IDENTIFYING DRY BEAN GENOTYPES AND GENOMIC REGIONS ASSOCIATED WITH ROOT ROT RESISTANCE WITH EMPHASIS ON *FUSARIUM SOLANI* F. SP. *PHASEOLI*

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Title

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The Supervisory Committee certifies that this disquisition complies with North Dakota State University's regulations and meets the accepted standards for the degree of

DOCTOR OF PHILOSOPHY

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ABSTRACT

Common bean (*Phaseolus vulgaris* L.) is the most produced legume in the U.S. and worldwide. Fusarium root rot (FRR) is a widespread soil-borne diseases causing up to 86% yield reduction in beans. Large-seeded cultivars are usually susceptible to root rot. Finding FRR resistant genotypes under naturally infected soil and mapping genomic regions involved in its resistance were the main objectives in this research. In addition, halo blight, days to flower, growth habit, plant survival, seed weight, and seed yield were studied. Fusarium root rot and halo blight diseases were highly epidemic during the research period. The objectives were accomplished through two consecutive steps. First, phenotyping a set of genotypes from Andean diversity panel (ADP) under field conditions during three years starting with 310 genotypes in 2013. A Randomized Incomplete Block Design with two replications was used as the experimental design. From three years phenotypic data, ADP462-PI527540B, ADP48-W6_6534, ADP624-Dolly, ADP68-Soya, and ADP438-46_1 genotypes were resistant to FRR and ADP73-Masusu, ADP601-Camelot, ADP636-Montcalm, and ADP511-Canario were susceptible. In addition, ADP84-Kablanketi-defu, ADP55-Kabuku, ADP122-Kranskop, ADP454-INIAP429, and ADP50-Salunde were among the most resistant to halo blight and ADP638-Redhawk, ADP676-CELRK, ADP677-Etna, ADP242-G9013, and ADP269-G13092 were among the most susceptible. Genotypes ADP48-W6_6534, ADP624-Dolly, ADP438-46_1, and VAX3 (check) were resistant to both diseases. These genotypes can be used as parents in the bean breeding programs. Second, for GWAS, 3525 filtered single nucleotide polymorphism (SNP) markers of 246 Andean genotypes were used to find significant ($P \leq 0.001$) trait-marker associations. After correcting for population structure and relatedness, genomic regions on three chromosomes were associated with five traits. The study provided insights into the genetic architecture for FRR, halo blight, days to flower, growth habit and plant survival. Resistant genotypes can be used in the breeding programs, genomic regions should be validated before using as molecular markers to accelerate the breeding process.

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DEDICATION

To my mom, dad, and Adriana, wherever they are, who taught me how to surmount difficulties and pursue challenges with joy. Nonetheless to my wife Alicia, my sons Alex and Santiago who always are by my side and for whom I do my best.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

ADP ..... Andean diversity panel

AFLP ..... Amplified fragment length polymorphism

AM ..... Association mapping

ANOVA ..... Analysis of variance

DNA ..... Deoxyribonucleic acid

EMMA ..... Efficient mixed linear model association

FRR ..... Fusarium root rot

Fsp ..... *Fusarium solani* f. sp. *phaseolicola*

GWAS ..... Genome-wide association study

LD ..... Linkage disequilibrium

MAF ..... Minor allele frequency

MAS ..... Marker assisted selection

MM ..... Mixed model

PC ..... Principal component

PCA ..... Principal component analysis

Psp ..... *Pseudomonas syringae* pv. *phaseolicola*

Pv ..... *Phaseolus vulgaris* L.

QTL ..... Quantitative trait loci

RFLP ..... Restriction fragment length polymorphism

RAPD ..... Random amplified polymorphic DNA

SSR ..... Simple sequence repeat

SNP ..... Single nucleotide polymorphisms

LIST OF APPENDIX TABLES

INTRODUCTION

Recent studies suggest that common bean (*Phaseolus vulgaris* L.) originated in Central America (Bitocchi et al., 2013; 2012) and confirmed the two centers of domestication (Mesoamerican and Andean) previously characterized by Singh et al. (1991) with well-defined races within each gene pool. Common bean is the most important grain legume in America, Africa, and Europe (Akibode and Maredia, 2011). It is cooked and consumed in a range of ways, as dry grain, fresh (threshed manually at physiological maturity), or as tender pods (snap or green beans).Dry bean production region in North Dakota and Minnesota produces more dry beans than any other area in the U.S. (43%). Within this region, a number of different market classes are produced, including pinto, navy, black, small red, great northern, and kidney (Knodel et al. 2016).

