Characterization of common bean (*Phaseolus vulgaris* L.) germplasm for morphological and seed nutrient traits from Western Himalayas

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Abstract
Common bean (*Phaseolus vulgaris* L.) is considered as one of the principle grain legume crops grown in Western Himalayas of Jammu and Kashmir, India. This region holds great diversity of common bean germplasm. The purpose of present study was to characterize 109 common bean genotypes collected from different hotspots for morphological traits—plant growth (growth habit, growth type, and twinning habit); leaf (color, size, and shape); flower (color, stripping on outer petal); pod (shape in relation to suture, shape of cross-section, shape of distal part, and stringiness), seed (color and shape) traits, and quantitative morphological traits (seed weight, length, and breadth). The preliminary analysis of trait data showed wide variation for different morphological traits. Furthermore, diverse 60 genotypes were selected out of 109 genotypes and were evaluated for seed micronutrients (Fe, Zn, and Cu) and seed macronutrients (K, Ca, P, and Mg). The analysis of seed micronutrient and macronutrient data indicated substantial variation for these minerals in the germplasm. Seed Mg, P, K, and Ca concentrations varied from 1,220.5 to 2,737.5 ppm, 1,980–4,050 ppm, 8,344.5–14,794 ppm, and 300–5,350 ppm, respectively. Similarly, seed micronutrients Fe, Zn, and Cu concentrations ranged from 80.5–180.6 ppm, 14.64–104.08 ppm, and 0.9–13.4 ppm, respectively. The evaluation for seed micronutrient and macronutrient led to the identification of candidate genotypes possessing high seed micronutrient and macronutrient. The candidate genotypes identified during the present study will prove useful in common bean breeding programs as donor genotypes, in development of useful genetic resources and in gene discovery programs through functional genomics and transcriptomics.

Keywords
common bean, macronutrients, micronutrients, morphological traits, phenotypic variation
INTRODUCTION

Common bean (Phaseolus vulgaris L) member of the family Fabaceae (legume or bean family) is a self-pollinated, diploid (2n = 2x = 22) legume crop with moderate genome size of 473 Mb (Priya & Manickavasagan, 2020). Common bean is cultivated throughout the world for its green pods as well as for dry seeds (Adikshita & Kansak, 2017). Based on evidences from archeological as well as morphological traits and phaseolin patterns, allozymes, and molecular markers, common bean has evolved from its closest wild common bean relative (Phaseolus vulgaris var. Mexicanaus) (Brucher, 1988; Gepts & Debouck, 1991; Salinas et al., 1988). Two geographically isolated and genetically recognized wild gene pools (Andean and Mesoamerican) evolved from a common wild ancestral parent about 10,000 years ago, and from these wild gene pools, nearly 8,000 years ago, common bean was independently domesticated in Mexico and South America (Bitocchi et al., 2013), and today the crop is being cultivated as a major food crop in many areas of the America, Europe, Africa, and Asia (Choudhary, Hamid, et al., 2018; Wortmann et al., 2006). Seed storage protein, phaseolin, helps in identifying cultivated and wild common beans. Two major phaseolin types that have been largely found in common bean are “S” and “T” type, with Mesoamerican and Andean genotypes possessing “S” and “T” type phaseolin patterns, respectively (Choudhary, Hamid, et al., 2018; Kami et al., 1995).

In India, common bean is cultivated in the states of Himachal Pradesh, Uttar Pradesh, Jammu and Kashmir, Maharashtra, Karnataka, Kerala, and Tamil Nadu (Kumar et al., 2017). Western Himalayas of Jammu and Kashmir holds great diversity of common bean landraces (Choudhary, Hamid, et al., 2018) and is a niche and cash crop (Sheikh et al., 2017). It is widely cultivated in Budgam, Baramulla, Shopian, Kulgam, Qazigund Rajouri, Poonch, Doda, Kishtwar, Bhaderwah, and Ramban, on an area of about 26.75 thousand hectares with an annual production of 14.2 thousand metric tons (Bhat et al., 2017; Choudhary, Bawa, et al., 2018; Choudhary, Hamid, et al., 2018; Mir et al., 2021).

In Jammu and Kashmir, common bean has gained the impetus because of high taste, texture, flavor, and palatability (Choudhary, Bawa, et al., 2018; Choudhary, Hamid, et al., 2018; Mir et al., 2021).

Because genetic diversity of valuable species is affected by anthropogenic factors, thus there is pressing need for conservation and utilization of local plant resources for breeding plant species (Stoilova et al., 2013). United Nations declared 2010 as “Year of Biodiversity” highlighting the need of conservation and utilization of biological diversity for human development. In common beans, landraces are an important component of plant biodiversity and constitute the foundation of present day crop breeding programs. They have assumed greater significance in view of deterioration of biophysical resource base and looming threats of climate change (Carovic-Stanko et al., 2017).

From the nutraceutical point of view, common beans are unique among plant diets, as they are cheap source of high quality protein (21%–25%) and are aptly designated as “Poor Man’s Meat” (USDA Dietary Guidelines, 2010). Beans are more than a foodstuff as they are rich in many other compounds like vitamins, especially B group vitamins (folates), antioxidants and polyunsaturated fatty acids, minerals like macronutrients, sulfur (S), potassium (K), phosphorus (P), calcium (Ca), magnesium (Mg), and magic wands, micronutrients, iron (Fe), zinc (Zn), copper (Cu), iodine (I), and manganese (Mn) (Akond et al., 2011). These minerals are required for proper functioning of our body systems. Fe and Zn, which are required in miniscule amounts, have been found at higher level in common beans than cereals and can potentially solve hidden hunger related problems faced by people falling at bottom of pyramid of societies economic strata (Blair et al., 2013). Likewise, macronutrients are needed to combat Alzhemier’s disease, Type 2 diseases, cardiovascular diseases, etc. (Hayat et al., 2014).

Earlier studies in common beans collected from different parts of world have reported substantial variation in the germplasm for various minerals (Grele et al., 2017; Ray et al., 2014). However, there are very few reports available from Western Himalayan regions of Jammu and Kashmir where bean germplasm from Jammu and Kashmir has been used in evaluation of seed micronutrients and macronutrients (Mahajan et al., 2015). Therefore, the aim of this study was to evaluate the seed micronutrients (Fe, Zn, and Cu) and seed macronutrients (K, Ca, P, and Mg) in a set of common bean germplasm collected from different hot-spot regions of Jammu and Kashmir harboring great diversity in common bean landraces. To the best of our discernment, we have succeeded in collection of bean landraces from those hot-spot regions, which were mostly unexplored in earlier studies.

MATERIALS AND METHODS

2.1 Germplasm collection

A set of 109 common bean genotypes were used during the present study. Among the 109 genotypes, 87 were collected from different hot spot regions of Jammu and Kashmir, and 15 were exotic genotypes from different countries (Syria, USA, Denmark, Ukraine, Turkey, Norway and Iran). Out of 109 genotypes, 52 genotypes were of Mesoamerican origin, and 57 genotypes were of Andean origin. The local bean landraces were collected from different districts of Kashmir Valley including Kupwara, Baramullah, Anantnag, and Bandipora and different districts of Jammu region including Poonch, Rajori, Kishtiar, Doda, and Badrewah (Figure 1; Table 1).

