

Genetic Insights into Color Traits in Tetraploid Andigenum Potatoes

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Abstract

The abstract serves both as a general introduction to the topic and as a brief, non-technical summary of the main results and their implications. Authors are advised to check the author instructions for the journal they are submitting to for word limits and if structural elements like subheadings, citations, or equations are permitted.

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1 Introduction

Potato (*Solanum tuberosum L.*) is the most important non-cereal crop in the world (worldwide) and is essential for food security (Reyes-Herrera et al., 2024). The origin of cultivated potatoes includes the Andean and Chilean landraces, with the Andean landraces being the most widely grown. In addition, Andean landraces have high morphological and genetic diversity (Spooner et al., 2005). Several studies from the



Fig. 1 Color variation in tuber skin and flesh among CCC accessions.

Andean region have reported color and nutritional diversity in Peru ([Bellumori et al., 2020](#)), Ecuador ([Balladares and Ramos, 2018](#)), Argentina ([Calliope et al., 2018](#)), and Colombia ([Berdugo-Cely et al., 2017, 2023](#)).

Plant color measurements have evolved over time. Initially, it relied on human perception, followed by color matching with predefined charts. Currently, more accurate and objective methods involve spectrometric and photographic color measurements ([Kasajima, 2019](#)). However, characterizations using color descriptors must be consistent, and for this purpose, it is necessary to relate characterizations with different descriptors.

2 Materials and Methods

The Colombian Central Collection of potatoes (CCC) is one of the most diverse collections in Colombia and the most important source of genetic variability for the improvement of this crop in Colombia ([Manrique-Carpintero et al., 2023](#)). Currently, the CCC clonal collection conserved in the field preserves 1225 accessions, with 68.8% consisting of *Solanum tuberosum* subsp. *andigenum* landraces. Most accessions were collected before 1985.

The regeneration of the CCC is conducted annually in the municipality of Zipaquirá (See Figure 2), located in the department of Cundinamarca, Colombia. This area is situated at an altitude of 2,950 m, with an average temperature of 15°C and a relative humidity of 75% ([Berdugo-Cely et al., 2017](#)).

2.1 Genotypic data

A set of 657 tetraploid accessions from the CCC, consisting of the *S. tuberosum* group Andigenum, was previously genotyped ([Berdugo-Cely et al., 2017](#)) using the Illumina



Fig. 2 Aerial image of the CCC field collection in 2022, with each furrow representing an accession, consisting of 20 plants. The orthophoto was created using images captured by a P4 UAV at an altitude of 12 meters in September 2022.

Infinium SolCAP SNP array (8303 SNP). The array was processed on the Illumina HiScan SQ system (Illumina, San Diego, CA) at AGROSAVIA, and the ClusterCall R package ([Schmitz Carley et al., 2017](#)) was used to obtain the dosage genotype calls from the Theta values and(?) raw data values, applying default parameters, and calibration from F1 populations supported by the software. This resulted in a genotype call matrix (0: AAAA, 1: AAAB, 2: AABB, 3: ABBC, and 4: BBBB) for each SNP across all accessions.

To ensure data quality and reliability for subsequent GWAS analyses, standard filtering criteria were applied. SNPs with a minor allele frequency (MAF) below 1% were excluded to eliminate rare variants that may lead to spurious associations due to insufficient statistical power ([Anderson et al., 2010](#)). Individuals with a genotype call missing rate (MIND) greater than 10% were removed to avoid bias introduced by low-quality samples. SNPs with a missing rate (GENO) of $\geq 10\%$ were filtered to maintain marker integrity and reduce imputation noise. Additionally, SNPs with

Hardy-Weinberg equilibrium (HWE) p-values below 1e-10 were excluded because extreme deviations may indicate genotyping errors, population structure artifacts, or selection (Wigginton et al., 2005). These thresholds are commonly used in polyploid GWAS studies and are consistent with established quality control practices (Lu et al., 2013; Pavan et al., 2020). Following this filtering process, 4,641 SNPs were retained for downstream genomic analyses.

2.2 Phenotypic data

Annual regeneration of CCC was used to characterize morphological traits. The field consists of seven square meters allocated for planting 20 seed tubers per accession. Due to the large size of the *S. tuberosum Andigenum* group collection and limited human resources, 600 accessions were evaluated over three years from 2015 to 2017. Color traits were characterized for stem (7 codes), berry (7 codes), and primary and secondary colors of the flower (8 and 9 codes, respectively), tuber skin (9 and 10 codes, respectively), tuber flesh (8 and 9 codes, respectively), and sprout (5 and 6 codes, respectively), using the descriptors proposed by Gómez (2000).

