456c	590b	593	105a	81b	75b	72b	83	310a	216b	181b	216b	231
COTX99338–1YR/Y	356b	511ab	362b	625a	464	79b	80b	96a	82b	84	274a	326a	202b	334a	284
NDTX4528–3P/PW	311b	347b	668a	299b	406	73b	74b	95a	59c	75	134bc	284a	96c	170b	171
NDTX4528–4P/PW	138b	109b	340a	370a	240	56b	66ab	78a	66ab	67	190b	289a	184b	272ab	234
NDTX4528–4BP/PW	173c	220bc	303ab	384a	270	60b	53b	80a	64ab	64	294a	223ab	137b	218ab	218
PATX99P32–2RY/YR	351c	648ab	521b	697a	554	95a	92a	98a	91a	94	560a	533a	533a	376a	501
PATX99P41–1RY/YR	425b	574ab	490b	725a	554	85b	85b	104a	88b	90	485a	474a	450a	454a	466
LSD[b]	70	44	190	44	51	16	7	12	8	6	105	116	88	103	50
mean by location (LSD)[e]	Dalhart,	337	McCook,	435	(14)	Dalhart,	78	McCook,	83	(2)	Dalhart,	378	McCook,	337	(14)
mean by year (LSD)[f]	Y1,	384	Y2,	387	(14)	Y1 -	87	Y2 -	73	(2)	Y1,	397	Y2,	318	(14)

[a] R = red, Y = yellow, P = purple, W = white skin/flesh color. [b] LSD is used to compare genotypes within columns. [c] Different letters across four columns for each parameter represent significant difference among four location and year combinations. [d] Mean values for genotypes averaged over two locations and two years. [e] Mean values for locations averaged over 25 genotypes and two years. [f] Mean values for years averaged over 25 genotypes and two locations.

was injected using the mobile phase acetonitrile (Solvent A) and nano pure water (pH adjusted to 2.3; Solvent B). Flow rate was 1 mL/min with a gradient 0/85, 6–35/85–0, 36–45/85 (min/%A) (*9, 19*). Peaks were identified by matching the spectra and retention times, and spiking with standard compounds.

Total Carotenoid Content. Total carotenoid content was determined by the absorbance of the ethanol and hexane extracts at 445 and 450 nm, respectively (*20*). Carotenoid content in the ethanol and hexane fractions was calculated using lutein and β-carotene standard curves, respectively. Total content was expressed as micrograms of lutein equivalents per 100 g of tuber (μg of LE/100 gfw).

Carotenoid Composition. Both ethanol and hexane extracts were concentrated by drying under a nitrogen stream to completion and resuspending in 1 mL of methanol with BHT (1 g/L). The concentrated sample was filtered through a 0.45 μm syringe filter before injection. A 20 μL sample was injected onto the HPLC. Solvent A consisted of methanol:water:triethylamine (90:10:0.1 v/v/v) and solvent B consisted of methanol:methyl tert-butyl ether (MTBE):triethylamine (6:90:0.1 v/v/v) (*21*). A YMC carotenoid column (4.6 × 250 mm, 5 μm, C-30 reverse-phase) was used at 35 °C with a 1 mL/min flow rate. The top five genotypes from McCook 2003 were analyzed for carotenoid composition. Peaks were identified both by spiking and matching the spectra and retention times.

Statistical Analysis. The effects of genotype, year, and location on AOA, TP, and TC were determined by three-way analysis of variance (ANOVA) using the SAS general linear model (GLM) procedure (*22*). Pair-wise multiple comparisons and mean separations were performed using Fisher LSD. Pearson correlation coefficients were determined using the SAS Proc Corr procedure. Estimates of variance components were calculated using the SAS Proc Mixed model, and the percent contribution of variance component i ($\%VC_i$) to the total variance was calculated as the proportion of its estimate (EVC_i) to the total of all estimated variance components including the error term ($\sum_{i=1}^{i=n} EVC_i$) as shown in the following equation

$$\%VC_i = \frac{EVC_i}{\left[\sum_{i=1}^{i=n} EVC_i\right]} \times 100$$

Principal component analysis was carried out using Excel Biplot by centering the data for genotype and environment.