Because the genotypes/landraces of common bean collected from farmer’s fields were invariably admixtures and heterogeneous, they were purified to ensure uniform seed sets within each accessions and to remove the off types that did not conform to the overall characteristics of that landrace (for details, see Choudhary, Hamid, et al., 2018; Mir et al., 2021).

2.2 Evaluation of germplasm

For the trait characterization, a set of 109 common bean genotypes were evaluated in Augmented Block Design (ABD) at Research Farm
FIGURE 1  Variation in seed testa color in common bean germplasm used during the present study. The figure shows the diverse nature of genotypes being used in the current study. A = French yellow; B = Canadian red; C = cream; D = olivaceous; E = light yellow; F = black eye; G = black; H = brown; I = light gray; J = light brown; K = great northern; L = red

TABLE 1  List of 109 genotypes along with their site of collection and origin used in the present investigation

| S. no | Accession number | Site of collection/source | Origin Indigenous/exotic |
|-------|------------------|--------------------------|--------------------------|
| 1     | SB101            | Cherward Lahroo, Anantnag, India | Indigenous |
| 2     | SB103            | Akingam, Anantnag, India | Indigenous |
| 3     | SB104            | Akingam, Anantnag, India | Indigenous |
| 4     | SB106            | Akingam, Anantnag, India | Indigenous |
| 5     | SB107            | Akingam, Anantnag, India | Indigenous |
| 6     | SB108            | Badasgam, Anantnag, India | Indigenous |
| 7     | SB11             | Watergam, Baramulla, India | Indigenous |
| 8     | SB110            | Badasgam, Anantnag, India | Indigenous |
| 9     | SB111            | Badasgam, Anantnag, India | Indigenous |
| 10    | SB113            | Kokernag, Anantnag, India | Indigenous |
| 11    | SB114            | Kokernag, Anantnag, India | Indigenous |
| 12    | SB115            | Kokernag, Anantnag, India | Indigenous |
| 13    | SB117            | Akingam, Anantnag, India | Indigenous |
| 14    | SB118            | Larnoo, Anantnag, India | Indigenous |
| 15    | SB119            | Larnoo, Anantnag, India | Indigenous |
| 16    | SB120            | Larnoo, Anantnag, India | Indigenous |
| 17    | SB121            | Larnoo, Anantnag, India | Indigenous |
| 18    | SB124            | Larnoo, Anantnag, India | Indigenous |
| 19    | SB125.2          | Larnoo, Anantnag, India | Indigenous |
| 20    | SB126            | Larnoo, Anantnag, India | Indigenous |
| 21    | SB127            | Larnoo, Anantnag, India | Indigenous |
| 22    | SB129            | Kansar, Doda, India | Indigenous |
| 23    | SB131            | Chilibalera, Badrewah, India | Indigenous |
| 24    | SB132            | Butla, Badrewah, India | Indigenous |

(Continues)
| S. no | Accession number | Site of collection/source | Origin Indigenous/exotic |
|-------|------------------|--------------------------|--------------------------|
| 25    | SB134            | Baderwah, India          | Indigenous               |
| 26    | SB135            | Baderwah, India          | Indigenous               |
| 27    | SB136            | Sartingil, Baderwah, India | Indigenous             |
| 28    | SB137            | Sartingil, Baderwah, India | Indigenous             |
| 29    | SB138            | Sartingil, Baderwah, India | Indigenous             |
| 30    | SB139.B          | Sartingil, Baderwah, India | Indigenous             |
| 31    | SB140            | Sartingil, Baderwah, India | Indigenous             |
| 32    | SB141.1          | Sartingil, Baderwah, India | Indigenous             |
| 33    | SB142            | Padder, Kashtiwar, India | Indigenous               |
| 34    | SB143            | Padder, Kashtiwar, India | Indigenous               |
| 35    | SB145            | Atholi Padder, Kishtiwar, India | Indigenous             |
| 36    | SB146            | Atholi Padder, Kishtiwar, India | Indigenous             |
| 37    | SB147            | Atholi Padder, Kishtiwar, India | Indigenous             |
| 38    | SB149            | Bandipora, India         | Indigenous               |
| 39    | SB150            | Bandipora, India         | Indigenous               |
| 40    | WB-493           | Sweden                   | Exotic                   |
| 41    | SB151            | Bandipora, India         | Indigenous               |
| 42    | SB152            | Bandipora, India         | Indigenous               |
| 43    | SB153            | Bandipora, India         | Indigenous               |
| 44    | SB155.2          | Bandipora, India         | Indigenous               |
| 45    | SB156            | Bandipora, India         | Indigenous               |
| 46    | SB159            | Haspulot Thanamandi, Poonch, India | Indigenous             |
| 47    | SB162            | Watergam, Baramulla, India | Indigenous             |
| 48    | SB163            | Watergam, Baramulla, India | Indigenous             |
| 49    | SB165            | Watergam, Baramulla, India | Indigenous             |
| 50    | SB167            | Watergam, Baramulla, India | Indigenous             |
| 51    | SB168            | Watergam, Baramulla, India | Indigenous             |
| 52    | SB169            | Watergam, Baramulla, India | Indigenous             |
| 53    | SB17             | Not known                | Exotic                   |
| 54    | SB170            | Pattan, Baramulla, India | Indigenous               |
| 55    | SB173            | Watergam, Baramulla, India | Indigenous             |
| 56    | SB174.1          | Watergam, Baramulla, India | Indigenous             |
| 57    | SB181            | Kupwara, India           | Indigenous               |
| 58    | SB182            | Kupwara, India           | Indigenous               |
| 59    | SB183.1          | Kupwara, India           | Indigenous               |
| 60    | SB184            | Kupwara, India           | Indigenous               |
| 61    | SB185            | Kupwara, India           | Indigenous               |
| 62    | SB186            | Kupwara, India           | Indigenous               |
| 63    | WB-792           | Bandipora, India         | Indigenous               |
| 64    | WB-923           | Bandipora, India         | Indigenous               |
| 65    | WB-650           | Bandipora, India         | Indigenous               |
| 66    | WB-1009          | Baramulla, India         | Indigenous               |
| 67    | WB-1199          | Baramulla, India         | Indigenous               |
| 68    | WB-1306          | Baramulla, India         | Indigenous               |
| 69    | WB-1187          | Baramulla, India         | Indigenous               |
| 70    | WB-1255          | Baramulla, India         | Indigenous               |
Experimental field was divided into six blocks. In each block, 17 genotypes and a check variety, Shalimar Rajmash 1 was sown. Each genotype was sown in two rows of 2 m length each, and 40 cm spacing between the rows and 15-cm plant-to-plant spacing was kept for better expression of traits for evaluation. Plots were kept free from weeds, diseases, and insect/pests throughout the growing season.