Additionally, in 2019, color characterization was performed using the fifth edition of the Royal Horticultural Society (RHS) color chart (Voss, 2002) to provide a more detailed color evaluation. This change expanded the codes from a maximum of ten options to a set of 884 codes. The chart was used to characterize the following nine traits: stem color (StemC), berry color (BerryC), primary flower color (PCFlower), primary tuber skin color (PCTuberskin), secondary tuber skin color (SCTuberskin), primary tuber flesh color (PCTuberflesh), secondary tuber flesh color (SCTuberflesh), primary sprout color (PCSprout), and secondary sprout color (SCSprout).

Moreover, the color characterization using the RHS color chart was converted to the Hue, Chroma, and Lightness (HCL or LCH) color space, as this model is closely aligned with human color perception and has been used in previous studies on potato color (Caraza-Harter and Endelman, 2020). The values of these LCH traits were derived from the transformation of the values of the potato color traits, measured using the Royal Horticultural Society (RHS) fifth edition color chart (<http://rhscf.orgfree.com/>) (Voss, 2002), into the three components: L, C, and H, of the Commission Internationale de l'Éclairage (CIE) LCH or CIE*L*C*h color space. Consequently, three components were obtained for each potato color trait, which will be referred to as LCH traits. Thus, the nine potato color traits were transformed into 27 LCH traits, which were used for genomic analyses (Fig. S1). As no outliers were detected, all available data were included in the analysis.

Correlation between two color descriptors

Two descriptors with different numbers of codes were used to characterize the color traits in CCC in different years. The correlation between the evaluations of both descriptors was calculated for each of the nine color traits using Cramer's V statistic (Lyman et al., 1986). Cramer's V measures the strength of the association between two qualitative variables, with values ranging from 0 to 1. Values below 0.6 indicate a weak association, while values of 0.6 or higher indicate a medium to strong association.

To study the genetics underlying color, we selected traits with a medium-to-strong association, indicating genetic influence.

Linking Color to Nutritional and Nutraceutical Variables

This study also examined the association between color traits and nutritional and nutraceutical values using data from a previous study [Berdugo-Cely et al. \(2023\)](#). The nutritional traits of the potatoes were represented by the Ascorbic Acid Content (AAC), while the nutraceutical traits were: Total Phenol Content (TPC) and Antioxidant Activity (measured by 2,2-Diphenyl-1-picrylhydrazyl Radical Scavenging Activity - DPPH and Ferric Reducing Antioxidant Power - FRAP assays). Given that the nutritional and nutraceutical variables were continuous, and the color traits were categorical, the determination coefficient was applied as a measure of association [Nagelkerke et al. \(1991\)](#). To evaluate these associations, data from 282 Andigenum accessions in the CCC collection, which included information on both sets of traits, were analyzed.

2.3 GWAS analysis

A previous GWAS study by [Berdugo-Cely et al. \(2017\)](#) employed the same genetic dataset and color descriptors as those defined by [Gómez \(2000\)](#). In contrast, the present study used the RHS color chart as a phenotype for color characterization, increasing the number of trait values from 30 to 884, thus achieving greater resolution.

We utilized MultiGWAS ([Garreta et al., 2021](#)), a tool that integrates the outputs from multiple GWAS methods. Specifically, we incorporated the results from GWASpoly ([Rosyara et al., 2016](#)) for tetraploid genotypes and GAPIT ([Tang et al., 2016](#)) for diploid genotypes. The analysis was conducted using the MultiGWAS Full Model (Q+K), which controls for population structure (Q, typically derived from principal component analysis) and kinship (K, based on a genetic relatedness matrix), thereby reducing the likelihood of false-positive associations.

In MultiGWAS, each tool implements a mixed linear model (MLM) (Phenotype Genotype + Q + K), but with method-specific adjustments. GWASpoly adapts the MLM for polyploid data, incorporating population structure and kinship as fixed and random effects, respectively. GAPIT employs a standard MLM, treating the population structure (Q) as a fixed effect (e.g., from PCA) and kinship (K) as a random effect via its kinship matrix. By unifying these approaches, MultiGWAS robustly controls for population stratification and relatedness while detecting marker-trait associations across ploidy levels (diploid and tetraploid).

