Seed coat color genetics and genotype × environment effects in yellow beans via machine-learning and genome-wide association

Rie Sadohara1 | Yunfei Long2 | Paulo Izquierdo1 | Carlos A. Urrea3 | Daniel Morris2 | Karen Cichy1,4

1 Dep. of Plant, Soil and Microbial Sciences, Michigan State Univ., 1066 Bogue St., East Lansing, MI 48824, USA
2 Dep. of Electrical and Computer Engineering, Michigan State Univ., 428 S Shaw Ln., East Lansing, MI 48824, USA
3 Panhandle Research & Extension Center, Univ. of Nebraska, 4502 Ave. I, Scottsbluff, NE 69361, USA
4 USDA–ARS, Sugarbeet and Bean Research Unit, 1066 Bogue St., East Lansing, MI 48824, USA

Correspondence
Karen Cichy, Dep. of Plant, Soil and Microbial Sciences, Michigan State Univ., 1066 Bogue St., East Lansing, MI 48824, USA. Email: Karen.Cichy@usda.gov

Assigned to Associate Editor Qijian Song.

Abstract
Common bean (Phaseolus vulgaris L.) is consumed worldwide, with strong regional preferences for seed appearance characteristics. Colors of the seed coat, hilum ring, and corona are all important, along with susceptibility to postharvest darkening, which decreases seed value. This study aimed to characterize a collection of 295 yellow bean genotypes for seed appearance and postharvest darkening, evaluate genotype × environment (G × E) effects and map those traits via genome-wide association analysis. Yellow bean germplasm were grown for 2 yr in Michigan and Nebraska and seed were evaluated for L*a*b* color values, postharvest darkening, and hilum ring and corona colors. A model to exclude the hilum ring and corona of the seeds, black background, and light reflection was developed by using machine learning, allowing for targeted and efficient L*a*b* value extraction from the seed coat. The G × E effects were significant for the color values, and Michigan-grown seeds were darker than Nebraska-grown seeds. Single-nucleotide polymorphisms (SNPs) were associated with L* and hilum ring color on Pv10 near the J gene involved in mature seed coat color and hilum ring color. A SNP on Pv07 associated with L*, a*, postharvest darkening, and hilum ring and corona colors was near the P gene, the ground factor gene for seed coat color expression. The machine-learning-aided model used to extract color values from the seed coat, the wide variability in seed morphology traits, and the associated SNPs provide tools for future breeding and research efforts to meet consumers’ expectations for bean seed appearance.

1 INTRODUCTION

Common bean (Phaseolus vulgaris L.) is a nutrient-dense food consumed worldwide, with an annual world production of 29 Tg (average of 2016–2019; FAOSTAT, 2021). Beans serve as an excellent source of protein, dietary fiber, and micronutrients and offer numerous health benefits including prevention and control of cardiometabolic diseases and certain types of cancer (Hayat et al., 2014; Messina, 2014). The seed appearance of beans is diverse with various shapes, sizes, colors, and patterns, the combinations of which form specific bean market classes (seed types) (González et al., 2006; Uebersax & Siddiq, 2012; Wortmann et al., 1998). Therefore,
bean breeders develop cultivars with morphological characteristics that meet the market demands in their target regions (Beebe, 2020; Castellanos et al., 1996; O. Voysest et al., 1994). In addition to the primary seed color and pattern, the hilum ring and corona color are also essential parts of seed appearance.

Since early in the 20th century, extensive research has been conducted to identify genes responsible for producing bean seed coat color. Prakken (1972, 1974) consolidated initial findings and developed a model for color expression in the bean seed coat, which, to date, is generally accepted. The model groups color-related genes into three categories: a ground factor gene, color genes, and color-modifying genes. A ground factor gene, P, is necessary for any seed color expression, and genotypes with homozygous recessive p produce a white seed coat. The P gene was later found to encode a transcription factor required for flavonoid biosynthesis (McClellan et al., 2018). Color genes include C, Z, and J genes. Multiallelic C locus is tightly linked with other genes, forming ’complex C locus’, which are involved in different color and pattern expressions (Bassett, 2007). The Z gene gives a brown hilum ring and is also involved in partly colored seed coat (Bassett et al., 1999). The J gene is involved in multiple traits such as seed coat color formation during maturation, a brown hilum ring, seed coat shininess, and postharvest darkening (Bassett, 1996; Prakken, 1970). Postharvest darkening refers to a phenomenon where seed color of some market classes darkens over time during storage. Postharvest darkening is an important trait for bean producers because consumers consider darkened seeds as old and long cooking, so darkened seeds may be of lower economic value (Junk-Knievel et al., 2008). Previous studies have shown that two unlinked interacting genes control postharvest darkening, J and sd, with the J genotype presenting postharvest darkening, jj genotype showing no darkening, and recessive sdsd paired with J showing slow darkening (Elsadr et al., 2011; Junk-Knievel et al., 2008). Gene sd has been confirmed to be an allele of the ground factor P and is denoted as psd (Islam et al., 2020). Color-modifying genes do not confer a color by themselves but intensify color expression of the color genes. Color-modifying genes include G for yellow-brown, B for greenish yellow-brown, V for purple to black, Rk for recessive red, R for dark red, and Gy for greenish-yellow (Bassett, 2002; Bassett et al., 2010; Beninger & Hosfield, 1999). The mechanism of color expression is complicated; some of the genes are multiallelic, and they interact with each other to collectively determine the colors and patterns of seed coat, hilum ring, corona, pods, and flowers (Bassett, 2007).

Although seed coat colors could be treated as a qualitative trait controlled by major genes, more recent research has quantitatively measured colors using CIE L*a*b* values (CIE International Commission on Illumination, 2004). The CIE L*a*b* expresses colors with three values, L*, a*, and b*, which measure lightness, greenness—redness, and blueness—yellowness, respectively defined as axes in a three-dimensional color space. L*a*b* values are perceptually uniform, meaning that the degree of difference between two colors corresponds to the Euclidean distance of them in the L*a*b* space (León et al., 2006). Expressing colors using numerical values enables an objective measurement of color rather than a subjective description. Traditionally, colorimeters were used to measure color values, but image-based, computer-vision technology has also been used (Wu & Sun, 2013). Image-based color measurement provides a better representation of samples because it can obtain L*, a*, and b* values from each pixel of an image, and a larger surface area can be sampled compared with conventional colorimeters (León et al., 2006). Depending on the type of samples, images can contain pixels that do not represent the specimen. In the case of bean seed coat color measurement, the nontarget pixels would be the white hilum, a hilum ring, and corona of seeds as well as the imaging background and light reflection. Measuring color values without excluding those could result in differences in color values because of a darker hilum ring and corona despite the same seed coat color of two bean samples. Machine learning presents a potential to segment seed coat from nontargets in bean seed images because machine learning has been used to separate target features from nontargets of plant images (Amatya et al., 2016; Ferentinos, 2018; Grinblat et al., 2016).

Numerous polyphenolic compounds exist in the seed coat of common bean such as flavonoids (Yang et al., 2018), which are considered to impart bean seed color (Beninger et al., 1998; Feenstra, 1960). Flavonoids present in the bean seed coat can be subclassified into flavonols, flavanols, and anthocyanidins (Reddy et al., 1985). Anthocyanidins are glycosides of anthocyanins, including cyanidin, pelargonidin, and delphinidin, and are found in pink, red, and black bean seeds (Rodríguez-Madrida et al., 2020; Takeoka et al., 1997). Proanthocyanidins (condensed tannins) are dimers or polymers of flavanols, including catechin and epicatechin (Dixon et al., 2005). Proanthocyanidins produce brown deposits upon

---

**Core Ideas**

- Postharvest darkening in yellow beans is associated with P gene.
- Environment influences yellow seed coat color independent of postharvest darkening.
- Imaging combined with machine learning is a useful way to measure bean seed coat color.
- Genotype and environmental differences in bean seed coat color are detectable via imaging.
oxidation in pinto bean seeds and are associated with postharvest darkening (Beninger & Hosfield, 2003; Marles et al., 2008). Proanthocyanidins are also involved in plant defense against pests and pathogens (Islam et al., 2003; Winkel-Shirley, 2001). In addition to seed coat color and plant defense responses, the concentrations of polyphenolic compounds influence quality attributes of beans such as cooking time, digestibility, and iron bioavailability (Bressani & Elías, 1979; Elia et al., 1997; Petry et al., 2010; Tako et al., 2014).

Yellow bean is an important market class in eastern and southern Africa and Latin America (Voysest, 2012; Wortmann et al., 1998). Yellow bean is diverse in seed morphology (Figure 1), and at least a dozen yellow-seeded market classes exist in Latin America alone (Voysest, 2012). One of the valuable attributes of some yellow bean cultivars is that they do not exhibit postharvest darkening. The susceptibility to postharvest darkening of yellow bean is mainly unknown except that genetic variability and a quantitative trait loci (QTL) for postharvest darkening near the J gene were reported among Manteca and green–yellow types and their progeny population (Bassett et al., 2021). Postharvest darkening is known to occur in carioca bean, which have light brown stripes on a cream background similar to pinto bean (Junk-Knievel et al., 2008); therefore, some yellow bean cultivars may be susceptible to postharvest darkening.