### TABLE 1 (Continued)

| S. no | Accession number | Site of collection/source | Origin Indigenous/exotic |
|-------|------------------|---------------------------|--------------------------|
| 71    | WB-1151          | Baramulla, India          | Indigenous               |
| 72    | WB-832           | Baramulla, India          | Indigenous               |
| 73    | WB-1184          | Baramulla, India          | Indigenous               |
| 74    | WB-473           | Denmark                   | Exotic                   |
| 75    | WB-416           | Iran                      | Exotic                   |
| 76    | WB-418           | Iran                      | Exotic                   |
| 77    | WB-469           | Norway                    | Exotic                   |
| 78    | WB-603           | Not known                 | Exotic                   |
| 79    | WB-413           | Not known                 | Exotic                   |
| 80    | WB-1131          | Pulwama                   | Exotic                   |
| 81    | WB-947           | Turkey                    | Exotic                   |
| 82    | WB-970           | Ukraine                   | Exotic                   |
| 83    | WB-330           | Bandipora, India          | Indigenous               |
| 84    | WB-665           | Bandipora, India          | Indigenous               |
| 85    | WB-1186          | Baramulla, India          | Indigenous               |
| 86    | R1               | Baramulla, India          | Indigenous               |
| 87    | WB-1189          | Baramulla, India          | Indigenous               |
| 88    | WB-634           | Kupwara, India            | Indigenous               |
| 89    | WB-1300          | Not known                 | Exotic                   |
| 90    | WB-956           | Syria                     | Exotic                   |
| 91    | WB-846           | Tailbal                   | Indigenous               |
| 92    | WB-934           | USA                       | Exotic                   |
| 93    | SB1              | Not known                 | Exotic                   |
| 94    | SB6              | NBPGR Shimla              | Indigenous               |
| 95    | SB7              | NBPGR Shimla              | Indigenous               |
| 96    | SB128            | Larnoo, Anantnag, India   | Indigenous               |
| 97    | SB127            | Larnoo, Anantnag, India   | Indigenous               |
| 98    | SB19             | NBPGR Shimla              | Indigenous               |
| 99    | SB22             | NBPGR Shimla              | Indigenous               |
| 100   | SB44             | Not known                 | Exotic                   |
| 101   | SB45             | Not known                 | Exotic                   |
| 102   | SB46             | Not known                 | Exotic                   |
| 103   | SB42             | Not known                 | Exotic                   |
| 104   | SB30             | NBPGR Shimla              | Indigenous               |
| 105   | SB43             | Not known                 | Exotic                   |
| 106   | SB9              | NBPGR Shimla              | Indigenous               |
| 107   | SB49             | Not known                 | Exotic                   |
| 108   | SRI              | Local                     | Indigenous               |
| 109   | WBRM-101         | USA                       | Exotic                   |
cropping cycle. Standard agronomic practices were followed for normal crop growth. Five plants were selected from each genotype for recording the data.

2.3 | Data collection

Data were recorded for various qualitative and quantitative morphological characteristics/traits like plant growth (growth habit, growth type, and twinning habit); leaf (color, size, and shape); flower (color and stripping on outer petal); pod (shape in relation to suture, shape of cross section, and shape of distal part and stringiness), seed (color and shape) traits, and quantitative morphological traits (seed weight, length, and breadth) from five randomly selected plants from each plot. Observations were recorded as per descriptor PPV and FRA (2007) at proper crop developmental stage.

2.4 | Seed mineral estimation

For evaluation of seed micronutrients and macronutrients, a set of 109 genotypes originally used for morphological characterization were reduced to 60 diverse genotypes. These 60 genotypes have been found diverse in terms of morphological traits and represent all hotspots/collection sites in Jammu and Kashmir. Out of 60 genotypes, 22 genotypes belonged to Mesoamerican gene pool, and 38 genotypes belonged to Andean gene pool. This diverse set of 60 genotypes was evaluated for macronutrients (K, P, Mg, and Ca) and micronutrients (Fe, Zn, and Cu) by di-acid digestion method (Ribeiro et al., 2012) using atomic absorption spectrophotometer (AAS). The protocol briefly involves:

I. Random sample of 10–12 seeds from each genotype was ground to powder using mortar and pestle.

II. Ground sample weighing 0.5 g was digested by 5-ml di-acid mixture (nitric acid: perchloric acid in the ratio of 3:1) on hot plate at 300°C till solution turns clear and colorless.

III. Digestion tubes were allowed to cool down, the peroxide was added to bleach the solution. The solution was again put for digestion on the hot plate, heated till solution appears colorless.

After the solution becomes clear, the final volume was made 50 ml with distilled water and shaken well. This aliquot was taken for estimation of micronutrients (Zn, Fe, and Cu) and macronutrients (K, Mg, P, and Ca) concentrations (ppm) using AAS (Agilent Technologies, 200 series) against standard solutions of known concentrations. Estimation of these minerals was carried out on three separate replications values. Concentrations of Fe, Zn, Cu Mg, K, Ca, and P were converted and expressed in ppm (mg/kg) from the absorbance using Atomic Absorption Spectroscopy.

IV. Data obtained were statistically analyzed using MS Excel 2007 for mean, range, standard error, and coefficient of variance.

2.5 | Phaseolin typing

The genomic DNA isolation was carried out by the method of (Doyle & Doyle, 1990). Analysis of phaseolin diversity at DNA level was done to figure out gene pools in the collected common bean germplasm. Primers for phaseolin gene were selected from (Choudhary, Hamid, et al., 2018; Kami et al., 1995). The primer sequence for the right primer was 5′-AGCATATTCTAGGGCCCTCC-3′, and the primer sequence for the left primer was 5′GCTCAGTTTCAATCTGTTTC-3′. The procedure adopted for the amplification of phaseolin locus, the PCR master mix components, and PCR profile is available elsewhere (see Choudhary, Hamid, et al., 2018; Kami et al., 1995).

### TABLE 2 Qualitative trait analysis of 109 common bean landraces studied during the present study

| S. no. | Variable                              | Observation | No. of accessions |
|-------|---------------------------------------|-------------|-------------------|
| 1     | Anthocyanin coloration                 | Absent      | 19                |
|       |                                       | Present     | 90                |
| 2     | Growth type                           | Erect       | 37                |
|       |                                       | Semi erect  | 24                |
|       |                                       | Spreading   | 48                |
| 3     | Plant growth habit                    | Indeterminate | 73           |
|       |                                       | Determinate | 36                |
| 4     | Plant twining habit                   | Vinyl       | 70                |
|       |                                       | Non vinyl   | 39                |
| 5     | Flower color                          | Pink        | 18                |
|       |                                       | White       | 44                |
|       |                                       | Violet      | 36                |
|       |                                       | Purple      | 6                 |
|       |                                       | Yellow      | 4                 |
|       |                                       | Red         | 1                 |
| 6     | Outer surface of standard petal       | Non stripped | 83            |
|       |                                       | Stripped    | 26                |
| 7     | Leaflet size                          | Small       | 5                 |
|       |                                       | Medium      | 41                |
|       |                                       | Large       | 63                |
| 8     | Leaf color                            | Green       | 31                |
|       |                                       | Dark green  | 78                |
| 9     | Leaf shape                            | Cordate     | 81                |
|       |                                       | Ovate       | 28                |
| 10    | Pod shape of cross section through seed | Ovate     | 38                |
|       |                                       | Elliptic    | 38                |
|       |                                       | Cordate     | 27                |
|       |                                       | Circular    | 6                 |
| 11    | Pod shape in relation to suture       | Concave     | 102               |
|       |                                       | Convex      | 3                 |
|       |                                       |Absent       | 4                 |
3 | RESULTS

3.1 | Morphological characterization

The evaluation of morphological trait data revealed wide variation for plant, leaf, flower, pod, and seed characteristics (Table 2). Results obtained from evaluation of these traits are presented in the following subheadings:

3.1.1 | Plant growth characteristics

Plant growth traits like growth habit, growth type, and twinning habit of plants were evaluated. Genotypes of spreading, semi-erect, and erect growth type were observed. Spreading growth type was predominant over semi-erect and erect growth types as it was observed in 44.03% genotypes. Vinyl and non-vinyl twining habit was observed, with predominance of vinyl twining habit (64.22%). In the genotypes studied, growth habit was either indeterminate or determinate type; however indeterminate, growth habit was frequent type observed in 66.97% genotypes. Anthocyanin pigmentation on stem was noticed in 82.56% of genotypes, and in 17.43% genotypes, this pigmentation was lacking.

