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Erratum

Erratum: Parra-Galindo, M.A., et al. Chromosomes I and X Harbor Consistent Genetic Factors Associated with the Anthocyanin Variation in Potato *Agronomy* 2019, *9*, 366

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The authors would like to make the following correction to the published paper [1]. These error corresponds to some percentage values (%) in the results Section 3.2. Genome-wide Association Study for Anthocyanidins Concentration, due to typing error.

The following paragraphs in Section 3.2. Genome-Wide Association Study for Anthocyanidins Concentration Regulation, has to be changed.

"The genetic basis of natural variation for anthocyanins levels from cooked potato tubers was explored, employing an association panel of 96 accessions genotyped with 7520 SNP markers for use in a GWAS of five anthocyanidins traits with a compression mixed linear model. A total of seven QTL were identified. These QTL would be involved in the genetic control of the anthocyanin content in cooked tubers (Supplementary Material 6). These QTL explain from 2.4% to 67% of the phenotypic variance (anthocyanidin content and composition). Three QTL map in chromosomes X, one in chromosome I, and one QTL in chromosomes II, XI, and XII (Table 1).

Two of the seven QTL were considered stable QTL, as they were detected for the five anthocyanidins. The QTLs identified as AnthoX_Chloro and AnthoX_STS, belonging to the X chromosome, were detected in a genome-wide association for the five traits. The strongest association signal was detected for pelargonidin with the peak SNP locus AnthoX_Chloro localized within the *Chloroplast threonine deaminase 1* gene (PGSC0003DMT400045363/*Chloroplast threonine deaminase 1* gene), explaining the 67% of the phenotypic variance. In a search window of 100 kb according to the LD decay, we found a *Phenylalanine ammonia-lyase*-gene (PAL-PGSC0003DMT400080548) within the flanking region of AnthoX_Chloro, which corresponds to the first enzyme involved in the anthocyanin biosynthetic pathway [51]. AnthoX_STS was localized at chr10:52261553 (PGSC0003DMT400045346/*STS14 protein* gene), and is strongly associated with pelargonidin, explaining30% of the phenotypic variance. On chromosome X, we also reported the QTL AnthoX_Adeny, colocalized at chr10:57301864 (PGSC0003DMT400060833/*Adenylyl-sulfate kinase* gene), explaining 67% of the phenotypic variance of pelargonidin. The QTL AnthoI_Ser/Thr belonging to the chromosome I, was associated with the concentration of cyanidin co-localized with chr01:50785405 (PGSC0003DMT400013570/*Serine/threonine-protein phosphatase* gene) and explained 31% of the phenotypic variance. The QTL AnthoII was associated with the petunidin concentration on chromosome II (chr02:48517142,), we found the *acetyl-CoA carboxylase*-gene (ACCase–PGSC0003DMT400052139) within the flanking region of 100 kb of AnthoII. The QTL AnthoXI was associated with the delphinidin concentration, co-localized chr11:40001900 (PGSC0003DMT400019149/conserved gene of unknown function) and explained 37% of the phenotypic variance. Finally, the QTL AnthoXII was associated with the petunidin concentration, is located inchr12:24259182 (PGSC0003DMT400090245/Hypothetical gene of unknown function) and explained 48% of the phenotypic variance (Table 1, Figure 3)".

The correct paragraphs should be:

"The genetic basis of natural variation for anthocyanins levels from cooked potato tubers was explored, employing an association panel of 96 accessions genotyped with 7520 SNP markers for use in a GWAS of five anthocyanidins traits with a compression mixed linear model. A total of seven QTL were identified. These QTL would be involved in the genetic control of the anthocyanin content in cooked tubers (Supplementary Material 6). These QTL explain from 31.3% to 44.4% of the phenotypic variance (anthocyanidin content and composition). Three QTL map in chromosomes X, one in chromosome I, and one QTL in chromosomes II, XI, and XII (Table 1).

Two of the seven QTL were considered stable QTL, as they were detected for the five anthocyanidins. The QTLs identified as AnthoX_Chloro and AnthoX_STS, belonging to the X chromosome, were detected in a genome-wide association for the five traits. One of the strongest association signal was detected for pelargonidin with the peak SNP locus AnthoX_Chloro localized within the *Chloroplast threonine deaminase 1* gene (PGSC0003DMT400045363/*Chloroplast threonine deaminase 1* gene), explaining the 43.9% of the phenotypic variance. In a search window of 100 kb according to the LD decay, we found a *Phenylalanine ammonia-lyase*-gene (PAL-PGSC0003DMT400080548) within the flanking region of AnthoX_Chloro, which corresponds to the first enzyme involved in the anthocyanin biosynthetic pathway [51]. AnthoX_STS was localized at chr10:52261553 (PGSC0003DMT400045346/*STS14 protein* gene), and is strongly associated with pelargonidin, explaining 43.3% of the phenotypic variance. On chromosome X, we also reported the QTL AnthoX_Adeny, colocalized at chr10:57301864 (PGSC0003DMT400060833/*Adenylyl-sulfate kinase* gene), explaining 41.1% of the phenotypic variance of pelargonidin. The QTL AnthoI_Ser/Thr belonging to the chromosome I, was associated with the concentration of cyanidin co-localized with chr01:50785405 (PGSC0003DMT400013570/*Serine/threonine-protein phosphatase* gene) and explained 31% of the phenotypic variance. The QTL AnthoII was associated with the petunidin concentration on chromosome II (chr02:48517142,), we found the *acetyl-CoA carboxylase*-gene (ACCase–PGSC0003DMT400052139) within the flanking region of 100 kb of AnthoII. The QTL AnthoXI was associated with the delphinidin concentration, co-localized chr11:40001900 (PGSC0003DMT400019149/conserved gene of unknown function) and explained 37.4% of the phenotypic variance. Finally, the QTL AnthoXII was associated with the petunidin concentration, is located inchr12:24259182 (PGSC0003DMT400090245/Hypothetical gene of unknown function) and explained 38.2% of the phenotypic variance (Table 1, Figure 3)".

The authors would like to apologize for any inconvenience caused to the readers by these changes. The authors and editorial office would like to apologize for any inconvenience caused to the readers by these changes. The changes do not affect the scientific results. The manuscript will be updated and the original will remain online on the article webpage.

References

1. Parra-Galindo, M.A.; Piñeros-Niño, C.; Soto-Sedano, J.C.; Mosquera-Vasquez, T. Chromosomes I and X Harbor Consistent Genetic Factors Associated with the Anthocyanin Variation in Potato. *Agronomy* **2019**, *9*, 366. [CrossRef]