Evidence is accumulating that a lemon-yellow seeded type, Manteca, is a promising breeding material because of its high digestibility, short cooking time, and high iron bioavailability (Cichy et al., 2015; Engleright et al., 1999; Hart et al., 2020; Hooper et al., 2016; J. Wiesinger et al., 2018; Wiesinger et al., 2019). Other yellow bean cultivars’ convenience and nutritional qualities have yet to be assessed despite their wide morphological diversity. Therefore, the Yellow Bean Collection (YBC) has been assembled with yellow-seeded P. vulgaris germplasm collected globally (Supplemental Figure S1). Although high heritability estimates (73–99%) were reported for color values with populations derived from yellow-seeded beans (Arns et al., 2018; Bassett et al., 2021; Possobom et al., 2015; Ribeiro et al., 2019), growing conditions could influence their seed coat colors (Kelly et al., 2021; Possobom et al., 2015). Thus, the genotype × environment (G × E) effects on the seed color of the YBC should be evaluated to develop bean cultivars that meet the consumers’ expectations in various bean production regions. Quantitative characterization of the seed coat colors of the YBC would enable an objective evaluation of their appearance, an important characteristic to consumers.

The objectives of this study were to (a) assess the genetic diversity of the YBC of 295 yellow bean genotypes for seed coat color values via a machine-learning aided procedure; (b) to assess the postharvest darkening of the YBC; and (c) investigate the genetic control and the G × E on these traits to aid breeding of beans with desired morphological, nutritional, and culinary characteristics.
2 MATERIALS AND METHODS

2.1 Plant materials

A yellow bean diversity panel, the YBC, comprising 295 genotypes, was used in this study. The YBC was grown in randomized complete block design with two field replications in two environments, Michigan and Nebraska, USA, in 2018 and 2019. The number of genotypes phenotyped for color, postharvest darkening, and hilum ring and corona colors are shown in Supplemental Table S1.

2.2 CIE L*a*b* of bean seed coat

The YBC contained solid-colored and patterned seed types, but the solid-colored types were used for seed coat color measurements. The genotypes used for color measurements were as follows: 37 Amarillo dark, 44 Amarillo light, six beige, seven brown, 83 Canary, six green–yellow including Njano, 11 Manteca, 56 Mayocoba, and three white genotypes. One layer of solid-colored, intact whole seeds were placed in a 70-by 70-mm box with matte black walls. Images of bean seeds from each of the two field replications were taken by using an image acquisition system described by Mendoza et al. (2017) with the shutter speed set to 1/100 s. To extract bean color from captured images via machine learning, a binary pixel classification was defined in which pixels representative of bean color are one category, and the remaining pixels, that is, background, hilum ring, corona, and specular reflection areas, are the second category. The pyramid convolutional neural network described in Long et al. (2019) to detect bean seed coat splits was retrained for this color pixel segmentation task. To train the network, semantic labels for 24 images (including 17 images for training and seven for validation) of various bean types and colors within the YBC were created manually and augmented by rotation (at 30° intervals) and flipping. The training was performed for eight epochs by using ADADELTA (Zeiler, 2012) as the optimizer with a learning rate of one and pixel-wise cross-entropy as the loss function. The network achieved 0.95 average precision in bean pixel classification on a validation set and so was able to effectively eliminate nondesired pixels (identified as pixels with predicted probability for the second category larger than 0.3) from images as illustrated in Figure 2. The source code, annotated images, and trained model are available online (https://github.com/longyunf/extract-bean-color).

Bean images were downsampled to 432 by 432 pixels using a custom MATLAB script (MATLAB, 2020), and the segmentation model was applied. The CIE L*, a*, and b* values were extracted from valid pixels in the images by scikit-image in Python (van der Walt et al., 2014). The L*a*b* values were calibrated using an image of Macbeth color checker chart (X-Rite) taken under the same conditions as the YBC at the start of image acquisition each year. The 24 color patches in the Macbeth color checker chart image were cut out into 100- by 100-pixel squares using ImageJ 1.52v (Schneider et al., 2012), and the L*a*b* values were extracted from each patch by the scikit-image in Python. The extracted L*a*b* values and the standard values of the patches were used to build a partial least squares model by the PLS package (Mevik et al., 2020) in R (R Core Team, 2017). Specifically, SIMPLS, a faster and improved partial least squares model (de Jong, 1993) with three components, was used to calibrate L*a*b* values of the YBC bean images, and calibration was carried out each year to accommodate potential changes in lighting intensity over the 1-yr period. The L*a*b* color values were evaluated for 252 genotypes in Michigan in 2018, 250 in Michigan 2019, 209 in Nebraska 2018, and 195 in Nebraska, depending on the seed availability and adaptation (Supplemental Table S1).

To evaluate the difference in seed coat colors between the environments, ΔL*, Δa*, and Δb* were calculated as the mean L*a*b* values in Michigan subtracted by those in Nebraska for each genotype. The ΔE was computed as follows: \[ \Delta E = \sqrt{\Delta L^2 + \Delta a^2 + \Delta b^2}. \]

2.3 Postharvest darkening

Postharvest darkening of MI2019 seeds (both solid-colored and patterned) was evaluated via an ultraviolet test developed by Junk-Knievel et al. (2007). In summary, ~10 seeds per sample per field replication were placed in a clear plastic seed tray. The tray held 60 samples in total. Trays containing seeds were placed ~10 cm under a UV light for 96 h. After that time period, the seeds were scored for darkening as 0 for non- or slow darkening and 1 for darkening. Some of the dark-seeded genotypes, such as brown and Amarillo (dark) types, were excluded from this evaluation.

2.4 Hilum ring and corona colors

The hilum ring and corona colors were evaluated of the MI2019 seeds (both solid-colored and patterned). The hilum ring colors were classified into two categories: 0 for yellow and 1 for dark. The corona colors were classified into two categories: 0 for light or yellow and 1 for dark.

2.5 Statistical analyses

The L*a*b* values were transformed using the Box–Cox method (Box & Cox, 1964) by using the MASS package.
FIGURE 2 (a) Original, (b) segmented by convolutional neural networks, and (c) masked images. The probability of each pixel of being seed coat is color-coded from dark blue (high) to yellow (low) in (b)

The genotype, environment, and year effects on the color values were estimated by the following mixed linear model:

\[ Y_{ijkl} = \mu + G_i + E_j + Y_k + EY_{jk} + GE_{ij} + GY_{ik} + GEY_{ijk} + B(EY)_{jkl} + e_{ijkl}, \]

where \( Y_{ijkl} \) is the phenotypic value of the \( i \)th YBC genotype grown in the \( l \)th block of the \( j \)th environment in the \( k \)th year; \( \mu \) is the grand mean; \( G_i \) is a random effect of the \( i \)th genotype; \( E_j \) and \( Y_k \) are fixed effects of the \( j \)th location and the \( k \)th year, respectively; \( EY_{jk} \), \( GE_{ij} \), and \( GY_{ik} \) are two-way interaction terms; \( GEY_{ijk} \) is a three-way interaction term; \( B(EY)_{jkl} \) is a random effect of the \( l \)th block nested in the \( j \)th environment and the \( k \)th year; and \( e_{ijkl} \) is the error term. The variance components of the model were used to estimate the broad-sense heritability of the phenotypic values (Fehr, 1987). To minimize the environment and year effect, best linear unbiased estimate (BLUE) was calculated for the \( L^* \), \( a^* \), and \( b^* \) values by setting the genotype as a fixed effect and all other terms as random effects using the emmeans package (Lenth, 2021) in R. All the models were fitted using the lme4 (Bates et al., 2015) and the lmerTest (Kuznetsova et al., 2017) packages in R. The BLUE values were used for principal component (PC) analysis and genome-wide association analysis. Principal component analysis was performed using prcomp function and was visualized using the factoextra package (Kassambara & Mundt, 2020) in R.