3.1.2 | Flower characteristics

Standard of the flower exhibited a marked variability. Pink, white, red, violet, and yellow colored flowers were found. However, white flower color was most predominant (44.86%). Stripping on outer standard petal was also observed in 23.85% genotypes, and in rest genotypes, it was absent.

3.1.3 | Leaf characteristics

In all 109 genotypes, leaf traits, namely, leaf shape, size, and color, were recorded. Two classes of leaf shape were found (Cordate and ovate). Cordate leaf shape was most predominant and was found in 78.31% genotypes. Three classes of leaf size were observed (large: predominant, medium, and small). Leaf color was, green, and dark green. Dark green leaf color was found to be the predominant as 71.55% genotypes had this leaf color.

3.1.4 | Pod characteristics

Pod color of 109 genotypes was green, pale green, and violet. Green color of pods was seen in 84.40% genotypes. Pod shape in relation to suture was found to be convex, concave and straight. Pods having concave shape in relation to suture were most common (93.75% genotypes). Shape of cross section of pod was seen as cordate, elliptical, and ovate. Cordate and elliptic shapes were most frequent. Shape of distal part of pods was found to be acute, truncate, and acute to truncate. Maximum genotypes (63.30%) had acute to truncate shape. Dry pods of maximum genotypes (55.04%) possessed strings, whereas in rest, it was absent. Also, pigmentation on pods was noticed only in 35.77% genotypes, but in rest of genotypes, it was absent.
3.1.5 Seed characteristics

A set of 109 accessions of common bean was also evaluated for seed shape, color, and size. Seeds of kidney, circular, elliptical, cuboidal, and circular to elliptical shapes were observed. Kidney (26.6%), cuboidal (28.4%), and circular to elliptical shapes (28.4%) were most predominant (Table 2). Variation was also noticed for seed testa color (Figure 1). Red (11.0%), cream (9.17%), cranberry (8.25%), purple (5.5%), black (0.9%), brown (6.42%), pink (0.9%), cannellini (0.9%), navy (0.9%), gray (1.83%), great northern (1.83%), and olivaceous (4.58%) colored seeds were observed. Different shades of red color were observed, namely, red painted lady (1.83%), Canadian red (3.66%), light red (2.75%), and dark red (7.33%). Likewise, painted black (2.75%) and black eye (0.9%) colors were also noticed. Similarly, different shades were seen in brown color and yellow colors (see Table 2 for more details).

The germplasm was also evaluated for three quantitative traits, namely, seed length, breadth, and weight. Good variation was noticed for these traits. In general, seed length ranged from 3 to 22.73 mm with mean value of 14.08 mm with standard error and variance of 2.63 and 18.82, respectively. Seed breadth ranged from 1.33 to 9.96 mm with mean value of 7.76 mm and with standard error and variance of 1.20 and 15.54, respectively. In genotype “SB30,” maximum seed length and breadth were observed. Genotype “WB1009” had minimum seed length and breadth. Seed weight also varied from 14.0 to 63 g with an average of 35.80 g. Genotype “WB413” was found to have maximum seed weight, and genotype “SB132” had minimum seed weight.

3.2 Trait phenotyping for microseed and macroseed minerals

A set of 60 genotypes evaluated for seed micronutrients and macronutrients depicted substantial variation for seed micronutrients (Fe, Zn, and Cu) and macronutrients (Mg, K, Ca, and P) (Table 3).

| Sample no | Genotype | Mg   | K      | Ca     | P      | Fe    | Zn    | Cu   |
|-----------|----------|------|--------|--------|--------|-------|-------|------|
| 1         | SB103    | 2.0125 | 12.397 | 4.125  | 2.490  | 115.4 | 38.31 | 9.4  |
| 2         | SB118    | 2.1241 | 13.654.5| 1.995  | 3.240  | 122.6 | 36.13 | 8.2  |
| 3         | SB128    | 1.9657 | 13.957 | 1.595  | 3.060  | 139.1 | 35.7  | 10.1 |
| 4         | SB49     | 1.8819 | 5.000   | 1.785  | 3.720  | 168.8 | 42.02 | 6.8  |
| 5         | SB46     | 1.2205 | 8.3445 | 2.101  | 2.160  | 95.7  | 25.63 | 10.3 |
| 6         | SB42     | 1.8027 | 13.964 | 1.2815 | 2.910  | 113.5 | 42.77 | 7.2  |
| 7         | SB44     | 1.8765 | 12.515.5| 2.1385 | 2.940  | 145   | 34.82 | 10.9 |
| 8         | SB43     | 1.7796 | 13.265 | 1.741  | 3.810  | 115.2 | 41.21 | 10.4 |
| 9         | SB45     | 2.3638 | 5.000   | 2.0605 | 3.300  | 149.3 | 40.97 | 12.1 |
| 10        | SB149    | 2.1524 | 14.3405 | 2.0485 | 3.900  | 138.1 | 40.49 | 9.6  |
| 11        | SB119    | 2.6118 | 14.8565 | 2.865  | 3.270  | 140.2 | 27.81 | 9.7  |
| 12        | SB334    | 2.0774 | 14.1415 | 2.590  | 3.300  | 152.2 | 40.36 | 7.6  |
| 13        | SB121    | 2.0309 | 12.821 | 4.300  | 2.760  | 124.8 | 30.85 | 0.9  |
| 14        | SB138    | 1.8727 | 14.5785 | 310    | 3.210  | 129.9 | 31.64 | 8.1  |
| 15        | SB147    | 2.0299 | 12.8145 | 3.205  | 2.940  | 124.5 | 34.51 | 10.9 |
| 16        | SB150    | 1.6408 | 5.000   | 3.050  | 3.660  | 171.3 | 52.44 | 9.7  |
| 17        | SB156    | 2.1534 | 14.2885 | 3.465  | 3.060  | 159.2 | 36.45 | 6.8  |
| 18        | SB102    | 1.679  | 14.794 | 3.135  | 3.090  | 145.9 | 36.31 | 8.9  |
| 19        | SB106    | 1.7908 | 5.000   | 3.650  | 3.420  | 180.6 | 104.08| 8.2  |
| 20        | SB111    | 2.2129 | 14.2525 | 3.140  | 3.780  | 136.8 | 42.22 | 9.7  |
| 21        | SB143    | 2.5817 | 14.683 | 2.535  | 3.450  | 129.1 | 41.73 | 7.9  |
| 22        | SB140    | 1.9924 | 12.337 | 2.895  | 2.970  | 130.1 | 34.24 | 8.6  |
| 23        | SB183.1  | 2.0181 | 5.000   | 2.730  | 3.090  | 128.7 | 27.07 | 7.9  |
| 24        | SB186    | 1.9514 | 5.000   | 4.050  | 2.940  | 130.3 | 38.97 | 9.4  |
| 25        | SB168    | 2.2771 | 13.9145 | 2.930  | 3.060  | 120.4 | 44.09 | 9.3  |
| 26        | SB158    | 2.4444 | 5.000   | 2.675  | 3.780  | 146   | 43.59 | 8.6  |
| 27        | SB159    | 2.489  | 5.000   | 4.780  | 3.930  | 135.2 | 22.34 | 8.9  |
| 28        | SB163    | 2.0926 | 13.632 | 2.810  | 3.210  | 133.4 | 45.15 | 7.4  |
Analysis of data revealed that seed Fe concentration ranged from 80.5 to 180.6 ppm with an average of 127.98 ppm in our collection. Maximum seed Fe concentration (180.6 ppm) was observed in genotype “SB106,” and minimum (80.5 ppm) was observed in genotype “SB42.”