RESULTS AND DISCUSSION

Effect of Genotype, Location, and Year on Antioxidant Activity, Total Phenolics, and Total Carotenoids. Previous reports (*8, 13, 14, 23*) have shown that genotype and environment play a role in antioxidant, phenolic, and carotenoid levels in potatoes. To identify the elite genotypes both high in the above parameters and suitable for different locations, it was necessary to investigate the effect of environment on AOA, TP, and TC. Significant differences ($p < 0.001$) were observed among the genotypes at each location and year for antioxidant activity (AOA), total phenolics (TP), and total carotenoids (TC) (**Table 3**). The main effects of genotype (G), location (L), and year (Y), and their interaction effects G × L, G × Y, L × Y, and G × L × Y, were significant for TP. For AOA, all above effects were significant except year and L × Y. For TC, all

interaction effects were significant except G × L and L × Y, indicating the importance of these effects in selecting varieties for different parameters.

Antioxidant activity ranged from 47 μg of TE/gfw for ATTX98444–4Y/Y in Year 2 at Dalhart to 783 μg of TE/gfw for CO112F2–2P/P in Year 1 at Dalhart (**Table 3**). Averaged across locations and years, the genotype CO112F2–2P/P had the highest AOA. This genotype showed intense purple skin and flesh color, indicating the presence of anthocyanins that can also contribute to AOA along with phenolic acids (*24*). ATTX98444–4Y/Y had the lowest AOA in both years at Dalhart, whereas ATTX 961014–1 and ATTX96750–1W/Y had the lowest AOA at McCook in Year 1 and Year 2, respectively. CO112F2–2P/P, COTX99086–4YR/Y, CO142F2–1R/R, and CO111F2–1P/P were significantly higher for AOA than other genotypes in Dalhart. In McCook, CO112F2–2P/P, ATTX98013–1R/R, CO142F2–1R/R, CO111F2–1P/P, PATX99P32–2RY/YR, and PATX99P41–1RY/YR were significantly higher for AOA compared to other genotypes (**Table 3**). This is consistent with findings of Reyes et al. (*25*) who reported variation in AOA among different genotypes of potato. Averaged across genotypes and years, McCook produced 29% more AOA than Dalhart. The higher TP concentrations found in McCook compared with Dalhart might be responsible for the higher AOA in genotypes grown in McCook. The significantly high positive correlation between AOA and TP (*8, 25*) further indicates the contribution of these compounds to AOA.

Total phenolics ranged from 41 mg of CGAE/100 gfw in ATTX96750–1W/Y in Year 2 at McCook to 155 mg of CGAE/100 gfw in CO112F2–2P/P in Year 1 at McCook. CO112F2–2P/P, CO111F2–1P/P, and ATTX98013–1R/R were significantly higher in TP compared to the other genotypes at Dalhart in both years. In McCook, CO112F2–2P/P was significantly higher for TP in the first year, but CO111F2–1P/P did not significantly differ from CO112F2–2P/P in the second year. Hale (*9*) and Friedman (*26*) also reported similar significant differences in TP among different genotypes. Averaged across genotypes and years, McCook had a higher TP than Dalhart. This may have resulted from the lower temperatures observed in McCook during the growing year (**Table 3**). Hamouz et al. (*13*) also observed significantly higher TP in tubers from traditional potato regions, which are cooler. Tubers from Dalhart Year 1 significantly differed from those in Year 2 in their TP when averaged across genotypes and locations, confirming the results that polyphenol content of potato tubers is influenced by the specific features of the given year (*27*). Tubers from Year 1 had 20% greater TP compared with Year 2.

Total carotenoid content ranged from 96 μg of LE/100 gfw in NDTX4528–3P/PW in Year 1 at McCook to 930 μg of LE/100 gfw in ATTX98493–1R/YR in Year 2 at McCook. Similarly, Nesterenko and Sink (*28*) reported TC ranging from 48 to 879 in white-, yellow-, and orange-fleshed potatoes. In Year 1, CO112F2–2P/P (purple flesh/purple skin) had the highest TC in both locations, whereas ATTX98493–1R/YR (dark yellowish red flesh/red skin) had the highest TC in Year 2. COTX00104–2P/Y, COTX00104–4R/Y, NDTX4528–3P/PW, and ATTX98012–5R/Y had the lowest TC in Dalhart Year 1, Dalhart Year 2, McCook Year 1, and McCook Year 2, respectively. Brown et al. (*29*) also reported that dark yellow flesh varieties had three to four times higher TC than light yellow cultivars. Unlike AOA and TP, Dalhart showed higher TC (13%) compared with McCook, when averaged across genotypes and years. Year 2 had higher TC than Year 1 when averaged across genotypes and locations. Similar significant differences among environments, genotypes, and genotype × environment interactions for yellow flesh intensity were reported by Haynes et al. (*14*).