### 3 RESULTS AND DISCUSSION

#### 3.1 Phenotypic diversity of seed coat, hilum ring, and corona colors and postharvest darkening

Employing the machine-learning technology, seed coat was successfully separated from hilum and corona of seeds, black background, and light reflection after feeding 24 hand-labeled images for training. The model correctly distinguished pixels of seed coat of \( >1,800 \) images of the YBC genotypes
TABLE 1 Descriptive statistics of L*a*b* values of the Yellow Bean Collection

| Trait | Environment–year | Min. | Max. | Median | Mean | SD |
|-------|------------------|------|------|--------|------|----|
| L*    | MI 2018          | 27.6 | 84.6 | 68.8   | 66.7 | 10.2|
|       | MI 2019          | 31.0 | 84.5 | 70.7   | 67.8 | 9.7 |
|       | NE 2018          | 33.5 | 85.3 | 71.6   | 69.9 | 10.0|
|       | NE 2019          | 31.9 | 86.0 | 73.1   | 71.7 | 9.8 |
| a*    | MI 2018          | −4.7 | 30.6 | 8.0    | 9.4  | 8.0 |
|       | MI 2019          | −3.5 | 32.1 | 8.4    | 9.9  | 8.0 |
|       | NE 2018          | −5.9 | 33.2 | 7.2    | 8.2  | 9.5 |
|       | NE 2019          | −5.6 | 35.0 | 5.8    | 7.4  | 9.7 |
| b*    | MI 2018          | 11.9 | 62.1 | 47.2   | 45.5 | 9.1 |
|       | MI 2019          | 12.6 | 62.2 | 47.8   | 46.9 | 9.0 |
|       | NE 2018          | 11.9 | 60.3 | 43.5   | 44.5 | 9.6 |
|       | NE 2019          | 12.3 | 63.6 | 45.5   | 45.7 | 10.1|

TABLE 2 Postharvest darkening of the Yellow Bean Collection genotypes by seed type

| Seed type                  | Non- or slow darkening | Darkening | Total |
|----------------------------|------------------------|-----------|-------|
| Amarillo (dark)            | 0                      | 2         | 2     |
| Amarillo (light)           | 4                      | 38        | 42    |
| Beige                      | 0                      | 6         | 6     |
| Brown                      | 0                      | 3         | 3     |
| Canary                     | 10                     | 64        | 74    |
| Green-yellow               | 3                      | 3         | 6     |
| Manteca                    | 11                     | 0         | 11    |
| Mayocoba                   | 39                     | 15        | 54    |
| White                      | 3                      | 0         | 3     |
| Amarillo dark and light mottled | 0         | 1         | 1     |
| Beige with brown stripes   | 0                      | 3         | 3     |
| White and red mottled      | 1                      | 0         | 1     |
| Total                      | 71                     | 135       | 206   |

without manual operation. The automation allows for more accurate measurement of seed coat color and saves a tremendous amount of time and labor that would have been spent on the manual processing of images. Automated separation of seed coat and hilum ring and corona areas are substantial because they are all under different genetic controls (Bassett, 2007). Bean seed colors have been measured traditionally with colorimeters (Arns et al., 2018; Erfatpour et al., 2018; Possobom et al., 2015) and more recently with ImageJ (Bassett et al., 2021; Bornowski et al., 2020; Varga et al., 2019), but the seed coat, hilum ring, and corona colors were not separated. Thus, this study has provided a novel, automated method to obtain color values from seed coat pixels.

The L* values range from 0 to 100 with 100 being the lightest; positive a* values indicate redness while negative a* indicates greenness; and positive b* indicates yellowness, while negative b* indicates blueness (León et al., 2006). A wide diversity in the seed coat color values were observed among the YBC genotypes: L* values ranged from 27.6 to 86.0, a* values from −5.9 to 35.0, and b* values from 11.9 to 63.6 (Table 1). The 2-yr average of L*a*b* values were highly correlated between the environments, but the correlation coefficient was slightly lower for the b* values (R = 0.88, p < .001), which measures yellowness, than L* and a* (R = 0.98, p < .001 for both; Supplemental Figure S2). The L* and a* values were negatively correlated (R = −0.69 in Michigan and R = −0.73 in Nebraska), and L* and b* values were moderately positively correlated (R = 0.5 in Michigan, R = 0.3 in Nebraska).

A total of 206 genotypes, excluding dark-colored seeds, were evaluated for susceptibility to postharvest darkening by the UV test. The UV test distinguished whether a sample darkened or not but did not distinguish nondarkening from slow-darkening samples. As a result, 71 were non- or slow darkening, and 135 genotypes showed a darkening phenotype (Table 2). The majority of Amarillo light and canary genotypes were darkening. All of Manteca were non- or slow darkening. ‘Prim’ Manteca bean was reported to contain no tannins (Beninger et al., 1998) and showed a jj genotype at the J locus, which would result in nondarkening (Bassett, 1999); therefore, Mantecas are expected to be nondarkening. For Mayocoba, 39 out of the 54 genotypes were slow- or non-darkening, and 14 of these were U.S. breeding lines. Because consumers highly value non- and slow-darkening seeds, as this trait is associated with freshness and shorter cooking time (Erfatpour et al., 2018; de Cássia Silva et al., 2018; Wiesinger et al., 2021), information on the postharvest darkening of the YBC is useful in developing and selecting yellow beans that meet consumers’ expectations.

A total of 258 YBC genotypes grown in MI2019 were classified based on their hilum ring and corona colors. Tables 3 and 4 show the number of genotypes in each category of hilum ring and corona colors by seed type. All the Manteca, Mayocoba, and white beans had a yellow hilum ring, and Amarillos, beige, brown, Canary, and green–yellow types had a dark hilum ring. For corona colors, Canary and Manteca types had dark corona, and Mayocoba type had light or yellow corona (Table 4), consistent with their characteristic seed appearance. Some Amarillos had light or yellow corona, and others had dark corona. Fifty-three out of the 71 non- or slow-darkening genotypes had a yellow hilum ring, and the other 18 had a dark hilum ring (Supplemental Table S2). The J gene is involved in both postharvest darkening and dark hilum ring color, and individuals with jj genotype are nondarkening (Elsad et al., 2011; Junk-Knievel et al., 2008). The Z gene is also involved in hilum ring color expression, and Z produces a dark hilum.

...
TABLE 3 Hilum ring (HR) color of the Yellow Bean Collection genotypes by seed type

| Seed type                                | Yellow HR | Dark HR | Total |
|------------------------------------------|-----------|---------|-------|
| Amarillo (dark)                          | 0         | 36      | 36    |
| Amarillo (light)                         | 0         | 42      | 42    |
| Beige                                    | 0         | 6       | 6     |
| Brown                                    | 0         | 7       | 7     |
| Canary                                   | 0         | 83      | 83    |
| Green-yellow                             | 0         | 6       | 6     |
| Manteca                                  | 11        | 0       | 11    |
| Mayocoba                                 | 56        | 0       | 56    |
| White                                    | 3         | 0       | 3     |
| Amarillo dark and light mottled          | 0         | 1       | 1     |
| Amarillo (dark) with brown mottles       | 0         | 1       | 1     |
| Amarillo (dark) with brown stripes       | 0         | 2       | 2     |
| Beige with brown stripes                 | 0         | 3       | 3     |
| White and red mottled                    | 0         | 1       | 1     |
| Total                                    | 70        | 188     | 258   |

TABLE 4 Corona color of the Yellow Bean Collection genotypes by seed type

| Seed type                               | Light or yellow corona | Dark corona | Total |
|-----------------------------------------|-------------------------|-------------|-------|
| Amarillo (dark)                         | 17                      | 19          | 36    |
| Amarillo (light)                        | 28                      | 14          | 42    |
| Beige                                   | 6                       | 0           | 6     |
| Brown                                   | 1                       | 6           | 7     |
| Canary                                  | 0                       | 83          | 83    |
| Green-yellow                            | 3                       | 3           | 6     |
| Manteca                                 | 0                       | 11          | 11    |
| Mayocoba                                | 56                      | 0           | 56    |
| White                                   | 3                       | 0           | 3     |
| Amarillo dark and light mottled         | 1                       | 0           | 1     |
| Amarillo (dark) with brown mottles      | 1                       | 0           | 1     |
| Amarillo (dark) with brown stripes      | 2                       | 0           | 2     |
| Beige with brown stripes                | 3                       | 0           | 3     |
| White and red mottled                   | 1                       | 0           | 1     |
| Total                                   | 122                     | 136         | 258   |

TABLE 5 The p-values for the factor effects on L*a*b* values and postharvest darkening traits

| Term          | L*  | a*  | b*  | Darkening* |
|---------------|-----|-----|-----|------------|
| Genotype (G)  | <.0001 | <.0001 | <.0001 | <.0001 |
| Environment (E)| <.0001 | <.0001 | .046 | –          |
| Year (Y)      | <.0001 | .086 | <.0001 | –          |
| G × E         | <.0001 | <.0001 | <.0001 | –          |
| G × Y         | .42 | .015 | 1 | –          |
| E × Y         | .026 | <.0001 | .84 | –          |
| G × E × Y     | <.0001 | <.0001 | <.0001 | –          |
| H^2b          | .99 | .98 | .93 | –          |

*Postharvest darkening was measured in Michigan in 2019.

b Broad-sense heritability.

