

Marker SNPs associated with texture in tubers of *Solanum tuberosum* group Phureja from the Colombian Central Core Collection

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Abstract

Solanum tuberosum, is a specie of the Solanaceae family that grown in different regions of the world. In the Andean region is a staple food in fresh consumption or process (chips and French fries). However mostly of the current potato cultivars does not have the require characteristics in texture quality for the industry, so there is a significant need to improve the quality of potatoes. Breeding programs need to build large populations, successive selections and estimate the trait or traits of interest. Due to the complexity of these traits, such as texture their improvement work is difficult and expensive. The use of molecular approaches and an accurate phenotyping are a feasible alternative to optimize breeding programs supporting the classical breeding. In this research 110 accessions from of the Colombian Core Collection (CCC) of *Solanum tuberosum* group Phureja. We harvested fresh tubers and standardized a cooking method, using data of tubers midpoint temperature after cooking. Phenotyping was performed in two different ways, first we calculated the content of total starch (%) in tubers using an enzymatic methodology and we found in the CCC clones percentages ranging from 7.05% to 8.95% of. Second we performed a texture assay profile (TPA) using a texturometer and TA-XTPlus texture analyzer® software. Third, we carried out a sensorial texture analysis, with a panel of experts and finally, we carried out an association genetic analysis for the trait.