Table 4. Phenolic Composition of Specialty Potato Genotypes Grown at Two Texas Locations[a]

		(μg/gfw)							
		CGA		CA		GA		CAT	
ID	genotype	D	M	D	M	D	M	D	M
1	ATTX98013–1	642	654	34	36	61	63	83	88[b]
2	ATTX961014–1	170	359[b]	35	35	63[b]	39	85	86
3	ATTX96750–1	149	275[b]	33	35	57	60	84	84
4	ATTX98012–5	262[b]	176	33	34	57[b]	43	83	85
5	ATTX98444–16	224	263	33	36[b]	59	66[b]	83	86
6	ATTX98444–4	209	183	39	34	45[b]	33	85	86
7	ATTX98462–3	164	162	36	35	55	46	84	85
8	ATTX98491–3	253	184	35	34	63	61	83	85
9	ATTX98493–1	289	242	35	34	52[b]	34	85	85
10	ATTX98500–2	214	346	34	35	50	58[b]	84	86
11	ATTX98500–4	211	485[b]	33	35	46	54	82	86[b]
12	ATTX99325–1	175	140	35	34	48	59	84	86
13	CO111F2–1	519	641	35	35	42	45	86	87
14	CO112F2–2	591	683	40	36	56	66	89[b]	85
15	CO141F2–1	216	353	35	34	42	60[b]	81	85[b]
16	CO142F2–1	321	411	34	34	43	53	82	86
17	COTX00104–2	223	174	34	35	49	51	84	84
18	COTX00104–4	190	192	34	34	54	50	83	85
19	COTX99086–4	450	221	37	34	57	43	86	86
20	COTX99338–1	271	344	33	35	48	62	83	85
21	NDTX4528–3	241	231	34	34	48	49	84	85
22	NDTX4528–4	132	281[b]	33	34	45	47	85	84
23	NDTX4528–4B	142	247[b]	31	33	46	60[b]	84	85
24	PATX99P32–2	255	390[b]	35	34	68[b]	64	86	85
25	PATX99P41–1	227	427[b]	34	35	61	60	83	85
	LSD	95	101	4	1	9	7	2	2

[a] Each value is a mean of six observations (3 replications and 2 years). Two years within the same location were pooled together because the year effect was not significant. [b] Significant difference ($p < 0.01$) between two locations for the same genotype for a single parameter. The LSD was used to compare genotypes within columns. CGA, chlorogenic acid; CA, caffeic acid; GA, gallic acid; CAT, catechin; D, Dalhart; M, McCook.

Theses results show that genotypes differ in their AOA, TP, and TC in different locations and years. Genotype CO112F2–2P/P had the highest AOA and TP in both locations and years and the highest TC in both locations in Year 1.

Effect of Genotype, Location, and Year on Phenolic Composition. Chlorogenic acid (CGA), caffeic acid (CA), gallic acid (GA), and catechin (CAT) were significantly different among genotypes. Year and the genotype × year interaction were not significant for the above four phenolic compounds. Therefore, the phenolic compounds were averaged across years (**Table 4**).

Chlorogenic acid was the major phenolic compound present, with concentrations ranging from 132 to 683 μg/gfw. ATTX98013–1R/R and CO112F2–2P/P had significantly higher CGA content compared to other genotypes tested in Dalhart. In McCook, CO112F2–2P/P, ATTX98013–1R/R and CO111F2–1P/P were significantly higher than other genotypes in their CGA content, but they did not differ significantly from each other. Location and interaction effects (G × L, G × L × Y) were significant for CGA content. McCook had significantly higher CGA content for seven genotypes. One genotype (ATTX98012–5R/Y) had higher CGA content in Dalhart than in McCook. This corroborates the findings of Emmons and Peterson (*30*), where location significantly affected the concentration of five phenolics in oats. All the other genotypes did not differ significantly between the two locations. Averaged across genotypes and years, McCook showed 20% more CGA content than Dalhart. This

Table 5. Correlation Coefficients between Antioxidant Activity (AOA), Total Phenolics (TP), Total Carotenoids (TC), and Four Phenolic Compounds, Chlorogenic Acid (CGA), Caffeic Acid (CA), Gallic Acid (GA), and Catechin (CAT)

	TP	TC	CGA	CA	GA	CAT
AOA	0.653[a]	0.050	0.668[a]	0.108	0.156	0.246[a]
TP		0.042	0.781[a]	0.220[a]	0.216[a]	0.128
TC			0.058	0.036	0.145	0.102
CGA				0.192[a]	0.186[a]	0.255[a]
CA					0.058	0.113
GA						0.020

[a] Significant ($p < 0.01$).

higher level of CGA accounts for the corresponding higher level of TP in McCook.