11 Mantecas were among the non- or slow-darkening genotypes with dark corona, and all the six beige genotypes were among the darkening genotypes with light or yellow corona. Genotypes of other seed types had different corona color and postharvest darkening (Supplemental Table S4). Mayocobas with yellow corona must be carrying gy, which expresses greenish-yellow corona color (Bassett, 2002). The 11 genotypes that had yellow hilum ring and the dark corona (Supplemental Table S4) were all Mantecas, showing the uniqueness of this market class. ‘Prim’ Manteca had v^lae, which gives dark corona (Bassett, 1999); thus, the dark corona of the 11 Manteca genotypes likely is due to v^lae.

3.2 G × E effects

The effects of genotype, environment, year, and interaction effects for the L*a*b* values are shown in Table 5. The genotype effect was significant for all the color values and postharvest darkening. The environment, G × E, and G × E × year effects for L*, a*, and b* values were significant, indicating that there is a G × E interaction for the color values. The genotype × year interaction was significant for a*, suggesting that a* of the seed colors in the YBC varied between years. However, the variation of a* as a result of year seems minimal because the ranges of a* were almost the same across the years and environments (Table 2) and the a* of the genotypes grown in each year were highly correlated (R ≥ 0.97). The heritability estimates of the color values were high (R ≥ 0.93; Table 5). This finding is consistent with other studies that reported high heritability of L*a*b* values with populations that had yellow or carioca bean as parental lines (H^2 > 0.73; Arns et al., 2018; Bassett et al., 2021; Possobom et al., 2015; Ribeiro et al., 2019). High heritability estimates of the color values indicate that genetic variance predominates in total phenotypic variance; thus, gain from selection is expected to be high.
3.3 | Principal component analysis

Best linear unbiased estimation of color values adjusted for environment and year effects were used for PC analysis (Figure 3). Principal component 1 separated brown and Amarillo dark beans from the rest of the market classes explaining >60% of the total variance. Principal component 2 separated genotypes based on b* values, explaining 33% of the total variance. Together, PC1 and PC2 explained 94% of the total variance, indicating that the color values of the YBC could be compressed to two dimensions instead of three without losing much information. This seemed to be because of the high negative correlation between L* and a* values (Supplemental Figure S2). The L* and a* values are correlated mainly because of the Amarillo dark genotypes having higher a* and lower L* values than the other market classes of the YBC. Amarillo light, Canary, and green–yellow genotypes overlapped with one another in the biplot (Figure 3), showing the similarity of seed colors of these color types, which corresponds to our observation. Manteca and Mayocoba bean formed a relatively distinct cluster characterized by higher L* values than other seed types. Overall, the large and continuous variability of color values, even within market classes, indicated that the YBC is a source of various yellow colors that can meet specific consumer preferences.

3.4 | Color differences between environments

Although the heritability for the L*a*b* values were high, G × E effect was significant (Table 5); therefore, the seed colors of Michigan- and Nebraska-grown seed were compared via ΔL*, Δa*, and Δb*, such that positive values indicate higher color values of the Michigan-grown seeds. The total differences were calculated as ΔE, a positive value that measures the degree of total color difference. The difference between two colors with ΔE of three or larger will be noticeable to the human eye (Haeghen et al., 2000). Many of the genotypes had ΔE larger than three (Figure 4a), indicating that their Michigan- and Nebraska-grown seeds had noticeably different colors. The ΔL* value was negative for almost all the genotypes regardless of the seed types, indicating that Michigan-grown seeds were darker than Nebraska-grown seeds (Figure 4b). The absolute values of ΔL* values were larger for some of the dark-colored seeds, such as brown and Amarillo dark types, so they were even darker in Michigan vs. Nebraska than the lighter-colored yellow classes such as beige and Amarillo light. It agreed with previous literature and our observation that beans grown under humid conditions tend to produce darker seeds than those grown under dry conditions (Osorno et al., 2018; Possobom et al., 2015). Higher seed coat lightness (L*) was also reported when a black × carioca population was grown in a dry season than in a rainy season (Possobom et al., 2015). Almost all the Amarillo light, Beige, Canary, Manteca, and Mayocoba beans had positive Δa* values, indicating that the seeds produced in Michigan were redder (Figure 4c). Amarillo dark and brown beans had lower Δb* values, meaning that they were less yellow in Michigan than in Nebraska (Figure 4d). Mayocoba and Canary had varying Δb* values. Light-colored beans, such as beige and Manteca types, had higher b* values, thus yellower in Michigan. Some Mayocoba-type beans tend to produce paler colors under cool and wet fall in the U.S. Midwest (Kelly et al., 2021). Indeed, 17 Mayocobas had negative Δb*, meaning that Michigan-grown beans were less yellow than Nebraska-grown beans. The other 33 Mayocobas, however, had positive Δb*, which means yellower seeds were produced in Michigan, highlighting the importance of evaluating the color expression of Mayocoba beans in their target environments. Various factors could cause the difference in seed colors, such as humidity, rain, shorter exposure to sunlight, and increased pressure of certain diseases that favor moist conditions. Postharvest darkening was associated with the decrease in polymerization of proanthocyanidins in a regular-darkening pinto bean (Beninger et al., 2005) and is characterized by the presence of proanthocyanidins and their precursors in regular-darkening cranberry bean (Chen et al., 2015), but further studies are needed to comprehensively understand the relationships between growing conditions, seed color, and polyphenolic profiles.

It was hypothesized that the genotypes that had darker seeds in Michigan (lower ΔL*, Δa*, or Δb* values) might be darkening types if darkening was already initiated before the images were taken. However, no clear separation in the color difference between darkening and non- or slow-darkening YBC lines was observed except for the b* values of Canary
Flavonoids, kaempferols in specific, are present in the seed coat of Canary bean (Hart et al., 2020), and it is possible that kaempferols present in darkening Canary bean grown in Michigan had started forming kaempferol-catechin adduct, which increased in regular-darkening pinto bean after darkening (Beninger et al., 2005).

3.5 Genome-wide association analysis

The Manhattan and quantile–quantile plots for the \(L^*a^*b^*\) values, postharvest darkening, and hilum ring and corona colors are shown in Figure 5. Eighteen SNPs were significantly associated with \(L^*\) value, 10 with \(a^*\), nine with \(b^*\), five for postharvest darkening, nine for hilum ring color, and seven for corona color (Supplemental Table S5). Three SNPs were significant for multiple traits: Chr02pos23133217 for \(a^*\) and \(L^*\); Chr07pos29169848 for \(a^*\), \(L^*\), postharvest darkening, hilum ring color, and corona colors; and Chr10pos43341167 for \(a^*\) and \(L^*\). Several SNPs were in proximity. Chr01pos41574533 for postharvest darkening and Chr01pos42211164 for \(b^*\) were 637 kb apart. Chr02pos44319551 for \(L^*\) and Chr02pos44931551 for \(L^*\) were 612 kb apart. Chr02pos45646751 for hilum ring color, Chr02pos45663695 for \(a^*\), and Chr02pos46287738 for \(L^*\) were all within the range of a 641-kb region. Chr05pos2078923 for hilum ring color and Chr05pos2408324 for corona color were 329 kb apart. Chr09pos18409319 for \(b^*\) and Chr09pos18733021 for \(a^*\) were 324 kb apart. Chr10pos42388055 for \(L^*\) and Chr10pos42797440 for hilum ring color were 409 kb apart, and the latter was 544 kb apart from Chr10pos43341167 for...
FIGURE 5  Quantile-quantile and Manhattan plots for $L^*$, $a^*$, $b^*$, postharvest darkening, hilum ring color, and corona color. The gray dotted lines are false discovery rate-adjusted threshold at $\alpha = 0.05$. $P$ is the ground factor gene for seed coat color, of which $p^{sd}$ allele confers slow darkening trait (Islam et al., 2020; McClean et al., 2018). $Sb^*4.1$, $Sa^*3.1$, $Sb^*3.1$, $SL^*3.1$, quantitative trait loci reported by Basset et al. (2021). $J$ and other QTL on Pv10 are the $J$ gene and previously found QTL or significantly associated SNPs. $J$ is the gene responsible for postharvest darkening (Elsadr et al., 2011). All the significant single nucleotide polymorphisms in this study for $L^*$ were within the ranges of Sa*.10.1, Sb*.10.1, SL*.10.1, and ND.10.1 (Basset et al., 2021). Chr10pos42388055 was within the range of $L^*10.1BB$ (I) (Bornowski et al., 2020). Chr10pos42388055 was within the range of $a^*10.1BB$ (I) (Bornowski et al., 2020).

$a^*$ and $L^*$. Chr11pos4985949 for postharvest darkening and Chr1pos5038396 for hilum ring color were 52 kb apart. The phenotypic effect was larger for the SNPs for $L^*$ than $a^*$ and $b^*$, reflecting the wider distribution of $L^*$ (Table 1).

