

CORRECTION

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Correction to: Novel SNP markers in *InvGE* and *Sssl* genes are associated with natural variation of sugar contents and frying color in *Solanum tuberosum* Group Phureja

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Correction

After the publication of this work [1], we detected some mistakes in the reverse primers of *InvGE* and *BMV-8/2* and in the forward primer of *PWD* shown in Table 1. Additionally, we made some editions in the primer sequences from Additional files 2 and 3. Please see the corrected Table 1 and Additional files 2 and 3 below.

Additional files

Additional file 2: Amplicon sequences of candidate genes with associations to sugar contents and frying color in *Solanum tuberosum* Group Phureja with the SNP alleles and SNP positions in the potato reference genome (version 4.03) [28, 43]. The sequences were retrieved from the SPUD data base [44]. Primer sequences are underlined, markers with associations are highlighted in blue and SNPs previously reported for tetraploid potatoes are shown in italics. The numbers indicate the position of the sequence and the SNPs in the chromosomes (chr). Exonic regions are represented with red letters while introns are represented in black letters according to the gene models from the SPUD data base [44]. (DOCX 23 kb)

Additional file 3: Amplicon sequences of additional candidate genes studied in *Solanum tuberosum* Group Phureja with the SNP alleles and SNP positions in the potato reference genome (version 4.03) [28, 43]. The sequences were retrieved from the SPUD data base [44]. Primer sequences are underlined and the SNPs previously reported for tetraploid potatoes are highlighted in yellow. Exonic regions are represented with red letters while introns are represented in black letters according to the gene models from the SPUD data base [44]. (DOCX 26 kb)

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Reference

1. Duarte-Delgado D, Juyó D, Gebhardt C, Sarmiento F, Mosquera-Vásquez T. Novel SNP markers in *InvGE* and *Sssl* genes are associated with natural variation of sugar contents and frying color in *Solanum tuberosum* group Phureja. *BMC Genomics*. 2017;18:23.

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Table 1 Loci (PGSC0003DMG******) from the reference genome [28, 43] analyzed in 112 *Solanum tuberosum* Group Phureja accessions

Gene Acronym (GenBank Accession No.)	Locus	Chr.	Primer Sequences 5'-3'	Ta (°C)	Amplicon size (bp)	No. SNPs Scored (Scored previously) ^e
<i>Stp23</i> (PHO1) ^a (D00520)	PGSC0003DMG400007782	III	*f-cagatattgtacatactctacc r-tcattagtcacaactttatcgg	59	963	4 (0)
<i>StpL</i> (PHO1) ^a (X73684)	PGSC0003DMG400028382	V	*f-ttacattgcacaagcacaagc r-gtgtacatacaatactctatcc	57	982	14 (1) [67]
<i>Sssl</i> (Y10416)	PGSC0003DMG402018552	III	f-aacaataggaattaccataacc *r-atattccaacaaaacagagc	57	970	12 (0)
<i>InvGE</i> (INV-cw) ^a (AJ133765)	PGSC0003DMG400008943	IX	f-caattctcgattcttcatagg *r-acagcacctatgtattataatgg	57	798	9 (8) [39]
<i>Pain1</i> (INV) ^a (X70368)	PGSC0003DMG400013856	III	f-catacattactatagatcc *r-aattgaagcagatcatgtagg	56	926	5 (2) [39,40]
			f-caaaatgaatacatattaagagg ^b *r-cttaagcagttgcttagagc	56	707	4 (0)
<i>UGPase</i> (D00667)	PGSC0003DMG401013333	XI	f-atgatgttctccactaaaagc *r-ttcagatttcagaagagagg	56	805	11 (1)[42]
			*f-tgattaacgatactatagctcc r-ttaaaacttccttatactatag	56	931	12 (1) [42]
<i>GWD</i> (Y09533)	PGSC0003DMG400007677	V	f-ttctgttatctactagttacg *r-gttttatatctgtctcttgg	56	992	5 (3) [7,41]
<i>BMY-8/2</i> (AF393847)	PGSC0003DMG400001855	VIII	f-gctactggagcatggtgacaga ^f *r-ttacatagaggtctgtcctgcttgag	57	560	9 (9) [5]
<i>PWD</i> (AY747068)	PGSC0003DMG400016613	IX	*f-ggtctgatgatctatctgattgc ^c r-cgacatcttgaggagaaccaaact	57	871	16 (16) [7,41]
			f-gcttctgtgcttggctc ^d *r-gataggcatacgaccaggtcagaaatcaa	60	985	8 (3) [37]

Chr, chromosome; Ta, annealing temperature

* Primer used for amplicon sequencing

^a These parenthesis include the alternative acronyms used in the starch-sugar interconversion pathway scheme adapted by Schreiber et al. [7]^b From a region downstream of the *Pain1* candidate gene^c From Schreiber et al. [7]^d From Fischer et al. [37]^e The studies where the SNPs or the related amino acid changes were previously reported in tetraploid potatoes are indicated