Caffeic acid concentration ranged from 31 to 40 μg/gfw. CO112F2–2P/P had the highest CA content in both locations but was not significantly different from most of the genotypes tested. Location effect and all the interaction effects were not significant for CA content.

Gallic acid concentration ranged from 33 to 68 μg/gfw. PATX99P32–2RY/YR had the highest GA content in Dalhart, whereas CO112F2–2P/P was highest in McCook. However, CO112F2–2P/P was not significantly different from many other genotypes tested. Though the overall location effect was not significant, some genotypes significantly differed in their GA content between locations (**Table 4**). The interaction effects G $\times$ L, L $\times$ Y, and G $\times$ L $\times$ Y were significant for GA content.

Catechin content ranged from 81 to 89 μg/gfw. CO112F2–2P/P and CO111F2–1P/P had the highest CAT content in Dalhart and McCook, respectively. The location effect was significant. Over all, McCook had higher CAT content than Dalhart. Genotypes ATTX98013–1R/R, ATTX98500–4P/Y, CO141F2–1P/P, and CO111F2–1P/P differed significantly in their CAT content between locations, whereas the first three had the highest content in McCook. The interaction effects G $\times$ L, L $\times$ Y, and G $\times$ L $\times$ Y were also significant for CAT content. Over all, chlorogenic acid showed significant differences among genotypes and between locations with 550 μg/gfw differences between the highest and the lowest genotypes.

Correlation Coefficients Among Different Parameters. Significant positive correlations were observed among AOA, TP, and CGA (**Table 5**). Vinokur et al. (*31*) and Scalzo et al. (*32*) also reported significant correlations between AOA and TP. Abundance of chlorogenic acid (*26*) might be responsible for its strong correlation with AOA and TP. The AOA and CAT, TP and CA, TP and GA, CGA and CA, CGA and GA, and CGA and CAT combinations also showed significant positive correlations between each other. In wheat, also similar significant correlations were observed between TP and AOA, TP and ferulic acid, AOA and ferulic acid, and TP and CA (*33*). Total carotenoid content was not correlated with AOA measured by the DPPH radical, probably because of the DPPH radical having no similarity to the highly reactive peroxyl radicals and singlet oxygens in the lipid phase where carotenoids exert their antioxidant functions (*34*). This may be the reason for the lack of correlation between TC and AOA. The TC did not show any correlation with TP or individual phenolic compounds. The AOA did not exhibit any correlation with CA or GA. The CAT showed no correlation with TP, CA, or GA.

Relative Influence of Variance Components on Different Parameters. The percent contribution of genotype, location, year, and interactions to the total variation was calculated as the proportion of individual estimates to the total estimates of variance components for each parameter including error term. The results are presented in **Table 6**. Variation due to genotype was significant for all measured parameters and was largest when compared with location, year, and their interactions. This study is the first to quantify the relative influence of genotype, location, year, and their interactions on potato phenolic compounds. Main effects and interaction effects together accounted for 87– 91% of total variation for AOA, TP, and TC. Genotype variation alone explained about 50% of the total variation for AOA, TP, and TC. Similar results were observed in blackberry, where 40–92% of total variation in anthocyanins accounted for cultivar main effects (*35*). Location influence was significant for AOA, TP, and TC and ranged from 1 to 11%. Year variation was significant for only TP and TC (18 and 7%, respectively). Genotype variation contribution was 53, 10, 29, and 16% for CGA, CA, GA, and CAT, respectively. For CA, the variance components genotype and L $\times$ Y were significant, and all other variance components were not significant. All the variance components together accounted for only 22% of the total variation. Variation due to location was significant for CGA and CAT. All two-way interactions were significant for TP. In blackberries as well, year, cultivar $\times$ year, and cultivar $\times$ location interactions accounted for 22, 34, and 20% of total variation for AOA, respectively. Though the three-way interaction variation was significant for all measured parameters except CA, it accounted for only 0–17% of total variation. Mpofu et al. (*33*) reported similar results in wheat.