Chr01pos50086405 on Pv01 was in a region where disease resistance genes are clustered, specifically for Colletotrichum lindemuthianum (Kelly & Bornowski, 2018). Polyphenolics play an important part in plant defense mechanisms against pests and pathogens (Bennett & Wallsgrove, 1994; Islam et al., 2004). If a gene is involved in the expression of seed colors important for consumers and disease resistance important for growers, the breeders’ job would be to select genotypes that carry favorable alleles for both traits. It could be challenging and merit further research because an instance is reported that purple seed coat color and bean common mosaic virus resistance on Pv02 are tightly linked.
(or caused by a pleiotropic effect) and that it was not possible to introduce the resistance to other color types (Temple & Morales, 1986). Despite being beneficial in insect control, some polyphenols may act as an iron absorption inhibitor and adversely affect iron bioavailability (Hart et al., 2017); therefore, breeders need to balance the benefits and tradeoffs.

Some of the significant SNPs on Pv03, Pv04, and Pv10 in this study were in the QTL regions found in QTL studies for seed coat color: one with a pale lemon-yellow × green-yellow bean recombinant inbred line population (Bassett et al., 2021) and one with a black bean population (Bornowski et al., 2020), respectively (Figure 5). These SNPs will be a useful reference in future studies on yellow color expression in common bean.

Chr07pos29169848 was significant for L*, a*, postharvest darkening, hilum ring color, and corona color with low p values and large phenotypic effects (−10.0 for L*, +9.2 for a*, +0.59 for postharvest darkening, +0.90 for hilum ring color, and +0.64 for corona color; Supplemental Table S5). The minor allele group genotypes at this SNP had a larger L*, a lower a*, a higher percentage of genotypes resistant to darkening, and light-colored hilum ring and corona (Supplemental Table S5). Intriguingly, all the minor allele group genotypes (47 genotypes for L*, a*, b*, hilum ring color, and corona color; 45 for postharvest darkening) were Mayocoba at this SNP. Among them, 22 were from the United States or Canada, and another 22 were from International Center for Tropical Agriculture, Colombia, whereas Mayocoba genotypes from other parts of the world such as Africa, Europe, and Mexico were found in the major allele group. Since the breeding materials from International Center for Tropical Agriculture and those from the United States are closely related, this SNP may indicate the importance of color for the selection of Mayocoba type. This SNP is located near the ground factor P gene (395 kb apart); the dominant P allele is necessary for seed coat color expression by other color genes (Bassett & Miklas, 2007; McClean, 2002; McClean et al., 2018). A QTL study with a Mayocoba × white bean population may reveal the potential role of the P gene (or another gene tightly linked to P) in giving the greenish-yellow color in some of the Mayocoba beans. This SNP was also significant for postharvest darkening, and 36 out of the 45 Mayocoba genotypes in the minor allele group at this SNP were non- or slow-darkening genotypes. Allele $p_{sd}$, an allele of $P$, is involved in slow darkening in the presence of $J$; genotypes with homozygous recessive $p_{sd}$ shows a slower rate of darkening than regular-darkening genotypes (Elsadr et al., 2011; Islam et al., 2020; Junk-Knievel et al., 2008). The postharvest darkening genotype at Chr07pos29169848, background information, hilum ring color, corona color, and BLUE of the L*a*b* values of the YBC genotypes are summarized in Supplemental Table S6. Surprisingly, 10 Canaries were non- or slow-darkening genotypes, although Canaries were reported to have proanthocyanidins (Hart et al., 2020). They had the major allele at this SNP same as Mantecas, which do not have proanthocyanidins and are considered to be carrying $j$ (Beninger et al., 1998; Hart et al., 2020). The difference between the non- or slow-darkening Canaries and Mantecas may be related to the other significant SNPs associated with postharvest darkening on Pv01, Pv04, and Pv11 (Supplemental Table S5).

The Chr08pos3300438 associated with corona color on Pv08 was 69 kb apart from the Gy gene. The Gy gene is considered to be responsible for the greenish-yellow seed coat, hilum ring, and corona colors of Mayocoba type (Bassett, 2002). However, the minor allele group of this SNP included 11 Amarillos, two beige, and one white types that had light or yellow corona, and Mayocobas were all in the major allele group. The role of the gy gene in non-Mayocoba types is yet to be researched. None of the significant SNPs were close to known color genes such as Z, G, R, and V that interactively impart yellow to brown seed coat, hilum ring, and corona colors (Bassett, 2007); however, despite the >2 Mbp distance, some SNPs associated with L*, a*, and corona color were on the same chromosomes as the color genes $B$ on Pv02, $G$ on Pv04, and $V$ on Pv06. There is no preceding study that quantitatively measured yellow seed color besides Bassett et al. (2021), thus further investigation will be necessary on genes and their interactions that produce the wide diversity of yellow colors.

The region of a candidate J gene for brown hilum ring color and postharvest darkening has been narrowed down to 41,141,057–41,591,985 bp on Pv10 (Erfatpour et al., 2018), but Chr10pos42797440 associated with hilum ring color was ~1.2 Mbp away from that region. A higher marker density and more SNPs closer to the J gene would help investigate the hilum ring color and postharvest darkening of yellow beans. Gene $J$ was detected in this study for postharvest darkening but just below the significance threshold: Chr10pos42038959 on Pv10 near the $J$ (447 bp apart) had a false discovery rate-adjusted $p$ value of .083. Nevertheless, a SNP (Chr10pos42797440) associated with hilum ring color within a range of a previously found QTL for postharvest darkening, ND.10.1 (3.98–43.85 Mbp; Bassett et al., 2021), lends support to the role of this region containing J. Another consideration for hilum ring color is that J and other genes are interacting—J is involved in the expression of dark hilum ring by $l^{fw}$ with the absence of Z:hr (Bassett et al., 1999; Bassett, 2003), thus, hilum ring color may not be only determined by the genotype at J. Interestingly, Chr10pos40877199 on Pv10 associated with L* was close to the J gene (264 kb apart). The J gene is involved in mature seed coat color development and postharvest darkening by regulating the biosynthesis pathways of polyphenolic compounds (Bassett, 2007; Elsadr et al., 2011; Erfatpour et al., 2018).
CONCLUSIONS

In this study, the seed coat color of yellow beans was measured by masking noise in bean images such as hilum ring, corona, background, and light reflection using machine-learning. As the trained model automatically segments seed coat from noise, it provides an efficient means to extract L*a*b* values from the seed coat. A large phenotypic diversity was observed for the L*a*b* values of the seed coat of the YBC genotypes grown in Michigan and Nebraska, USA. Despite the high heritability estimate for the color values, the G × E effects were significant. Most of the YBC lines grown in Michigan and Nebraska had a noticeable color difference, and those grown in Michigan with high humidity were darker. Genome-wide association analysis discovered SNPs associated with the color values, postharvest darkening, and hilum ring and corona colors of the YBC genotypes. The L*, a*, postharvest darkening, hilum ring color, and corona color mapped near the

ACKNOWLEDGMENTS

This work was supported by the USDA National Institute of Food and Agriculture AFRI (Award Number #: 2017-67013-26212), Michigan State University, the National Science Foundation Research Traineeship Program (DGE-1828149) awarded to Rie Sadohara and Yunfei Long, the Nebraska Hatch Project (NEB43-116), and USDA, Agricultural Research Service Project, 5050-21430-010-00D. The authors thank Anna Akariza, Amber Bassett, Gasana Ingabiregasana, Miranda Haus, Sharon Hooper, Queen Iribagiza, Hannah Jeffery, Hannah Peplinski, Scott Shaw, Jason Wiesinger, and Evan Wright for assistance with field operations and image acquisition.

AUTHOR CONTRIBUTIONS

Rie Sadohara: Data curation; Formal analysis; Investigation; Methodology; Validation; Visualization; Writing—original draft. Yunfei Long: Formal analysis; Methodology; Software; Writing—review & editing. Paulo Izquierdo: Investigation; Methodology; Writing—review & editing. Carlos A. Urrea: Funding acquisition; Investigation; Methodology; Writing—review & editing. Daniel Morris: Methodology; Software; Supervision; Writing—original draft. Karen A. Cichy: Conceptualization; Funding acquisition; Project administration; Resources; Supervision; Writing—review & editing.

CONFLICT OF INTEREST

There are no conflicts of interest to be disclosed.