Material and methods

Plant material

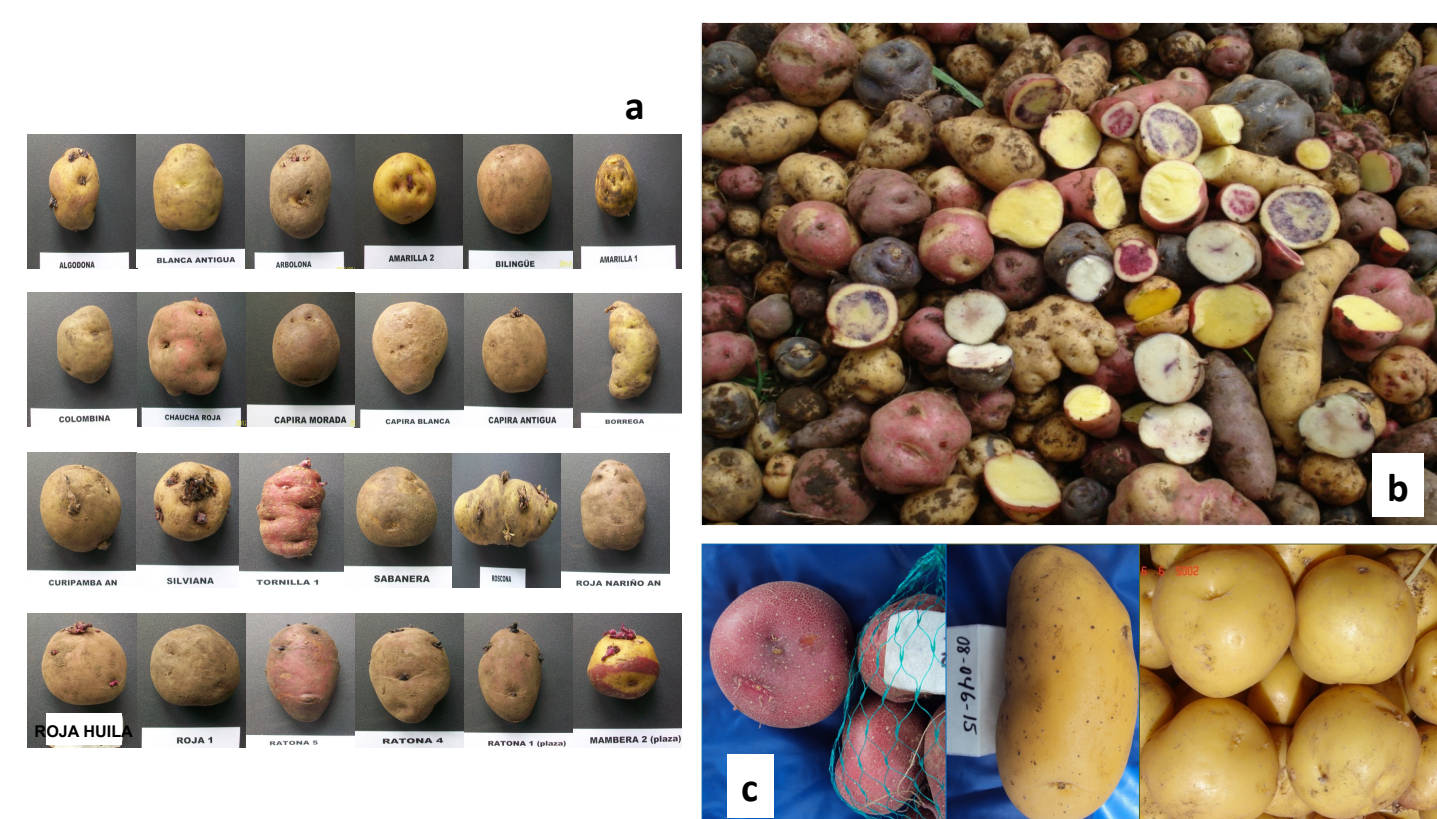


Figure 1. Plant material employed was *S. tuberosum* group Phureja. a) Native varieties, b) *S. phureja* from CCC. d) Advanced clones

Methodology

We employed raw and cooked potatoes to get the samples. Tubers were classified according to their sizes and the cooking was optimized. Genetic association analysis was carried out for each trait. Figure 2 shows the flow chart of general methodology.