To address the issue of multiple testing, the MultiGWAS tool applies the Bonferroni correction. However, instead of adjusting the *p-values*, MultiGWAS adjusts the threshold to determine a significant *p-value*. Specifically, this threshold is set to α/m , where α represents the significance level and m is the number of tested markers from the genotype matrix. The CMPlot library ([Yin et al., 2021](#)) was used to generate Manhattan and Circos plots to visualize significant SNP markers.

Candidate Marker Identification

Given the evaluation of multiple traits and the integration of results from the four GWAS tools in MultiGWAS, we developed a proprietary scoring function called GSCORE. This function was designed to rank markers by incorporating the outputs from the MultiGWAS. Specifically, GSCORE selected the top 50 markers with the lowest p-values from each tool, resulting in 100 markers (2 tools \times 50 markers). GSCORE is calculated as the sum of three weighted terms: inflation factor (I), contributing 70% of the score. Replicability (R) accounts for 10%, and significance (S) accounts for the remaining 20%. The scoring function is represented by the following equation:

$$GSCORE(M) = 0.7 * I + 0.1 * R + 0.2 * S$$

I is the inflation factor score, defined as $I = 1 - |1 - \lambda(M)|$, where $\lambda(M)$ is the inflation factor for marker M. This score is the highest when $\lambda(M)$ is close to 1. In addition, R is the number of SNPs shared among the three GWAS tools. Finally, S is a binary value (1 or 0) that indicates whether the SNP is significant (p-value \leq threshold). Marker M achieves a high $GSCORE$ when it has an inflation factor $\lambda(M)$ close to one, identifies a large number of shared SNPs across tools, and is statistically significant. In contrast, the score is low if $\lambda(M)$ is either too low (close to 0) or excessively high, identifies few shared SNPs, or is not significant. In other scenarios, the score is determined by a balance between the inflation factor, shared SNP count, and significance. This approach prioritizes markers that are statistically robust, consistent across tools, and highly significant.

Marker annotation

Markers were annotated by taking information from the Potato Genome Sequencing Consortium (PGSC) public data based on the double monoploid *S. tuberosum* Group Phureja from assembly DMv6.1([Pham et al., 2020](#)) obtained from the SpudDB website. Annotation was performed by associating marker identifiers with information from both the high confidence gene models annotation, the InterProScan assigned GO terms for the working gene models, the InterProScan search results for the working gene models, and the SolCAP 69 K SNP positions on the DMv6.1 assembly available in SpudDB. Furthermore, for each trait, the amino acid sequences were analyzed using BlastKOALA ([Kanehisa et al., 2016](#)) for KEGG mapping to identify common functional categories among the significant markers.

2.4 Heritability

Narrow-sense heritability h^2 , defined as the proportion of phenotypic variance explained by additive effects ([de los Campos et al., 2015](#)), was estimated for all LCH components using by the following equation:

$$h^2 = \frac{\sigma_a^2}{\sigma_y^2}$$

where σ_a^2 denotes additive genetic variance and σ_y^2 denotes phenotypic variance. These variances were obtained by fitting a whole-genome regression model using Bayesian regression implemented in the BGLR package in R ([Pérez and de los Campos, 2014](#)).

2.5 Genomic Prediction (GP)

We used 12 Genomic Prediction (GP) models with a large number of genetic markers to generate genomic estimated breeding values (GEBVs) for each of the 27 LCH traits. The genomic prediction (GP) models encompassed three categories: parametric models—including Genomic Best Linear Unbiased Prediction (GBLUP), Estimated Best Linear Unbiased Prediction (EGBLUP), Ridge Regression (RR), and Least Absolute Shrinkage and Selection Operator (LASSO); semiparametric models—comprising Reproducing Kernel Hilbert Spaces (RKHS), Random Forest (RF), and Support Vector Machine (SVM); and Bayesian models—including Bayesian Ridge Regression (BRR), Bayesian LASSO (BL), Bayes A, Bayes B, and Bayes C. Additionally, to identify the optimal number and type of markers for estimating GEBVs, various subsets of markers generated through GWAS were tested. The R package for the Breed Wheat Genomic Selection Pipeline (BWGS) ([Charmet et al., 2020](#)) was used. Furthermore, 5-fold cross-validation, repeated five times, was employed to assess the performance of the 12 models for each LCH trait. The parameter values for running each model were set to the default settings provided by the BWGS library.

2.5.1 GP using marker subsets

To determine the optimal number of markers for genomic prediction (GP) of each LCH color trait component, GP was conducted using subsets containing varying numbers of markers. These markers were selected based on GWAS results and prioritized according to their relevance using our custom GSCORE scoring function (see Section [2.3](#)).