Seed Zn concentration ranged from 14.64 to 104.08 ppm with an average of 36.21 ppm. Maximum seed Zn concentration (104.08 ppm) was found in genotype “SB106,” and minimum (14.64 ppm) was found in genotype “WB330.”

Cu concentration in seeds of 60 genotypes ranged from 0.9 to 13.4 ppm with an average of 8.16 ppm. Evaluation of macronutrients including seed K, Mg, Ca, and P in the current study depicted good variation among 60 genotypes. Seed Mg concentration ranged from 1,220.5 to 2,737.8 ppm with an average of 1,974.2 ppm. Similarly, seed K concentration ranged from 8,344.5 to 14,794 ppm with an average of 13,351.16 ppm. Seed calcium concentration ranged from 300 to 5,350 ppm with an average seed calcium concentration of 2,735.2 ppm. Seed phosphorus concentration ranged from 1,980 to 4,050 ppm with an average concentration of 2,828 ppm.

Coefficient of variation for all these macronutrients varied from 9.4 to 37.7, with an average of 20.46 and that of micronutrients varied from 13.7 to 32.50 with an average of 23.59.

Further analysis of data helped us to select a set of 10 candidate genotypes out of 60 genotypes that possess high and low concentration of each mineral (Table 4). For seed Mg, we selected candidate genotypes for low and high Mg that contains less than 1,600 ppm and more than 2,271 ppm, respectively. Based on estimation of seed phosphorus, a set of 10 candidate genotypes for low and high P were selected that contain less than 2,250 ppm and more than 3,420 ppm.

| Sample no | Genotype | Mg     | K       | Ca     | P       | Fe     | Zn     | Cu     |
|-----------|----------|--------|---------|--------|---------|--------|--------|--------|
| 29        | SB108    | 2,046.8| 13,697.5| 2,120  | 3,120   | 117.2  | 21.73  | 12.2   |
| 30        | SB139B   | 2,289  | 5,000   | 3,015  | 4,050   | 139.2  | 32.3   | 8      |
| 31        | SB153    | 1,872.4| 13,659.5| 5,345  | 2,610   | 131.1  | 53.83  | 9.5    |
| 32        | SB167    | 2,542.2| 14,029.5| 3,570  | 2,310   | 121    | 32.5   | 7.6    |
| 33        | WB473    | 2,046.6| 13,834  | 3,110  | 2,580   | 115.9  | 34.12  | 6.4    |
| 34        | WB469    | 1,822.3| 14,185  | 3,030  | 2,220   | 117.7  | 34.56  | 7.5    |
| 35        | WB1255   | 1,806.3| 12,378.5| 3,175  | 2,280   | 118.5  | 26.5   | 5.9    |
| 36        | WB330    | 1,687.7| 10,984  | 1,645  | 2010    | 80.5   | 14.64  | 4      |
| 37        | WB493    | 1,486  | 14,765.5| 3,360  | 2,190   | 103.8  | 30.51  | 7.2    |
| 38        | WB429    | 1,733.2| 12,337.5| 3,185  | 2,340   | 110.8  | 32.78  | 7.7    |
| 39        | WB1186   | 2,737.8| 12,856.5| 2,195  | 2,610   | 126.4  | 25.34  | 5.4    |
| 40        | WB1131   | 1,545.8| 12,073  | 2,820  | 2,160   | 111.5  | 38.37  | 6.7    |
| 41        | WB1184   | 2,067.9| 12,336  | 3,410  | 2,370   | 130.1  | 40.62  | 7.1    |
| 42        | WB832    | 1,893.5| 12,318.5| 2,405  | 2,370   | 120    | 36.37  | 6.8    |
| 43        | WB665    | 1,728  | 12,407.5| 3,375  | 2,430   | 136    | 28.06  | 6.7    |
| 44        | WB634    | 2,372.9| 12,878.5| 2,300  | 2,400   | 128    | 31.81  | 7.7    |
| 45        | WB934    | 1,572  | 12,657  | 2,585  | 2,430   | 107.6  | 25.36  | 7.7    |
| 46        | WB1199   | 1,968.7| 12,709  | 1,060  | 2,430   | 131.3  | 28.94  | 6      |
| 47        | WB1151   | 1,776.9| 11,916.5| 1,870  | 2,250   | 127.8  | 30.14  | 7.3    |
| 48        | WB1189   | 1,970.3| 12,437.5| 5,350  | 2,250   | 124    | 25.84  | 6.1    |
| 49        | WB650    | 1,823.4| 11,065  | 995    | 1,980   | 120.8  | 27.8   | 7.1    |
| 50        | WB846    | 1,423.9| 12,719.5| 1,295  | 2,730   | 132.8  | 24.27  | 9      |
| 51        | WB418    | 2,054.3| 14,149.5| 4,425  | 2,940   | 131.3  | 38.31  | 9.1    |
| 52        | WB1187   | 1,907.6| 11,925  | 2,435  | 2,160   | 135.9  | 36.13  | 7.6    |
| 53        | WB792    | 1,998.4| 13,080  | 1,630  | 2,400   | 121.5  | 35.7   | 8.8    |
| 54        | WB413    | 1,681.2| 12,642  | 2,530  | 2,460   | 134    | 42.02  | 7.8    |
| 55        | WB947    | 1,898.8| 13,887.5| 1,715  | 2,760   | 130.1  | 25.63  | 4.9    |
| 56        | WB956    | 1,819.2| 12,900.5| 4,565  | 2,400   | 118.2  | 42.77  | 13.4   |
| 57        | WB970    | 2,161.4| 13,328.5| 2,845  | 2,730   | 123.6  | 34.82  | 8      |
| 58        | WB1009   | 1,672.1| 11945.5| 1,865  | 2,640   | 110.7  | 41.21  | 6.8    |
| 59        | SR1      | 1,670.7| 12,713  | 2,920  | 2,220   | 105.3  | 40.97  | 9.6    |
| 60        | SB1      | 2,251.4| 12,868  | 1,985  | 2,400   | 95.3   | 47.13  | 10     |
TABLE 4  A set of 10 candidate lines/genotypes containing high and low concentration of micronutrients (Fe, Zn, and Cu) and macronutrients (Mg, K, P, and Ca) used in the current study