There are many foliage and root diseases of beans throughout the world (Miklas et al., 2006) and some occur in ND/MN region. Among foliage disease are White Mold (Knodel et al., 2016), caused by *Sclerotinia sclerotiorum* (Lib.) de Bar] and bacterial blights (Markell and Pasche, 2014), caused by *Xanthomonas axonopodis* pv. *phaseoli* (Smith) Dye, *Pseudomonas syringae pv. phaseolicola* (Burkholder) Young et al. (Psp) , and *Pseudomonas syringae pv. syringae* van Hall. Among root diseases are FRR, caused by *Fusarium solani* (Mart.) f. sp. *phaseoli* (Burkholder) Snyder and Hansen; Fusarium wilt, caused by *F. oxysporum* Schlech. f. sp. *phaseoli* Kendrick & Snyder] (Fsp), and Rizoctonia root rot, caused by *Rhizoctonia solani* Kuhn [(telemorph *Thanatephorus cucumeris* (Frank)) Dark]. Fusarium root rot is major yield-limiting root disease of dry bean in this region (Estevez de Jensen, 2000, Bilgi et al., 2008).

Few sources of partial resistance to FRR rot are available within *P. vulgaris* species. Most commercial cultivars grown in Minnesota are susceptible to FRR. Cultivars within the red kidney bean market class have been suffering more losses due to FRR than some of the other market classes grown in the region (Bilgi, 2008) due to Andean origin. Cultivars and landraces from Andean gene pool are more susceptible than from Mesoamerican gene pool (Beebe el al., 1981).

Searching for useful germplasm for a breeding program is indispensable for sustained crop improvement. Improving breeding strategies and efficiencies on a continuous basis is also equally important. Thus, plant breeders typically look for germplasm that has favorable alleles that are lacking in

their own breeding programs. Breeders usually introduce new genes using conventional and new techniques and technologies to improve the breeding process.

It is a longstanding goal to identify genotypes or germplasm that can be used to improve disease resistance in Andean cultivars. The cultivars derived from the Nueva Granada race, such as Montcalm (http://bean.css.msu.edu/100Years.cfm), Redhawk (Kelly et al., 1998a), and others, are extensively used in Minnesota but are very susceptible to root t pathogens.

Traditionally, traits have been mapped to chromosomes through bi-parental population use. More recently, association mapping (AM) has been used to map quantitative trait loci (QTL) in naturally collected genotypes without parent-derived off-springs. Association mapping takes advantage of linkage disequilibrium (LD) to detect non-random marker-marker or trait-marker associations. Genome-wide association study is a variant of AM to detect trait-marker association utilizing phenotypic and genotypic data. The current study utilizes the GWAS approach to identify FRR resistant loci across a set of germplasm from Andean Diversity Panel (ADP). In addition to FRR, days to flower, determinacy growth habit, halo blight, plant survival, seed weight, and seed yield were studied.

The BARCBean 6K_3 SNP chip (Song et al., 2015) is utilized to localize markers in populations of common bean. Therefore, it could be used in finding significant markers associated with FRR and identifying potential candidate genes that control this trait. Identification of highly diagnostic markers within the Andean gene pool (mainly Nueva Granada race) could provide an opportunity to develop improved cultivars in a more efficient manner when incorporated into the breeding program. This will help the breeders in enhancement of genetic diversity, whereas maintaining commercially desired phenotypic characteristics of common bean.

Andean diversity panel field experiments were conducted at Perham, MN and screened mainly for FRR, the prevalent root disease in the area. An initial collection of 310 genotypes from the Andean diversity panel was phenotyped to identify genomic regions associated with it and other traits through GWAS.

LITERATURE REVIEW

Common bean is an important cash crop with high nutritional value and is produced on about 693,000 ha in the U.S. (USDA-NASS, 2015). The average harvested area in the U.S. was 605,000 ha during 2009-2013 period. The three leading commercial classes produced during this period were: Pinto (39%), navy (15%), and black (13%). Moreover, red kidney (6%), great northern (5%), and others (20%, including garbanzo) were produced in lower amounts. North Dakota and Minnesota produced 517,000 (43%) out of total 1.2 million metric tons leading bean production is the U.S. (Zahniser and Farah, 2014).

The region spanning across North Dakota and Minnesota, is the largest dry bean producing area in the U.S. The most important commercial classes are pinto, navy, and black bean in North Dakota, whereas kidney, navy, black, pinto and are in Minnesota. In addition, great northern and small red classes are grown on limited areas (Knodel et al., 2016). The growth type of the most modern cultivars is upright (determinate and indeterminate bush) with a life cycle 85 to 105 days from planting to harvest date. The seed yield average is 2100 kg ha^{-1} (Zahniser and Farah, 2014).