3 Results

The distribution for the three components of the color traits can be seen in Figure S1 in the supplementary information.

3.1 Correlation between descriptors

The correlations between the values of the color traits measured with the two color descriptors over different years are presented in Figure [3 A](#). Among the traits, only berry color and primary tuber flesh color exhibited weak correlations, leading to their exclusion from the genetic study. In contrast, the remaining seven color traits showed moderate to strong correlations, ranging from 0.65 to 0.97. Although some color traits were correlated with others, all moderate to strong correlations, as expected, were concentrated along the diagonal of the correlation matrix. In particular, there were correlations between primary and secondary tuber skin colors, between primary tuber skin color and both primary and secondary tuber flesh colors, and between primary and secondary sprout colors.

3.1.1 Linking Color to Nutritional and Nutraceutical Variables

In Figure [3 B](#), the heatmap presents the determination coefficient R^2 between the color traits measured using the RHS color scale and nutritional/nutraceutical variables. R^2

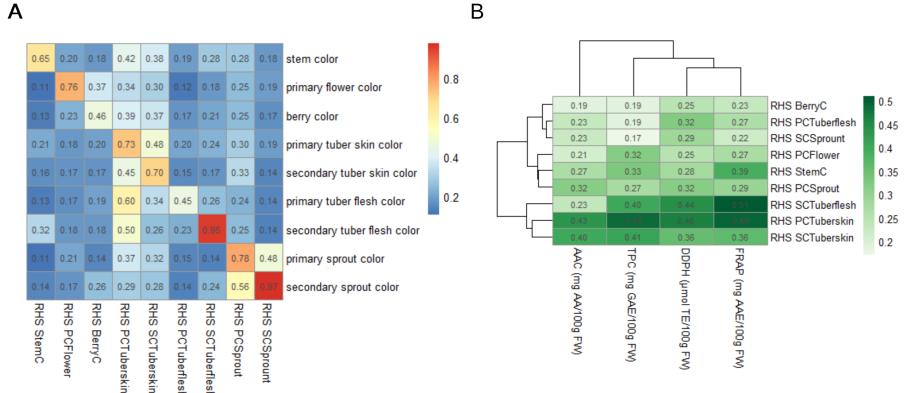


Fig. 3 **A.** Heatmap showing the correlation matrix of potato color traits in CCC accessions, derived from color descriptors by Gómez (2000) and measured with RHS (Voss, 2002) color chart. The color bar is located in the top right, with blue indicating low correlation values and red representing high correlation values. **B.** Heatmap showing the determination coefficient between nutritional (AAC) and nutraceutical (TPC, DPPH, and FRAP assay reported by (Berdugo-Cely et al., 2023) components and potato RHS color traits. The color bar is located at the top right, with the intensity of green representing the determination coefficient.

below 0.3 reflect a weak association (blue cells), while R^2 between 0.3 and 0.51 reflects a moderate association between color traits and nutritional variables (yellow and red). Three specific traits—the secondary color of the tuber flesh and the primary and secondary colors of the tuber skin—exhibited notable associations with nutritional variables. Antioxidant activity (measured using FRAP and DPPH assays) showed the strongest correlation with these traits. Additionally, Total Phenol Content and Ascorbic Acid Content demonstrated the highest association with the primary color of the tuber skin. Stem color, meanwhile, showed a moderate association with antioxidant activity and Total Phenol Content.

3.2 GWAS Analysis

GWAS analysis identified 21 significant SNPs associated with five traits: ten related to the secondary color of the tuber flesh, four to the primary color of the flower, three to the primary color of the sprout, two to the secondary color of the sprout, and two to the stem color. Manhattan plots for all seven traits are presented in Figure 4 (A-G). The most significant SNPs were associated with the Hue component and secondary color of the tuber flesh trait.

Notably, chromosome 2 accounted for 28.5% of the significant SNPs, followed by chromosomes 1 and 11, each contributing 19% and 14.29%, respectively. A Circos plot (Figure S2) combines the data for all seven traits and presents the density of SNP markers for chromosomes, allowing the visualization of SNP co-occurrence across different traits.