| Genotype | Mg   | Genotype | K   | Genotype | Cu   | Genotype | Fe   | Genotype | Zn   | Genotype | Ca   | Genotype | P   |
|----------|------|----------|-----|----------|------|----------|------|----------|------|----------|------|----------|----|
| Low nutrient candidate lines |
| SB46    | 1220.5 | SB46    | 8344.5 | SB121  | 0.9  | WB330    | 80.5 | WB330    | 14.64 | SB138    | 310  | WB650    | 1980 |
| WB846   | 1423.9 | WB330   | 10,984 | WB330  | 4    | SB1      | 95.3 | SB108    | 21.73 | WB650    | 995  | WB330    | 2010 |
| WB493   | 1.486  | WB650   | 11,065 | WB947  | 4.9  | SB46     | 95.7 | SB159    | 22.34 | WB1199   | 1,060 | SB46     | 2,160 |
| WB1131  | 1545.8 | WB1151  | 11916.5 | WB1186 | 5.4  | WB493    | 103.8 | WB846    | 24.27 | SB42     | 1281.5 | WB1113   | 2,160 |
| WB934   | 1.572  | WB1187  | 11,925 | WB1255 | 5.9  | SR1      | 105.3 | WB1186   | 25.34 | WB846    | 1,295 | WB1187   | 2,160 |
| SB150   | 1640.8 | WB1009  | 11945.5 | WB1199 | 6    | WB934    | 107.6 | WB934    | 25.36 | SB128    | 1,595 | WB493    | 2,190 |
| SR1     | 1670.7 | WB1131  | 12,073 | WB1189 | 6.1  | WB1009   | 110.7 | SB46     | 25.63 | WB792    | 1,630 | WB469    | 2,220 |
| WB1009  | 1672.1 | WB832   | 12318.5 | WB473  | 6.4  | WB429    | 110.8 | WB947    | 25.63 | WB330    | 1,645 | SR1      | 2,220 |
| SB102   | 1.679  | WB1184  | 12,336 | WB1131 | 6.7  | WB1131   | 111.5 | WB1189   | 25.84 | WB947    | 1,715 | WB1151   | 2,250 |
| WB413   | 1681.2 | SB140   | 12,337 | WB665  | 6.7  | SB42     | 113.5 | WB1255   | 26.5  | SB43     | 1,741 | WB1189   | 2,250 |
| High nutrient candidate lines |
| SB168   | 2277.1 | SB119   | 14856.5 | SB111  | 9.7  | SB119    | 140.2 | SB111    | 42.22 | SB167    | 3,570 | SB106    | 3,420 |
| SB139B  | 2.289  | SB49    | 14,857  | SB1    | 10   | SB44     | 145   | SB42     | 42.77 | SB106    | 3,650 | SB143    | 3,450 |
| SB45    | 2363.8 | SB45    | 14857.3 | SB128  | 10.1 | SB102    | 145.9 | WB956    | 42.77 | SB186    | 4,050 | SB150    | 3,660 |
| WB634   | 2372.9 | SB150   | 14857.4 | SB46   | 10.3 | SB158    | 146   | SB158    | 43.59 | SB103    | 4,125 | SB49     | 3,720 |
| SB158   | 2444.4 | SB106   | 14857.5 | SB43   | 10.4 | SB106    | 180.6 | SB168    | 104.08 | SB121    | 4,300 | SB111    | 3,780 |
| SB159   | 2.489  | SB186   | 14858.2 | SB44   | 10.9 | SB134    | 152.2 | SB163    | 45.15 | WB418    | 4,425 | SB158    | 3,780 |
| SB167   | 2542.2 | SB158   | 14,859  | SB147  | 10.9 | SB156    | 159.2 | SB1      | 47.13 | WB956    | 4,565 | SB43     | 3,810 |
| SB143   | 2581.7 | SB159   | 14859.3 | SB45   | 12.1 | SB49     | 168.8 | SB150    | 52.44 | SB159    | 4,780 | SB149    | 3,900 |
| SB119   | 2611.8 | SB139B  | 14859.5 | SB108  | 12.2 | SB150    | 171.3 | SB153    | 53.83 | SB153    | 5,345 | SB159    | 3,930 |
| WB1186  | 2737.8 | SB183.1 | 14,878  | WB956  | 13.4 | SB45     | 149.3 | SB106    | 104.08 | WB1189   | 5,350 | SB139B   | 4,050 |
of P, respectively. Similarly, we selected candidate genotypes for low and high calcium that possess less than 1.741 ppm and more than 3.570 ppm of seed calcium. For another seed macronutrient, K, we delineated candidate genotypes for low K that contain less than 12.337 ppm of K and candidate genotypes for high K that contain more than 14,856 ppm of K.

Based on estimation of seed micronutrients, namely, Fe, Zn, and Cu, a set of 10 genotypes have been selected that contain high Fe (>140.2 ppm), high Zn (>42 ppm), and high Cu (>9.7 ppm), and these genotypes are called as candidate genotypes for high Fe, Zn, and Cu. Similarly, a set of 10 genotypes have been selected that contain low Fe (<113 ppm), low Zn (<26.5 ppm), and low Cu (<6.7 ppm), and these genotypes are called as candidate genotypes for low Fe, Zn, and Cu.

Among these candidate genotypes for high micronutrients and macronutrients, certain genotypes were identified, which can be highly nutritious as they contain more than one mineral at higher concentration. Genotype “SB106” was found to possess K, Ca, P, Fe, and Zn in higher concentration. Genotype “SB45” was declared as a candidate genotype for high Mg, K, P, Fe, Zn, and Cu. Similarly, genotype “SB150” was found to contain high concentration of K, P, Fe, and Zn. Likewise other high nutrient candidate genotypes, namely, SB168 (Mg and Zn); SB139B (K, Mg, and P); SB158 (Mg, K, P, Fe, and Zn); SB159 (Mg, K, and Ca); SB167 and SB 143 (Mg and Ca); SB 119 (Mg, K, and Fe); SB 153 (Ca and Fe); SB 111P (Ca, Mg, and Zn); SB49 (K, P, and Fe); SB49 (P and Zn); SB 43 (P and Cu), and WB 956 (Fe and Zn), were identified during the present study.

It was found that genotype “SB46” contains low concentration seed Mg, K, P, Fe, and Zn. Genotype “WB330” was found to contain low concentration of K, Ca, P, Fe, Zn, and Cu. In genotype “WB113,” low concentration of Mg, K, P, Fe, and Cu was observed. The other low nutrient candidate genotypes like “WB846” low for Mg, Ca, and Zn; WB1009 low for Mg, P, and Fe; WB934 low Mg, Fe, and Zn; WB 650 low for Ca, P, and K; WB1151 and WB 1187 low for K and P; WB1186 and WB1255 low for Zn and Cu; WB947 low for Ca, Zn, and Cu; WB1199 low for Ca and Cu; WB1189 low for P, Zn, and Cu; and SB 42 low for Ca and Fe were identified.