There are abiotic (excess of rainfall, drought) and biotic constraints (pathogens, weeds) present in the ND/MN region. During the 2014 growing season, excess of rainfall was ranked as the first production problem in the region and diseases as the second. White mold (Knodel et al., 2016) was the main foliar disease followed by bacterial blights (Markell and Pasche, 2014), however, FRR was the most significant problem in Minnesota (Estevez de Jensen, 2000).

Fusarium root rot

Fusarium root rot is one of the most common dry bean root diseases distributed worldwide. Under stress conditions, it can reduce bean yield up to 86% (Abawi and Pastor-Corrales, 1990). Large-seeded kidney beans cultivated are most affected (Beebe et al., 1981). This pathogen has been consistently isolated from areas of intensive bean cropping.

Initial symptoms appear as longitudinal narrow, reddish lesions on the hypocotyl and primary roots about one or two weeks after seedling emergence. As infection progresses, lesions become numerous, coalescent, and the entire underground stem and root systems may become covered with reddish brown external and internal lesions. There are no pronounced wilting symptoms although severely infected plants are stunted, chlorotic, and exhibit premature defoliation (Abawi, 1989).

Most isolates of *F. solani* produce appressed mycelia growth (pseudopionnotes) on artificial agar media. Fungal colonies are usually blue to blue-green, but occasionally are white to buff in color. Three types of asexually spores are produced by all isolates: microconidia, macroconidia, and chlamydospores. Microconidia are usually produced on simple short conidiophores. Macroconidia are sickle shaped, multiseptate and usually produced on sporodochia. The dark and thick chlamydospores are produced abundantly on or in infected host tissues and are long-term survival structures.

The pathogen survives in soil or in the infected decaying tissue primarily as thick-walled resting spores called chlamydospores. These overwintering spores germinate readily in response to plant root exudates and infect plants through stomata and wounds (Abawi, 1989).The pathogen is disseminated into the bean field by multiple means such as movement of infected soil, infected host tissues, colonized debris, irrigation water, and contaminated seed. Once into the field, the pathogen becomes uniformly distributed at high densities after two or three cycles of common bean cropping.

Fusarium root rot reaction is a complex inherited trait controlled by many different genes with low heritability, consequently difficult to manipulate by cross breeding (Mukankusi et al., 2011). Limited attempts to transfer resistant genes found in Middle American gene pool into Andean bean cultivars have been made. Genetic resistance has been identified in Mesoamerican common bean varieties such as PI 203958 (N203) (Boomstra and Bliss, 1977); Puebla 152, Porrillo Sintetico, ICA-Pijao (Beebe et al., 1981), T-39, VAX 3, Rojo chiquito (Bilgi et al., 2008), and G40001 (tepary bean, P. acutifolius A. Gray) (Mejia-Jimenez et al., 1994). However, it is still a challenge to find Andean germplasm with high levels of resistance since the genetic base is narrow.

Phenotyping

Collection of high-quality phenotypic data is essential in genome-wide association studies. Newly discovered candidate genes in mapping studies can only be tested if we have existing robust and accurate phenotypic data, which is usually collected over years in multiple locations (Flint-Garcia et al., 2005). To increase the mapping power, when screening large number of genotypes, it is necessary to consider efficient field designs such as incomplete block designs (e.g., α-lattice), and appropriate statistical methods (Eskridge, 2003).

Fusarium root rot and halo blight are the two main biotic constraints at Perham, MN under field conditions. Although screening for FRR was the main objective of the project, halo blight and other agronomic traits of economic importance were also studied.

Halo blight was epidemic during the three consecutive years as had been reported by Markell and Pasche (2014), and Vasquez et al. (2015b). Susceptible genotypes from the ADP were severely attacked under field conditions. The high winds and rains created wounds in the plant tissue, providing an entry for this pathogen. Early symptoms begin as small greasy spots on plant tissue, eventually surrounded by a yellow halo. Infection is favored by plant wounding and rainfall. Optimal temperatures range from the high 20 °C to low 15 °C (Markell and Pasche, 2014).Halo blight can reduce seed yield up to 45%. Nine races have been identified. Resistant cultivars, among others, are Chase (under field conditions), US14, CAL143 and PI150414. Early inheritance studies observed both monogenic and polygenic resistance (Singh and Schwartz, 2010). Monogenic resistance can be dominant or recessive (Duncan et al., 2014). Resistant genes have been named Pse-1, Pse-2, Pse-3, Pse-4, and Pse5. In addition, Miklas et al. (2014) found another major resistant gene named Pse-6 conferring specific resistance to Races 1, 5, 7, and 9 on Pv04 by using 76 F_9–derived lines from cross BelNeb-RR-1/A55. On the other hand, Duncan et al. (2014) reported another cultivar, US14HBR6, with specific recessive resistance to Race 6.