ORCID

Rie Sadohara https://orcid.org/0000-0003-2861-5288
Yunfei Long https://orcid.org/0000-0002-3252-5763
Paulo Izquierdo https://orcid.org/0000-0002-2153-0655
Carlos A. Urrea https://orcid.org/0000-0002-1336-3199
Daniel Morris https://orcid.org/0000-0003-3032-5511
Karen Cichy https://orcid.org/0000-0002-4311-0774

REFERENCES

Amatya, S., Karkee, M., Gongal, A., Zhang, Q., & Whiting, M. D. (2016). Detection of cherry tree branches with full foliage in planar architecture for automated sweet-cherry harvesting. Biosystems Engineering, 146, 3–15. https://doi.org/10.1016/j.biosystemseng.2015.10.003
Arns, F. D., Ribeiro, N. D., Mezozo, H. C., De Marco Steckling, S., Kläseren, G. R., & Casagrande, C. R. (2018). Combined selection in carioca beans for grain size, slow darkening and fast-cooking after storage times. Euphytica, 214, 66. https://doi.org/10.1007/s10681-018-2149-8
Bassett, A., Kauvaramu, D. N., Song, Q., & Cichy, K. (2021). QTL mapping of seed quality traits including cooking time, flavor, and texture in a yellow dry bean (Phaseolus vulgaris L.) population. Frontiers in Plant Breeding, 12, 670284. https://doi.org/10.3389/fpls.2021.670284
Bassett, M. J., Shearon, C., & McClean, P. (1999). Allelism found between two common bean genes, hilum ring color (D) and partly colored seedcoat pattern (Z), formerly assumed to be independent. Journal of the American Society for Horticultural Science, 124, 649–653. http://journal.ashspublications.org/content/124/6/649.short
Bassett, M. J. (1999). The seedcoat color genotype of ‘Prim’ and the Manteca and Coscorrón market classes of common bean. Hortscience, 34, 336–337. https://doi.org/10.21273/HORTSCI.34.2.336
Bassett, M. J. (1996). The margo (mar) seedcoat color gene is a synonym for the joker (j) locus in common bean. Journal of the American Society for Horticultural Science, 121, 1028–1031. https://doi.org/10.21273/JASHS.121.6.1028
Bassett, M. J. (2002). Classical and molecular genetic studies of the strong greenish yellow seedcoat color in ‘Wagenaa’ and ‘Enola’ common bean. Journal of the American Society for Horticultural Science, 127, 50–55. https://doi.org/10.21273/JASHS.127.1.50
Bassett, M. J. (2003). Inheritance of yellow corona and hilum ring in seedcoats of Mayocoba market class common beans with genotype P[Cr]gy J[g b v^cr] Rk. Journal of the American Society for Horticultural Science, 128, 721–723. https://doi.org/10.21273/JASHS.128.5.0721
Bassett, M. J. (2007). Genetics of seed coat color and pattern in common bean. In J. Janick (Ed.), Plant breeding reviews (pp. 239–315). John Wiley & Sons, Inc. https://doi.org/10.1002/9780470168028.ch8
Bassett, M. J., & Miklas, P. N. (2007). A new gene, bic, with pleiotropic effects (with T P V) for bicolor flowers and dark olive brown seed coat in common bean. Journal of the American Society for Horticultural Science, 132, 352–356. https://doi.org/10.21273/JASHS.132.3.352
Bassett, M. J., Miklas, P. N., Caldas, G. V., & Blair, M. W. (2010). A dominant gene for garnet brown seed coats at the Rk locus in ‘Dorado’ common bean and mapping Rk to linkage group 1. Euphytica, 176, 281–290. https://doi.org/10.1007/s10681-010-0247-3
Bates, D., Mächler, M., Bolker, B., & Walker, S. (2015). Fitting linear mixed-effects models using lme4. *Journal of Statistical Software, 67*, 1–48. https://doi.org/10.18637/jss.v067.i01

Beebe, S. (2020). Biofortification of common bean for higher iron concentration. *Frontiers in Sustainable Food Systems, 4*, 573449. https://doi.org/10.3389/fsufs.2020.573449

Beninger, C. W., Gu, L., Prior, R. L., Junk, D. C., Vandenbeng, A., & Bett, K. E. (2005). Changes in polyphenols of the seed coat during the after-darkening process in pinto beans (*Phaseolus vulgaris* L.). *Journal of Agricultural and Food Chemistry, 53*, 7777–7782. https://doi.org/10.1021/jf0500511

Beninger, C. W., & Hosfield, G. L. (1999). Flavonoid composition of three genotypes of dry bean (*Phaseolus vulgaris*) differing in seedcoat color. *Journal of Agricultural and Food Chemistry, 124*, 514–518. https://doi.org/10.12173/JASHS.124.5.514

Beninger, C. W., & Hosfield, G. L. (2003). Antioxidant activity of extracts, condensed tannin fractions, and pure flavonoids from *Phaseolus vulgaris* L. seed coat color genotypes. *Journal of Agricultural and Food Chemistry, 51*, 7879–7883. https://doi.org/10.1021/jf0304324

Beninger, C. W., Hosfield, G. L., & Nair, M. G. (1998). Flavonol glycosides from the seed coat of a new Maneteca-type dry bean (*Phaseolus vulgaris* L.). *Journal of Agricultural and Food Chemistry, 46*, 2906–2910. https://doi.org/10.1021/jf9801522

Bennett, R. N., & Walls Grove, R. M. (1994). Secondary metabolites in plant defence mechanisms. *New Phytologist, 127*, 617–633. https://doi.org/10.1111/j.1469-8137.1994.tb02968.x

Bornsowski, N., Song, Q., & Kelly, J. D. (2020). QTL mapping of post-processing color retention in two black bean populations. *Theoretical and Applied Genetics, 133*, 3085–3100. https://doi.org/10.1007/s00122-020-03656-3

Box, G. E. P., & Cox, D. R. (1964). An analysis of transformations. *Journal of the Royal Statistical Society: Series B (Methodological), 26*, 211–243. https://doi.org/10.1111/j.2517-6161.1964.tb00553.x

Bressani, R., & Elias, L. G. (1979). The nutritional role of polyphenols in beans. In J. H. Hulse (Ed.), *Polyphenols in cereals and legumes: 36th annual meeting of the Institute of Food Technologists* (pp. 61–68). International Development Research Centre. https://idl-bnc-idrc.dspacedirect.org/bitstream/handle/10625/20583/IDL-20583.pdf?sequence=1

Castellanos, J. Z., Guzman-Maldonado, S. H., Jimenez, A., & Acosta-Gallegos, J. A. (1996). Preferential habits of common bean (*Phaseolus vulgaris* L.) consumers in Mexico. In *Reports of Bean Improvement Cooperative and National Dry Bean Council Research Conference, 182*–183. https://handle.nal.usda.gov/10113/IND20562914

Chen, P. X., Tang, Y., Marcone, M. F., Pauls, P. K., Zhang, B., Liu, R., & Tsao, R. (2015). Characterization of free, conjugated and bound tannin fractions, and pure flavonoids from cranberry beans (*Phaseolus vulgaris* L.). *Food Chemistry, 185*, 298–308. https://doi.org/10.1016/j.foodchem.2015.03.100

Cichy, K. A., Wiesinger, J. A., & Mendoza, F. A. (2015). Genetic diversity and genome-wide association analysis of cooking time in dry bean (*Phaseolus vulgaris* L.). *Theoretical and Applied Genetics, 128*, 1555–1567. https://doi.org/10.1007/s00122-015-2531-z

CIE International Commission on Illumination. (2004). *CIE 15: Technical Report: Colorimetry*. (3rd ed.). https://www.cdvplus.cz/file/3-publikace-cie15-2004/

de Cássia Silva, F., Pereira, H. S., Melo, P. G. S., & Melo, L. C. (2018). Selection of parents and segregating populations of common bean with high agronomic potential and slow seed-coat darkening. *Pesquisa Agropecuária Tropical, 48*, 75–82. https://doi.org/10.1590/1983–40632018v48n519

de Jong, S. (1993). SIMPLS: An alternative approach to partial least squares regression. *Chemometrics and Intelligent Laboratory Systems, 18*, 251–263. https://doi.org/10.1016/0169-7439(93)85002-X

Dixon, R. A., Xie, D.-Y., & Sharma, S. B. (2005). Proanthocyanidins – a final frontier in flavonoid research? *New Phytologist, 165*, 9–28. https://doi.org/10.1111/j.1469-8137.2004.01217.x

Duitama, J., Quintero, J. C., Cruz, D. F., Quintero, C., Hubmann, G., Foulquié-Moreno, M. R., Verstrepen, K. J., Thevelein, J. M., & Tohme, J. (2014). An integrated framework for discovery and genotyping of genomic variants from high-throughput sequencing experiments. *Nucleic Acids Research, 42*, e44. https://doi.org/10.1093/nar/gkt1381

Elia, F. M., Hosfield, G. L., Kelly, J. D., & Ueberras, M. (1997). Genetic analysis and interrelationships between traits for cooking time, water absorption, and protein and tannin content of Andean dry beans. *Journal of American Society for Horticultural Science, 122*, 512–518. https://doi.org/10.21273/JASHS.122.4.512

Elshad, H. T., Wright, L. C., Peter Pauls, K., & Bett, K. E. (2011). Characterization of seed coat post harvest darkening in common bean (*Phaseolus vulgaris* L.). *Theoretical and Applied Genetics, 123*, 1467–1472. https://doi.org/10.1007/s00122-011-1683-8