3.3 | Gene pools of common bean germplasm by phaseolin typing

Phaseolin assay discriminated a set of 109 lines in two major gene pools, Mesoamerican and Andean, based on phaseolin type they possess. Two major phaseolins that have been largely found in common bean are “S” type and “T” type; “S” type belongs to genotypes having Mesoamerican origin, whereas “T” type to genotypes of Andean origin. It has been observed that genotypes that possess “T” type phaseolin produced three homoduplex bands whereas “S” type phaseolin produced 2 homoduplex bands on agarose gels. The same PCR product when run on PAGE displayed more complex/multiple banding pattern. The expected product size/band size of 240-300 bp was amplified for all the genotypes evaluated during the present study (Figure 2). These lower size bands are true amplification products, whereas bands larger in size (greater than 300 bp) are not true amplification products and are heteroduplexes resulted from various combinations from lower size bands during annealing and denaturation reactions of PCR (Kami et al., 1995). However, presence of this extra band having high molecular weight in “T” type phaseolin helps in discriminating genotypes of Andean origin from genotypes of Mesoamerican origin which lack this extra high molecular weight bands.

3.4 | Seed characteristics in Mesoamerican versus Andean beans

The set of 109 genotypes used during the present study was subjected to phaseolin typing. The analysis of phaseolin patterns led to the classification of 109 genotypes into Mesoamerican and Andean types. Average seed size and seed weight of Andean common bean genotypes was found more than seed size and seed weight of Mesoamerican genotypes. The average seed length, breadth, and weight of Andean genotypes was 15.3 mm, 8.04 mm, and 39 g, respectively, whereas the average seed length, breadth, and weight in Mesoamerican genotypes was 12.97 mm, 7.8 mm and 32.9 g, respectively. Similarly, the analysis of seed nutrients in these two different gene pools revealed that genotypes belonging to Mesoamerican gene pool possess higher average concentration of seed Mg, K, Ca, P, and Fe, whereas average seed Zn and Cu concentration was found higher in genotypes belonging to Andean gene pool. The average concentration of seed Mg, K, Ca, P, Fe, Zn, and Cu of genotypes of Mesoamerican gene pool was 2.061, 12.289, 2.058.06, 2.930.45, 131.51, 33.70, and 7.85 ppm, respectively. In contrast to Mesoamerican genotypes, the average seed Mg, K, Ca, P, Fe, Zn, and Cu concentrations in genotypes of Andean gene pool was 1.923.83, 1.1630.57, 2.548.38, 2.768.68, 125.9, 37.6, and 8.32 ppm, respectively.
DISCUSSION

4.1 Morphological trait diversity

Common bean is a major legume crop in Western Himalayan region of India. Huge diversity exists for plant type, growth habit, grain morphology, and in agro-ecological adaptation of landraces cultivated in this region (Choudhary, Bawa, et al., 2018; Choudhary, Hamid, et al., 2018; Singh, 2001). Presence and high magnitude of genetic variability in crop germplasm is the basic requirement of utmost importance for launching a crop improvement program (Appalaswamy & Reddy, 2004). Genetic variability of crop plants is maintained and conserved in ex situ manner in gene banks. Characterization of germplasm that is conserved in gene banks for various traits is essential for its practical application and exploitation in various breeding programs (Junqueira et al., 2010). In the present study, an effort was made to collect and characterize the common bean landraces from various hotspots of Jammu and Kashmir possessing high diversity for common bean landraces. Substantial variation was recorded for various morphological traits in the collection of 109 common bean genotypes, and these results are in accordance with earlier published results (Okii et al., 2014; Sofi et al., 2014). The predominance of indeterminate vinyl/climbing types may be due to the fact that common bean is mostly intercropped with maize and seldom grown as monocrop in Western Himalayas. Maize plants provide excellent trellis for the beans of climbing types to grow. Similar results were observed while evaluating 297 genotypes of common bean from Jammu and Kashmir in an earlier study (Sofi et al., 2014). However, determinate growth habit is commonly selected by farmers/breeders as determinate genotypes are mostly insensitive to day length (Kwak et al., 2012). Substantial variation was also noticed for leaf color, size, and shape in our common bean germplasm collection. The variation in leaf morphology may indicate variation in photosynthetic rates among genotypes (White & Montes-r, 2005). In our germplasm, different size and color of pods were found. Size and color of pods are important traits in deciding the marketability of a crop. All the genotypes evaluated had acceptable green pod color and pod size. Furthermore, shape of cross section of pods when looked through seeds was cordate, elliptical, and ovate. Cross section of pods is the characteristic feature of snap beans as they have low fiber, whereas elliptical cross section is associated with dry beans (Wallace et al., 2018). In 55.04% genotypes, dry pods were found, as they possessed strings; when pods were broken at full green mature stage, these strings help pods to resist breakage during transportation. Similar observations were also recorded by Sofi et al. (2011) during characterization of local common bean landraces under agro-climatic conditions of Jammu and Kashmir.

Seed traits like color, size, and shape in common bean show considerable variation and important trait for consumer preference because different people have different preferences for these traits (Beninger & Hosfield, 2003). Substantial variation for seed quantitative traits is comparable with earlier studies (Choudhary, Bawa, et al., 2018; Choudhary, Hamid, et al., 2018; Raffi & Nath, 2004; Sultan et al., 2014).

4.2 Trait phenotyping for seed nutrients

Common bean is an excellent source of micronutrients and macronutrients in addition to carbohydrates, proteins, vitamins, and antioxidants (Guzmán-Maldonado et al., 2000). These minerals in beans are readily available, thus can mitigate deficiencies and other health-related problems associated with their inadequate intake. In the current study, substantial variation for micronutrients and macronutrients was observed in a collection of 60 selected diverse genotypes.

The average values of Fe (127.98 ppm) and Zn (36.21 ppm) indicated less, moderate, and high density Fe and Zn genotypes in our collection. Several reports are already available on evaluation of common bean germplasm for seed Fe and Zn concentrations (Blair et al., 2009; Gouveia et al., 2014; Islam et al., 2002; Paredes et al., 2009; Ribeiro et al., 2013; Silva et al., 2010; Talukder et al., 2010; Tryphone & Nchimbi-Msolla, 2010). However, there is hardly literature available on evaluation of beans for nutrients from north-western Himalayas. The results of these studies indicated availability of huge variability for seed micronutrients in common bean germplasm. In broader term, the range of seed Fe and Zn concentrations observed in the current study were comparable with those in earlier analyses of Fe and Zn in common beans (Di bella et al., 2016; Paredes et al., 2009; Philippe et al., 2020; Ribeiro et al., 2013; Silva et al., 2010). However, it is notable that in previous studies, seed Fe and Zn concentration in a germplasm was found quite low, namely, Zn (17.5–32.3 ppm) and Fe concentration (63.5–86.9 ppm) (Islam et al., 2002). Fe concentration (53–69 ppm) and Zn concentration (25–32 ppm) (Moraghan & Grafton, 2001); Fe concentration (40.0–84.6 ppm) and Zn concentration (17.7–42.4 ppm) (Blair et al., 2009); Fe concentration (8.9–112.9 ppm) and Zn concentration (30.90–64.60 ppm) (Akond et al., 2011). Such differences in seed Fe and Zn concentration between this study and earlier studies are attributed to differences among cultivars/genotypes, inclusion of different number of genotypes, differences in soil types, and environmental conditions. Despite these germplasm evaluations, understanding the genetic control of seed Fe and Zn is essential to improve breeding process for these important nutritional traits. Seed Fe and Zn concentrations are predominantly quantitative/metric traits (Guzmán-Maldonado et al., 2003; Tryphone & Nchimbi-Msolla, 2010), whereas previous studies have shown monogenic inheritance for seed zinc (Cichy et al., 2005; Forster et al., 2002; Gelin et al., 2007).