Table 6. Relative Influence (%) of Genotype (G), Location (L), Year (Y), and Their Interactions on Antioxidant Activity (AOA), Total Phenolics (TP), Total Carotenoids (TC), and Phenolic Composition of 25 Specialty Potato Genotypes Grown in Two Texas Locations and Two Years[a]

	genotype (24)[b]	location (1)	year (1)	G $\times$ L (24)	G $\times$ Y (24)	L $\times$ Y (1)	G $\times$ L $\times$ Y (24)
AOA	52[c]	11[c]	0	2[c]	9[c]	0	17[c]
TP	44[c]	1[c]	18[c]	3[c]	1[c]	7[c]	17[c]
TC	48[c]	3[c]	7[c]	0	26[c]	0	4[c]
CGA	53[c]	4[c]	0	11[c]	1[c]	0	16[c]
CA	10[c]	0	2	7	0	3[c]	0
GA	29[c]	0	0	26[c]	5	7[c]	11[c]
CAT	16[c]	7[c]	1	13[c]	6	5[c]	11[c]

[a] Each value in the table is the proportion of individual estimate of variance component to the total of all estimated variance components. CGA = chlorogenic acid, CA = caffeic acid, GA = gallic acid, CAT < catechin. [b] The number in parentheses represents degrees of freedom. [c] Significant ($p < 0.01$).

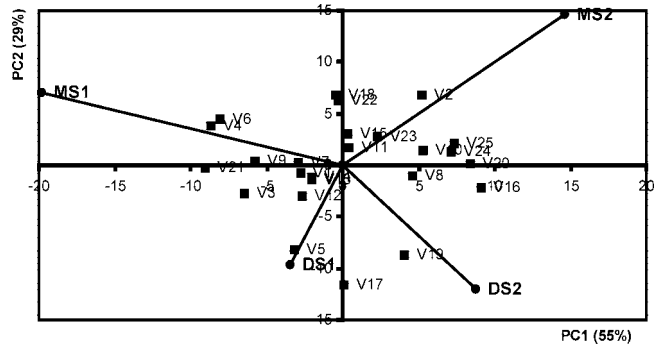

Figure 1. Principal component analysis biplot for antioxidant activity of 25 genotypes in four environments. Environments are in upper case with first letter representing location (M = McCook, D = Dalhart) Y1 and Y2 represent Year 1 and Year 2, respectively. Genotypes are in lower case. Principal component 1 values are on the *x*-axis and principal component 2 values are on the *y* axis. V1 to V25 correspond to the genotypes 1–25 in **Table 4**.

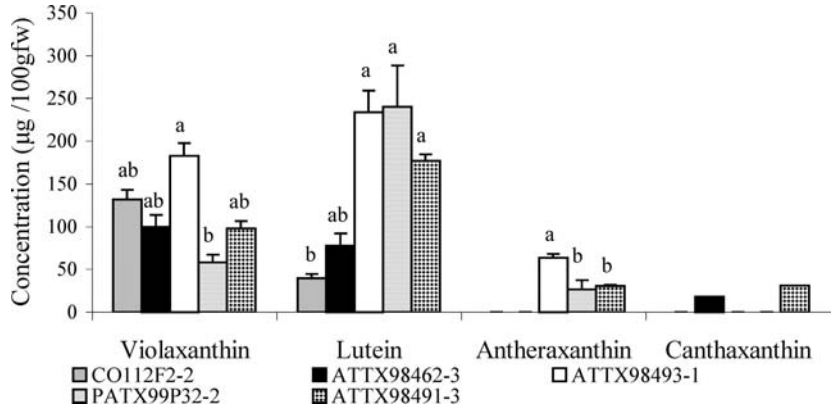

Figure 2. Individual carotenoid content in specialty potato genotypes. Each value is a mean of three replications. Different letters on the bars represent significant differences ($p < 0.01$) among genotypes for each carotenoid.