Elshire, R. J., Glaubitz, J. C., Sun, Q., Poland, J. A., Kawamoto, K., Buckler, E. S., & Mitchell, S. E. (2011). A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS ONE, 6*, e19379. https://doi.org/10.1371/journal.pone.0019379

Englericht, R., Beimiri, M., & Hosfield, G. (1999). Determination of total dietary fiber, indigestible starch, and indigestible protein in dry bean (*Phaseolus vulgaris* L.). *Annual Report of the Bean Improvement Cooperative, 42*, 123–124. https://handle.nal.usda.gov/10113/IND23288576

Erfatpour, M., Navabi, A., & Pauls, K. P. (2018). Mapping the non-darkening trait from ‘Wit-rood boontje’ in bean (*Phaseolus vulgaris*). *Theoretical and Applied Genetics, 131*, 1331–1343. https://doi.org/10.1007/s00122-018-3081-y

FAOSTAT. (2021). *No Title*. Food and Agriculture Organization of the United Nations. http://www.fao.org/faostat/en/#data/QC

Feenstra, W. J. (1960). *Biochemical aspects of seedcoat colour inheritance in Phaseolus vulgaris L*. Wageningen University & Research. https://library.wur.nl/WebQuery/wurpubs/525612

Fehr, W. R. (1987). *Principles of cultivar development*. Macmillan.

Ferentinos, K. P. (2018). Deep learning models for plant disease detection and diagnosis. *Computers and Electronics in Agriculture, 145*, 311–318. https://doi.org/10.1016/j.compag.2018.01.009

González, A. M., Monteagudo, A. B., Casquero, P. A., De Ron, A. M., & Santalla, M. (2006). Genetic variation and environmental effects on agronomical and commercial quality traits in the main European market classes of dry bean. *Field Crops Research, 95*, 336–347. https://doi.org/10.1016/j.fcr.2005.04.004

Grinblat, G. L., Uzal, L. C., Larese, M. G., & Granitto, P. M. (2016). Deep learning for plant identification using vein morphological patterns. *Computers and Electronics in Agriculture, 127*, 418–424. https://doi.org/10.1016/j.compag.2016.07.003

Haeghen, Y. V., Naeyaert, J. M. A. D., Lemahieu, I., & Philips, W. (2000). An imaging system with calibrated color image acquisition for use in dermatology. *IEEE Transactions on Medical Imaging, 19*, 722–730. https://doi.org/10.1109/42.875195
Hart, J. J., Tako, E., & Glahn, R. P. (2017). Characterization of polyphenol effects on inhibition and promotion of iron uptake by Caco-2 Cells. *Journal of Agricultural and Food Chemistry, 65*, 3285–3294. https://doi.org/10.1021/acs.jafc.6b05755

Hart, J. J., Tako, E., Wiesinger, J., & Glahn, R. P. (2020). Polyphenolic profiles of yellow bean seed coats and their relationship with iron bioavailability. *Journal of Agricultural and Food Chemistry, 68*, 769–778. https://doi.org/10.1021/acs.jafc.9b05663

Hayat, I., Ahmad, A., Masud, T., Ahmed, A., & Bashir, S. (2014). Nutritional and health perspectives of beans (*Phaseolus vulgaris L. *): An overview. *Critical Reviews in Food Science and Nutrition, 54*, 580–592. https://doi.org/10.1080/10408398.2011.596639

Hooper, S., Wiesinger, J. A., Echeverria, D., Thompson, H. J., Brick, M. A., Nchimbi-Msolla, S., & Cichy, K. A. (2016). Carbohydrate profile of a dry bean (*Phaseolus vulgaris L.*) panel encompassing broad genetic variability for cooking time. *Cereal Chemistry Journal, 94*, 135–141. https://doi.org/10.1098/CCHEM-04-16-0126-FI

Huang, M., Liu, X., Zhou, Y., Summers, R. M., & Zhang, Z. (2019). BLINK: A package for the next level of genome-wide association studies with both individuals and markers in the millions. *GigaScience, 8*, giy154. https://doi.org/10.1093/gigascience/giy154

Islam, F. M. A., Beebe, S., Muñoz, M., Tohme, J., Redden, R. J., & Basford, K. E. (2004). Using molecular markers to assess the effect of introgression on quantitative attributes of common bean in the Andean gene pool. *Theoretical and Applied Genetics, 108*, 243–252. https://doi.org/10.1007/s00122-003-1437-3

Islam, F. M. A., Rengifo, J., Redden, R. J., Basford, K. E., & Beebe, S. E. (2003). Association between seed coat polyphenolics (tannins) and disease resistance in common bean. *Plant Foods for Human Nutrition, 58*, 285–297. https://doi.org/10.1023/B:QUAL.0000042833.51023-c2

Islam, N. S., Bett, K. E., Pauls, K. P., Marsolais, F., & Dhaubhadel, S. (2020). Postharvest seed coat darkening in pinto bean (*Phaseolus vulgaris*) is regulated by *P*∗, an allele of the basic helix-loop-helix transcription factor *P. Plants, People, Planet, 2*, 663–677. https://doi.org/10.1002/ppp.10132

Junk-Knievel, D. C., Vandenberg, A., & Bett, K. E. (2007). An accelerated postharvest seed-coat darkening protocol for pinto beans grown across different environments. *Crop Science, 47*, 694–700. https://doi.org/10.2135/cropsci2006.05.0325

Junk-Knievel, D. C., Vandenberg, A., & Bett, K. E. (2008). Slow darkening in pinto bean (*Phaseolus vulgaris L.*) seed coats is controlled by a single major gene. *Crop Science, 48*, 189–193. https://doi.org/10.2135/cropsci2007.04.0227

Kassambara, A., & Mundt, F. (2020). factoextra: Extract and visualize the results of multivariate data analyses. https://cran.r-project.org/package=factoextra

Kelly, J. D., Awale, H. E., Wiersma, A. T., Cichy, K. A., & Wright, E. M. (2021). Registration of ‘Yellowstone’ yellow bean. *Journal of Plant Registrations, 15*, 265–270. https://doi.org/10.1006/jprr.2020.0757

Kelly, J. D., & Bornowski, N. (2018). Marker-assisted breeding for economic traits in common bean. In S. S. Gosal & S. H. Wani (Eds.), *Andean gene pool*. Springer International Publishing. pp. 211–238.

Kuznetsova, A., Brockhoff, P. B., & Christensen, R. H. B. (2017). *lmerTest* package: Tests in linear mixed effects models. *Journal of Statistical Software, 82*, 1–26. https://doi.org/10.18637/jss.v082.i13

Lenth, R. V. (2021). emmeans: Estimated marginal means, aka least-squares means. R package version 1.5.5-1. https://CRAN.R-project.org/package=emmeans

León, K., Mery, D., Pedreschi, F., & León, J. (2006). Color measurement in *L*a*b* units from RGB digital images. *Food Research International, 39*, 1084–1091. https://doi.org/10.1016/j.foodres.2006.03.006

Lipka, A. E., Tian, F., Wang, Q., Peiffer, J., Li, M., Bradbury, P. J., Gore, M. A., Buckler, E. S., & Zhang, Z. (2012). GAPT: Genome association and prediction integrated tool. *Bioinformatics, 28*, 2397–2399. https://doi.org/10.1093/bioinformatics/bts444

Lobaton, J. D., Miller, T., Gil, J., Ariza, D., de la Hoz, J. F., Soler, A., Beebe, S., Duitama, J., Gepts, P., & Raatz, B. (2018). Resequencing of common bean identifies regions of inter–gene pool introgression and provides comprehensive resources for molecular breeding. *The Plant Genome, 11*, 170068. https://doi.org/10.3835/plantgenome2017.08.0068

Long, Y., Bassett, A., Cichy, K., Thompson, A., & Morris, D. (2019). Bean split ratio for dry bean canning quality and variety analysis. Proceedings of the IEEE/CVF conference on computer vision and pattern recognition (CVPR) workshops. https://openaccess.thecvf.com/content_CVPRW_2019/html/CVPPP/Long_Bean_Split_Ratio_for_Dry_Bean_Canning_Quality_and_Variety_CVPRW_2019_paper.html

Marles, M. A. S., Vandenberg, A., & Bett, K. E. (2008). Polyphenol oxidation activity and differential accumulation of polyphenolics in seed coats of pinto bean (*Phaseolus vulgaris L.*) characterize postharvest color changes. *Journal of Agricultural and Food Chemistry, 56*, 7049–7056. https://doi.org/10.1021/jf8004367

MATLAB. (2020). MATLAB: R2020a (9.8.0.1538580). The Math-Works Inc.