Availability of substantial variation for seed Fe and Zn in our germplasm suggests that genotypes with high Fe and Zn can be utilized in future biofortification programs, transcriptomics studies, and other genomics studies. As for biofortification programs for higher seed Fe concentrations, genotypes should have seed Fe concentration more than 95 ppm (Ribeiro et al., 2013), and seed Zn concentration should be greater than 31 ppm according to the classification proposed by Tryphone and Nchimbi-Msolla (2010). In the current study, we found genotypes possessing seed Fe concentration>95 ppm and Zn concentration >31 ppm, respectively. Such genotypes are therefore apt for biofortification programs for improving Fe and Zn concentration in commercial cultivars.
Similarly, range of seed Cu concentration observed in the current study is comparable with those found in previous studies (Di Bella et al., 2016; Poersch et al., 2013; Ribeiro et al., 2013; Steckling et al., 2017). There is hardly any report available on evaluation for seed Cu concentrations of bean germplasm from Jammu and Kashmir. Thus, it is imperative to state here that our bean germplasm set with substantial Cu concentration can be potentially used in copper biofortification programs and as a genetic resource in genomics programs. It is desirable to elevate the copper concentration in common bean grains for alleviating copper deficiency, such as hypochromic anemia, neutropenia, and skeletal disorders (Maziero et al., 2016).

Determination of seed macronutrients including seed K, Mg, Ca, and P in our current study revealed good variation for these macronutrients. Similar results have been reported in some earlier studies (Di Bella et al., 2016; Moraghan & Grafton, 2001; Ribeiro et al., 2013). Seed Ca concentration is usually more in seed coat than embryo and is generally 80%–96% (Ribeiro et al., 2012). In earlier breeding programs, biofortification with Ca has been performed successfully, and genotypes with more than Ca 1,400 ppm have been obtained (Ribeiro et al., 2013). It is important to mention here that calcium concentration in some of our genotypes exceeds 1,400 ppm; therefore, these genotypes will serve as donors in future common bean breeding programs and will be useful in future biofortification programs. However, it is advised to include beans in a food along with seed coats to ensure substantial supply of calcium for keeping calcium-related deficiencies at bay. This is because of calcium oxalates present in seed coat restricts movement of calcium to embryo, resulting in its less concentration in embryo (Moraghan et al., 2006). For seed phosphorus concentration, substantial variation was reported in our germplasm. Parallel variation for seed phosphorus was observed common bean germplasm prior to this study (Blair et al., 2009; Ribeiro et al., 2019). The high nutritious candidate genotypes identified in this study can be highly recommended to meet dietary requirements and are appealing target for biofortification programs. These genotypes can also be used for development of Multi-Parent Advanced Generation Inter-cross (MAGIC) population and biparental mapping population and can be used in transcriptomics for accessing differential gene expression level for these nutrients. These genotypes can also be used in transfer of micronutrients and macronutrients into local common cultivars deficient or having less concentration of these nutrients. The low nutrient candidate genotypes can be recommended to persons requiring these nutrients in less amounts/concentration. Also, these low nutrient candidate genotypes are apt for hybridization program aimed for gene/QTL discovery for these nutrients because QTL mapping involves use of contrasting parents for development of mapping populations. Although researchers have been successful in identifying QTLs associated seed minerals in common beans (Beebe et al., 2000; Blair et al., 2009, 2010; Casanas et al., 2013; Cichy et al., 2005; Gelin et al., 2007; Guzmán-Maldonado et al., 2000; Izquierdo et al., 2018) in the world, but to the best of our knowledge, very few studies have been conducted in Jammu and Kashmir for identification of genes for these seed micronutrients and macronutrients (Mahajan et al., 2015).

So the current study shall pave a way for identification of genes associated with the seed minerals in common bean germplasm of Jammu and Kashmir.

4.3 Trait variability in Mesoamerican versus Andean beans

Seed size variability has been documented among the beans of Mesoamerican and Andean gene pools. Genotypes of Mesoamerican origin carrying “S” type phaseolin are smaller in size than the genotypes of Andean origin carrying “T” phaseolin which tended to have large seed. This association between seed size and phaseolin banding pattern of common bean has also been observed in earlier studies where cultivars carrying T phaseolin have larger seeds than cultivars carrying “S” phaseolin (Gepts et al., 1986). Domestication in Middle America would have resulted in small-seeded cultivars with “S” phaseolin patterns, and an independent domestication involving the Andean beans would have led to large-seeded cultivars with a “T” phaseolin type. Presence of both S and T types in local landraces of Jammu and Kashmir suggests that domestication of common bean in this region has been attempted multiple times (Choudhary, Hamid, et al., 2018). Multiple domestications in time and/or space may have been one of the key determinants in structuring the genetic diversity present in common bean. The analysis of data of seed Fe and Zn concentrations revealed substantial variation is present in genotypes of Andean or Mesoamerican origin collected by us from different hotspots of Jammu and Kashmir. Genotypes of Mesoamerican gene pool tend to have higher average seed Fe concentration than those of Andean gene pool. However, this trend was opposite for seed Zn concentration. In contrast to our results, higher seed Fe and Zn concentration was observed in genotypes of Andean gene pool and Mesoamerican gene pools, respectively (Blair et al., 2010; Islam et al., 2002).

5 Conclusion

In the present study, substantial genetic diversity was observed in a set of 109 genotypes for various quantitative and qualitative morphological traits. Conservation of this diversity is recommended for future breeding programs for improving various traits according to the interest of breeder. Substantial variation in germplasm for various micronutrients and macronutrients paves a way for further improvement of this germplasm. Augmentation of diets with genotypes having high concentration of the nutrients can ameliorate various deficiencies related to them. These findings endow some important facts that could be used to develop iron- and zinc-rich common bean varieties to potentially solve “hidden hunger” problem in the globe.

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CONFLICT OF INTEREST
The authors declare no conflict of interest.

AUTHORSHIP CONTRIBUTIONS
Reyazul Rouf Mir conceptualized and supervised this research. Sofora Jan conducted the experiments. Irshad Ahmad Rather and Mohd Altaf Wani facilitated collection of germplasm and in mineral estimation experiment. Sofora Jan, Reyazul Rouf Mir, Mohammad Ashraf Bhat, Parvaze Sofi and Farooq Ahmad Sheikh helped in writing and editing of the manuscript. All authors contributed to manuscript revision.

ETHICS STATEMENT
This article does not contain any human and animal subjects for experiments.

DATA AVAILABILITY STATEMENT
The data that support the findings of this study are available from the corresponding author up on request.

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