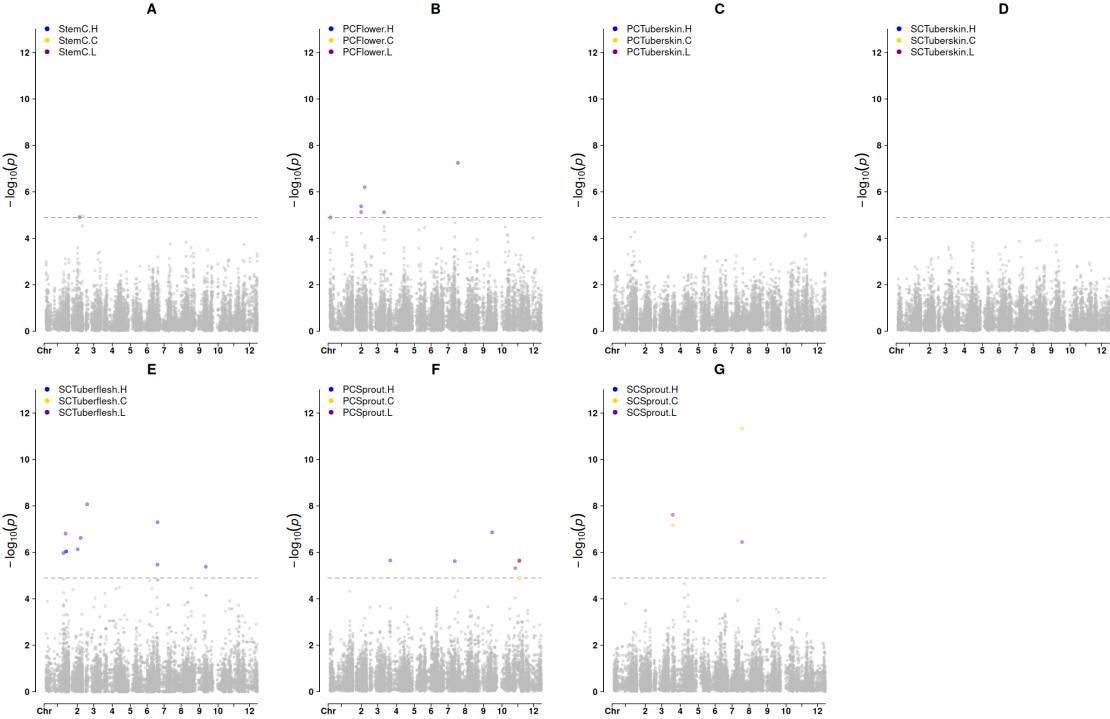


Fig. 4 (A-G) Manhattan plots show the markers linked to LCH traits, with colors indicating the significant SNPs associated with each LCH color component.

A total of 21 significant associations were detected across the nine HCL components that corresponded to five traits. These associations involved 21 SNP markers annotated with 21 genes, represented by a total of 33 transcripts. A total of eight functional pathway categories were identified based on genes annotated with significant SNPs: seven belonged to the metabolism category and one to the genetic information processing category. Information on the primary annotations linked to these markers, as retrieved from the SPUD database, is provided in Supplementary Table 1, and the specific functional categories per trait are provided in Supplementary Table 2.

Moreover, GWASpoly and GAPIT identified 50% of the significant SNPs, with both tools jointly predicting nine SNPs, representing 42.85% of the total. Although no common SNPs were found across the different traits, four SNPs were associated with distinct HCL components of the same trait.

3.3 Heritability

In general, most traits exhibit high average heritability values (≥ 0.5), with the exception of the secondary color of the sprout. Figure 5 A. shows the heritability of the selected LCH traits. The primary color of the flower and secondary color of the tuber flesh exhibited high heritability values (greater than 0.9) for the two LCH traits. Furthermore, the color of the stem showed heritability of ≥ 0.8 .

3.4 Genomic Prediction

The results for genomic prediction (GP) using all 4,641 markers from the potato dataset are in Figure 5 B. Predictive ability corresponds to the correlation between the observed phenotype values and the predicted genomic estimated breeding values (GEBV) in the validation set. Primary flower color and stem color exhibited the highest predictive abilities, followed by the primary color of the tuber skin and the primary color of the tuber sprout. However, the secondary colors of sprouts, tuber flesh, and tuber skin showed low predictive ability.