McCLean, P. E., Bett, K. E., Stonehouse, R., Lee, R., Pfieger, S., Moghaddam, S. M., Geffroy, V., Miklas, P., & Mamidi, S. (2018). White seed color in common bean (*Phaseolus vulgaris*) results from convergent evolution in the *P* (pigment) gene. *New Phytologist, 219*, 1112–1123. https://doi.org/10.1111/nph.15259

McCLean, P. E. (2002). Molecular and phenotypic mapping of genes controlling seed coat pattern and color in common bean (*Phaseolus vulgaris*). *Journal of Heredity, 93*, 148–152. https://doi.org/10.1093/jhered/93.2.148

Mendoza, F. A., Kelly, J. D., & Cichy, K. A. (2017). Automated prediction of sensory scores for color and appearance in canned black beans (*Phaseolus vulgaris L.*) using machine vision. *International Journal of Food Properties, 20*, 83–99. https://doi.org/10.1080/10942912.2015.1136939

Messina, V. (2014). Nutritional and health benefits of dried beans. *The American Journal of Clinical Nutrition, 100*, 437S–442S. https://doi.org/10.3945/ajcn.113.1071472.7

Mevik, B.-H., Wehrens, R., & Liland, K. H. (2020). *pls*: Partial least squares and principal component regression. https://cran.r-project.org/package=pls

Osorno, J. M., Vander Wal, A. J., Kloberdanz, M., Pasche, J. S., Schroder, S., & Miklas, P. N. (2018). A new slow-darkening pinto bean with improved agronomic performance: Registration of ‘ND-Palomino’. *Journal of Plant Registrations, 12*, 25–30. https://doi.org/10.3198/jpr2017.05.0026crc

Petry, N., Egli, I., Zeder, C., Walczyk, T., & Hurrell, R. (2010). Polyphenols and phytic acid contribute to the low iron bioavailability from common beans in young women. *The Journal of Nutrition, 140*, 1977–1982. https://doi.org/10.3945/jn.110.125369
Possobom, M. T. D. F., Ribeiro, N. D., Zemolin, A. E. M., & Arns, F. D. (2015). Genetic control of the seed coat colour of Middle American and Andean bean seeds. *Genetica*, 143, 45–54. https://doi.org/10.1007/s10709-014-9811-4

Prakken, R. (1970). Inheritance of colour in *Phaseolus vulgaris* L. II: A critical review. *Mededelingen van de Landbouwhogeschool Te Wageningen*, 70(23), 1–38.

Prakken, R. (1972). Inheritance of colours in *Phaseolus vulgaris* L. III. On genes for red seed coat colour and a general synthesis. *Mededelingen van de Landbouwhogeschool Te Wageningen*, 29, 1–82.

Prakken, R. (1974). Inheritance of colours in *Phaseolus vulgaris* L. IV. Recombination within the ‘complex locus C’. *Mededelingen van de Landbouwhogeschool Te Wageningen*, 24, 1–36.

R Core Team. (2017). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing. https://www.r-project.org/

Reddy, N. R., Pierson, M. D., Sathe, S. K., & Salunkhe, D. K. (1985). Dry bean tannins: A review of nutritional implications. *Journal of the American Oil Chemists Society*, 62, 541–549. https://doi.org/10.1007/BF02542329

Ribeiro, N. D., Mezzomo, H. C., & dos Santos, G. G. (2019). Genetic parameters and combined selection for seed coat color and macrominerals in Mesoamerican common bean lines. *Genetics and Molecular Research*, 18, gmr18224. https://doi.org/10.4238/gmr18224

Rodríguez Madrera, R., Campa Negrillo, A., Suárez Valles, B., & Ferreira Fernández, J. J. (2020). Characterization of extractable phenolic profile of common bean seeds (*Phaseolus vulgaris* L.) in a Spanish diversity panel. *Food Research International*, 138, 109713. https://doi.org/10.1016/j.foodres.2020.109713

Schneider, C. A., Rasband, W. S., & Eliceiri, K. W. (2012). NIH Image to ImageJ: 25 years of image analysis. *Nature Methods*, 9, 671–675. https://doi.org/10.1038/nmeth.2089

Takeoka, G. R., Dao, L. T., Full, G. H., Wong, R. Y., Harden, L. A., Edwards, R. H., & Berrios, J. D. J. (1997). Characterization of black bean (*Phaseolus vulgaris* L.) anthocyanins. *Journal of Agricultural and Food Chemistry*, 45, 3395–3400. https://doi.org/10.1021/jf970264d

Tako, E., Beebe, S. E., Reed, S., Hart, J. J., & Glahn, R. P. (2014). Polyphenolic compounds appear to limit the nutritional benefit of biofortified higher iron black bean (*Phaseolus vulgaris* L.). *Journal of Nutrition*, 144, 5–20. https://doi.org/10.3944/jn.2012.453

Temple, S. R., & Morales, F. (1986). Image processing in Python. *PeerJ*, 2, e453. https://doi.org/10.7717/peerj.453

Uebersax, M. A., & Siddiq, M. (2012). Market classes and physical and physiological characteristics of dry beans. In M. Siddiq & M. A. Uebersax (Eds.), *Dry beans and pulses production, processing and nutrition* (pp. 55–74). Blackwell Publishing Ltd. https://doi.org/10.1002/9781118448298.ch3

van der Walt, S., Schönberger, J. L., Nunez-Iglesias, J., Boulogne, F., Warner, J. D., Yager, N., Gouillart, E., & Yu, T. (2014). scikit-image: Image processing in Python. *PeerJ*, 2, e453. https://doi.org/10.7717/peerj.453

Varga, F., Vidak, M., Ivanović, K., Lazarević, B., Širić, I., Srećec, S., Šatović, Z., & Carović-Stanko, K. (2019). How does computer vision compare to standard colorimeter in assessing the seed coat color of common bean (*Phaseolus vulgaris* L.)? *Journal of Central European Agriculture*, 20, 1169–1178. https://doi.org/10.5513/JCEA01/20.4.2509

Venables, W., & Ripley, B. (2002). *Modern applied statistics with S* (4th ed.). Springer. https://www.stats.ox.ac.uk/pub/MASS4/

Voysest, O. (2012). Yellow beans in Latin America. *Annual report of the Bean Improvement Cooperative*, Vol. 55. http://arsfifthbean.uprm.edu/bic/wp-content/uploads/2018/05/BIC_2012_Annual_Report.pdf

Wiesinger, J. A., Glahn, R. P., Cichy, K. A., Kolba, N., Hart, J. J., & Tako, E. (2019). An *in vivo* (*Gallus gallus*) feeding trial demonstrating the enhanced iron bioavailability properties of the fast cooking Manetcia yellow bean (*Phaseolus vulgaris* L.). *Nutrients*, 11, 1768. https://doi.org/10.3390/nu11081768

Wiesinger, J. A., Osorno, J. M., McClean, P. E., Hart, J. J., & Glahn, R. P. (2021). Faster cooking times and improved iron bioavailability are associated with the down regulation of procyanidin synthesis in slow-darkening pinto beans (*Phaseolus vulgaris* L.). *Journal of Functional Foods*, 82, 104444. https://doi.org/10.1016/j.jff.2021.104444

Wiesinger, J., Cichy, K., Tako, E., & Glahn, R. (2018). The fast cooking and enhanced iron bioavailability properties of the Manetcia yellow bean (*Phaseolus vulgaris* L.). *Nutrients*, 10, 1609. https://doi.org/10.3390/nu10111609

Winkel-Shirley, B. (2001). Flavonoid biosynthesis. A colorful model for genetics, biochemistry, cell biology, and biotechnology. *Plant Physiology*, 126, 485–493. https://doi.org/10.1104/pp.126.2.485

Wortmann, C. S., Kirkby, R. A., Eleedu, C. A., & Allen, D. J. (1998). Atlas of common bean (*Phaseolus vulgaris* L.) production in Africa. *CIAT Publication*, 297, 131. http://hdl.handle.net/10568/54312

Wu, D., & Sun, D.-W. (2013). Colour measurements by computer vision for food quality control – A review. *Trends in Food Science & Technology*, 29, 5–20. https://doi.org/10.1016/j.tifs.2012.08.004

Yang, Q.-Q., Gan, R.-Y., Ge, Y.-Y., Zhang, D., & Corke, H. (2018). Polyphenols in common beans (*Phaseolus vulgaris* L.): Chemistry, analysis, and factors affecting composition. *Comprehensive Reviews in Food Science and Food Safety*, 17, 1518–1539. https://doi.org/10.1111/1541-4337.12391

Yin, L. (2020). *CMplot: Circle Manhattan Plot*. R package version 3.6.2. https://cran.r-project.org/package=CMplot

Zeiler, M. D. (2012). ADADELTA: An adaptive learning rate method. arXiv:1212.5701. https://arxiv.org/abs/1212.5701

**SUPPORTING INFORMATION**

Additional supporting information may be found in the online version of the article at the publisher’s website.