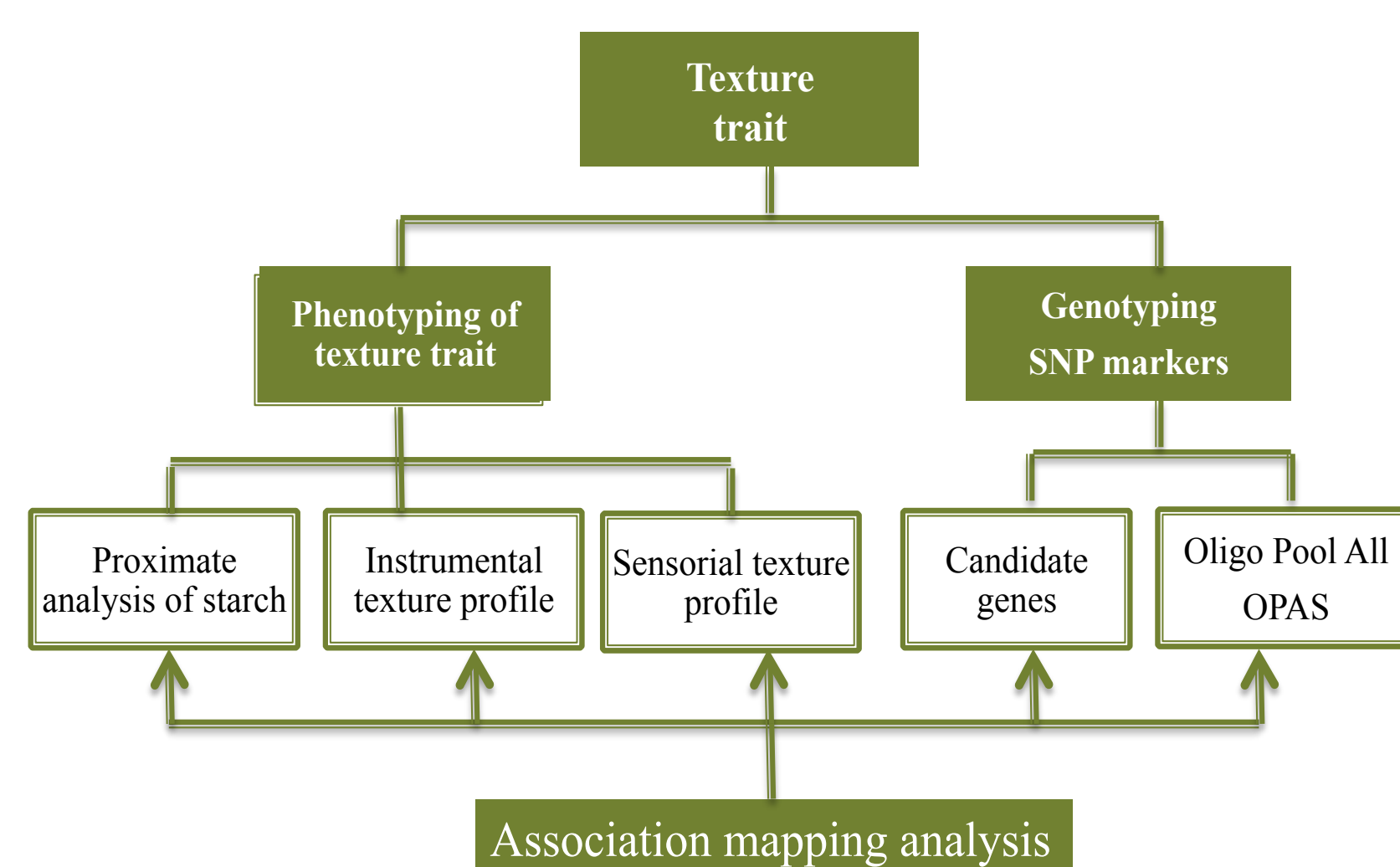


Figure 2. Flow chart applied for the texture study. Main steps are showed.

Results and Discussion

We carried out an integral study of the texture trait. The parameters to conform this trait, hardness (Hard), fracturability (Frac), adhesiveness (Adh), springiness (Spr), cohesiveness (Coh), gumminess (Gum) and chewiness (Che) were estimated through chemical analysis measuring starch content (Table 1), instrumental texture profile (Table 2) and sensorial texture profile. For starch content we found all the genotypes have lower starch content to compare with the control (maize) but advanced clones presented in average more starch for Colombian germplasm, what is useful for processing.

Table 1. Content of total starch in genotypes of *S. tuberosum* group Phureja.

Plant material	Range (%)	Average (%)
CCC (Colombian Core Collection)	6.110 - 17.943	11.925 ± 2.443
CA (Advanced clones)	12.83 - 33.28	24.71 ± 7.04
N (Native varieties)	10.721-10.181	10.462 ± 0.219
Commercial cultivars		
1. Capiro		10.6 ± 0.102
2. Pastusa Suprema		10.43 ± 0.66
3. Criolla Paisa		15.3 ± 0.82
4. Criolla Colombia		20.3 ± 7.83
5. Criolla Galeras		13.4 ± 0.134
Starch control / (standard-maize)		33.9 ± 2.583

Analysis of texture profile using instrumental estimation allows us to identify two allelic variants (Figure 3) in two genes that mapped in chromosomes 6 and 8. All genotypes grouped in three groups (Table 2) for texture parameters. Medium values for these parameters are desirable because extreme values may be undesirable traits for people.

Table 2. Averages calculated for each trait of instrumental texture profile

Clusters	Traits for texture													
	Hard	StD	Frac	StD	Adh	StD	Spr	StD	Coh	StD	Gum	StD	Che	StD
1	813.35	200.15	372.21	169.04	-31.4	11.47	0.22	0.05	0.08	0.01	59.1	13.21	12.86	4.35
2	1504.3	296.34	820.23	313.59	-29.1	5.41	0.25	0.06	0.069	0.01	99.15	23.29	25.04	8.59
3	2612.77	653.9	1412.85	882.7	-28.73	4.79	0.32	0.08	0.068	0.01	182.52	67.8	56.87	18.86

Genetic association analysis using a null model with out population structure was applied and we could identify six allelic variants (Table 3, figure 4) for texture parameters in the instrumental analysis. For the sensorial analysis we identified four allelic variants in four candidate genes (Table 4, figure 5).