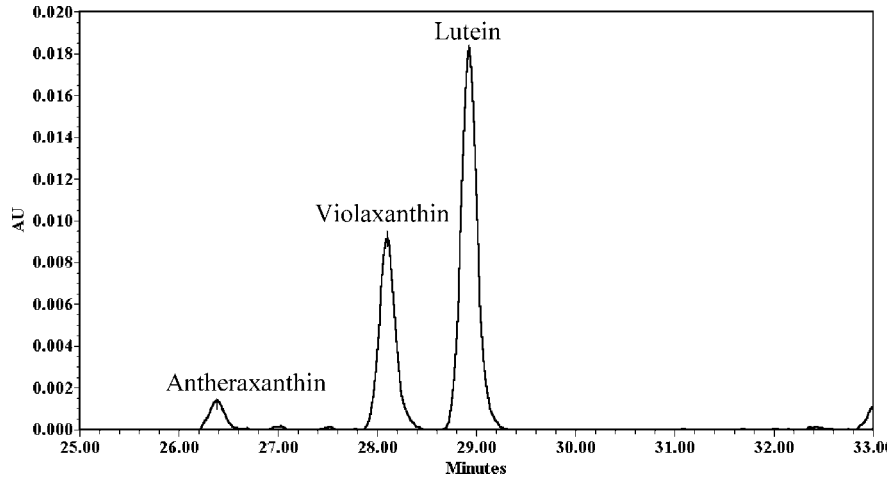

Figure 3. HPLC chromatogram of specialty potato genotype ATTX98493–1R/YR showing retention times on the *x*-axis and absorbance on the *y*-axis.

Principal component analysis (PCA) was done to determine the deviation of the genotypes and environments from their averages for AOA, and to identify the stable genotypes across locations and years. PCA is an exploratory tool used to identify patterns or trends in data of multiple dimensions, by performing a covariance analysis between variables. Results are graphically displayed in a biplot (*36*) to show relationships among variables. Principal component 1 (PC 1) (55%) and principal component 2 (PC2) (29%) together explained 84% of variation (**Figure 1**). Genotypes ATTX98013–1R/R, ATTX98462–3RY/RY, ATTX98500–4P/Y, CO111F2–1P/P and CO112F2–2P/P were relatively stable for AOA across environments, because of less interaction effect. Genotype CO112F2–2P/P was not only stable, but also had significantly higher AOA, TP and TC. Genotypes furthest from the origin (**Figure 1**) had a large interaction effect and deviated substantially from the average performance (*37*).

Carotenoid Composition. Five genotypes with high total carotenoids were analyzed for carotenoid composition, and they differed significantly in both carotenoid content and composition. Lutein and violaxanthin were the two major carotenoids present in all five genotypes analyzed. Antheraxanthin and canthaxanthin were present only in some genotypes. Violaxanthin content ranged from 58 to 183 μg/100 gfw. ATTX98493–1R/YR had significantly higher lutein content compared to the other four genotypes. Lutein was highest in PATX99P32–2RY/YR (240 μg/100 gfw), but not significantly different from ATTX98493–1R/YR (234 μg/100 gfw) (**Figure 2**). ATTX98493–1R/YR, PATX99P32–2RY/YR, and ATTX98491–3YR/Y contained antheraxanthin and ATTX98493–1R/YR had significantly higher antheraxanthin content (63.7 μg/100 gfw) than all other genotypes (**Figure 3**). Canthaxanthin was detected in two of the five genotypes (ATTX98462–3RY/RY and ATTX98493–1R/YR). Earlier reports also suggested the presence of lutein, violaxanthin, lutein-5,6-epoxide, zeaxanthin, and neoxanthin in potatoes (*12*, *24*).

In conclusion, genotype and location significantly affected AOA, TP, TC, and phenolic composition in potatoes. Overall, CO112F2–2P/P had significantly higher AOA and TP. McCook had significantly higher AOA (29%), TP (7%), and CGA (20%), and Dalhart had significantly higher TC (13%). Year had a significant influence on TP and TC. Significant positive correlations were observed between AOA-TP, AOA-CGA, and TP-CGA. Relative influence of genotype was highly significant for AOA, TP, TC, and phenolic composition. Genotypic variance accounted for more than 55% of total variation for AOA, TP, TC, and CGA. Location, year, and interaction effects were significant. Individually, they accounted for 1–23% of total variation for all the measured parameters. Because CO112F2–2P/P was high in most of the measured parameters and was stable across environments, this genotype would be an ideal parent for use in breeding programs aimed at increasing antioxidant content in potato. Further research is needed to investigate the effects of individual environmental parameters, such as temperature, rainfall, irrigation, solar radiation, temperature stress, etc., on AOA, TP, TC, phenolic, and carotenoid composition.

ACKNOWLEDGMENT

We thank Dr. Jeannie Miller, Dr. Jairam Vanamala, Dr. Manjit S. Kang, and Ndambe Nzaramba for critically reviewing the manuscript. We appreciate the assistance of Jeff Koym and Douglas C. Scheuring, who provided the weather information and assisted with collection of samples.

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Received for review May 25, 2007. Accepted July 25, 2007. We are grateful to the CSREES Special Research Grant Program-Potato Research for partial funding of this research.

JF071543W