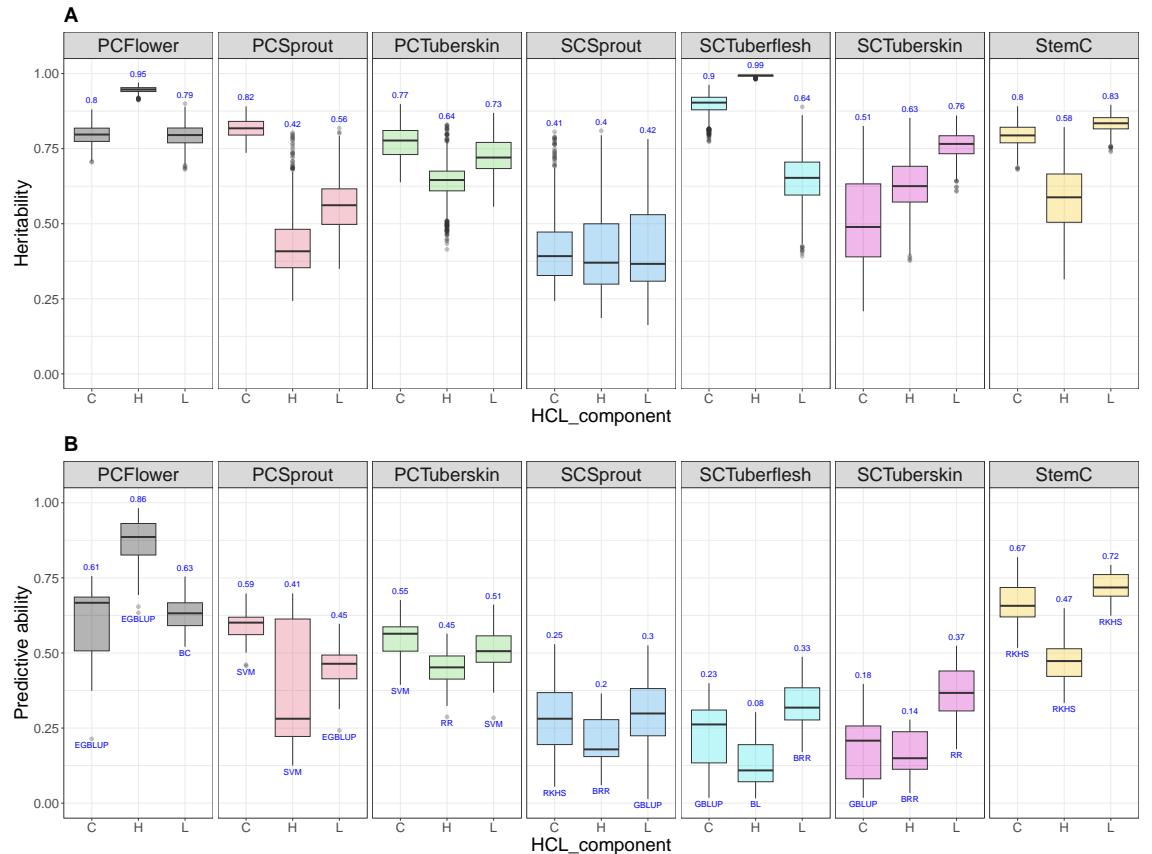


Fig. 5 A . Estimated heritabilities for LCH traits. At the top of each division is the name of the potato color trait, whereas at the bottom is the LCH component of that trait being evaluated. **B. Predictive abilities of GS models for LCH traits.** Comparison of genomic predictions for LCH components using the full set of markers. The horizontal axis represents the three LCH components for each of the seven potato color traits, while the vertical axis displays the predictive ability values ranging from 0 to 1. The mean predictive ability is displayed at the top of each boxplot, while the model that achieved the best prediction is indicated at the bottom.

3.4.1 GP using marker subsets

Genomic prediction was performed using marker subsets representing 5%–100% of the 4,641 SNPs. Predictive ability, assessed by the Pearson correlation between observed phenotypes and genomic estimated breeding values (GEBVs), varied by trait and marker density (see Figure S3).

In general, predictive ability increased rapidly with marker density up to 40%–50% of the total set, after which gains plateaued, indicating diminishing returns. This pattern held across most color traits and LCH components (Hue, Chroma, Lightness), suggesting that a moderate number of well-distributed, informative SNPs can achieve predictive performance comparable to that of the full marker set.

Stem color and primary flower color traits consistently showed higher predictive abilities, with correlations nearing 0.75 at full marker density. In contrast, secondary traits, such as secondary tuber flesh or sprout color, showed lower predictive values, even with more markers. This variability reflects differences in genetic architecture, with some traits likely controlled by major loci and others influenced by more polygenic and complex effects.

These results support the feasibility of cost-effective genomic selection for tetraploid *Andigenum* potatoes by using an optimized SNP subset. The top 50% of markers, selected via the GSORE metric (Section 2.3), effectively captured the relevant genetic variation, enabling accurate predictions while reducing the computational demand.

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