Table 3. Allelic variants identified using candidate genes approach for texture parameters.

Trait	Primer name	Chrm.	Position	Allelic variant	Effect	Percentage of effect	Described function
Hardness	TM18SNP88	6	52355675	C/T	10.936	12.54	Thylakoid lumenal 15 kDa protein 1, chloroplastic
Chewiness	TM18SNP88	6	52355675	C/T	451.735	12.53	Thylakoid lumenal 15 kDa protein 1, chloroplastic
	TM18SNP108	6	52355695	T/C	-432.521	-11.99	Thylakoid lumenal 15 kDa protein 1, chloroplastic
	MF19PHUSNP1	1	1155255	A/G	-368.725	-10.22	Extensin
	MF19PHUSNP6	1	1155436	G/A	-378.344	-10.49	Extensin
Springiness	MF19PHUSNP4	1	1155327	A/C	0.0647	14.17	Extensin
Gumminess	TM18SNP88	6	52355675	C/T	25.69	10.39	Thylakoid lumenal 15 kDa protein 1, chloroplastic
Adhesiveness	MF17PHUSNP4	11	41005304	T/C	0.2187	10.93	Calmodulin
	TM46PHUSNP3	7	50569932.0	A/G	-0.826	-12.71	Chloroplast thiazole biosynthetic protein
Sensorial hardness	TM46PHUSNP6	7	50570023.0	G/T	-0.9837	-15.14	Chloroplast thiazole biosynthetic protein
	TM46PHUSNP7	7	50570065.0	A/G	-0.9188	-14.13	Chloroplast thiazole biosynthetic protein
	TM46PHUSNP8	7	50570077.0	A/G	-0.8224	-12.65	Chloroplast thiazole biosynthetic protein
Sensorial adhesiveness	TM25SNP256	7	5179531	C/T	-0.5154	-10.31	Photosystem II 10 kDa polypeptide, chloroplastic
fracturability	TM47PHUSNP5	8	4677946	G/C	-1.236	-24.72	Photosystem I reaction center subunit

Table 4. Allelic variants identified using OPAs approach for texture parameters.

Trait	Primer name	Chrm.	Position	Allelic variant	Effect	Percentage of effect	Described function
Chewiness	MICRO.1882.C1_394	8	39670923	A/G	9.0206	10.344	Protein (Tipa)
	solcap_stsnp_c1_1317	11	39368633	G/A	15.9471	18.288	Sin anatación
	solcap_stsnp_c1_1319	11	39472273	A/G	12.3849	14.203	Proteasa
Hardness	MICRO.1882.C1_394	8	39670923	A/G	416.313	11.544	Protein (Tipa)
	solcap_stsnp_c1_1317	11	39368633	G/A	693.602	19.233	Sin anatación
	solcap_stsnp_c1_1319	11	39472273	A/G	568.315	15.759	Proteasa
Gumminess	solcap_stsnp_c1_1317	11	39368633	G/A	37.9	15.3	Sin anatación
	solcap_stsnp_c1_1319	11	39472273	A/G	31.4	12.7	Proteasa
Sensorial adhesiveness	solcap_stsnp_c1_7569	4	660102	G/A	-0.3826	-19.13	Phosphoenolpyruvate carboxylase
Sensorial hardness	solcap_stsnp_c1_126	3	59316627	A/G	-0.9249	-14.229	Transcription initiation factor IIE alpha subunit family protein

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References

Ducreux L. *et al.*, 2008. Journal of Experimental Botany 59(15): 4219 - 4231.
 Li L. *et al.*, 2008. Theor Appl Genet 116:1167–1181
 Zeeman S.C. 2010. Annual Review of Plant Biology 61:209 – 34

Conclusions

We optimized the protocols to evaluate texture using chemical analysis, instrumental texture profile analysis and sensorial texture profile. Genetic association analysis identified seven candidate genes involved in the trait employing candidate gene approach and four allelic variants for the texture trait using OPA approach. the complexity of the feature can be observed through the number of allelic variants identified.