Genotyping

Traditional family-based linkage mapping uses bi-parental mapping populations like F_2, doubled haploids, recombinant inbred lines, near isogenic lines, and inbred backcross lines. Mostly RAPD markers along with composite interval mapping approach have been used to localize markers associated with FRR (Hagerty et al., 2015).Traditional mapping has also been called QTL mapping. Navarro et al. (2008) found polymorphism for root rot complex employing RAPDs, cosegregates S18.1500 and AD9.950 on linkage group Pv06 in recombinant inbred lines derived from cross Eagle/Puebla 152. The marker AD9.950 was genotyped in root rot resistant Puebla 152 accession and S18.1500 was genotyped in the susceptible cultivar Eagle. Contrastingly, Roman-Aviles and Kelly (2005) found RAPD markers associated with FRR resistance on linkage groups Pv02 and Pv05 of the integrated bean map. These authors used two inbred backcross lines derived from Red Hawk//Negro San Luis and C97407//Negro San Luis. Redhawk and C97407 are susceptible recurrent parents from Andean origin, whereas Negro San Luis is

resistant non-recurrent parent from Mesoamerican origin.These results are similar to findings made from Schneider et al. (2001). These authors found, using RAPDs, a marker $P7_{700}$ associated with FRR on linkage group Pv02 using F_4-derived recombinant inbred lines from a cross made among susceptible Montcalm and Isles with resistant FR266.Bi-parental population approach has some advantages, however, Mamidi et al. (2011) concluded that the loci discovered are often specific to those populations. In addition, Al-Maskri et al. (2012) stated that, bi-parental approach is very costly, has low resolution due to lower number of recombination events, and evaluates few alleles simultaneously in a relatively longer time scale.

Song et al. (2015) developed a SNP BARCBean6K_3 Beadchip. The BeadChip captured polymorphism of 5352 SNP markers in 502 Phaseolus genotypes, approximately 3 SNPs/kb. All SNPs are distributed across the 11 chromosomes of cultivars and landraces. The BeadChip is a useful tool for genetics and genomics research and it is widely used by common bean breeders and geneticists in the U.S. and abroad.

The availability of SNP BARCBean6K_3 BeadChip has created an opportunity to dissect FRR and other agronomical, physiological and nutritional traits, with enhanced resolution because of the smaller LD blocks in an association panel than in bi-parental mapping populations (Myles et al., 2009). The smaller LD blocks result from historical diverse panel, as opposed to bi-parental mapping populations where the LD blocks are longer because short-lived recombination resulting from the few generation-recombinations (Zhu et al., 2008).

Single nucleotide polymorphic markers (SNPs) are currently known as valuable markers for genotyping, due to their abundance, stability, and simplicity (Shi et al., 2011). SNPs represent most frequent polymorphisms (Cho et al., 1999).SNP markers in common bean reflect dual domestication events and inter gene pool hybridization in both gene pools. SNPs allowed the identification of three Andean and three Mesoamerican clusters corresponding to races (Cortes et al., 2011; Schmutz et al., 2014). Due to greater polymorphism and race structure, Mesoamerican gene pool shows higher genetic diversity with SNPs than the Andean (Cortes, 2013; Cichy et al., 2015).

Using SNP markers to map FRR resistance in a snap bean RIL population, Hagerty et al. (2015) found QTLs FRR3.1 on chromosome Pv03 and FRR7.1 on chromosome Pv07 highly associated with

FRR resistance in RR138 F6-derived population from RR6950/OSU5446 cross. RR6950 is highly FRR resistant, small seeded black indeterminate type IIIA accession of unknown origin, whereas OSU5446 is a highly FRR susceptible determinate type I Blue Lake 4-sieve breeding line. Previously, Bello et al. (2014), using an F5-derived recombinant inbred population (RR138, n=168) from the same cross, found a reliable association between FRR trait and the QTL genomic region on chromosomes Pv01, Pv04, Pv09, and Pv11. It should be pointed out that the population was evaluated at the F6 generation in the field, whereas the F5 generation was under greenhouse conditions.

Genome-wide association, identify loci by examining the significant trait-marker associations that can be attributed to the strength of LD between markers and functional polymorphisms across a set of diverse germplasm. In association mapping, a natural population is surveyed to determine trait-marker associations using LD (Flint-Garcia et al., 2005).Gupta et al. (2005) make a difference among AM and LD. Linkage disequilibrium refers to non-random association between: a) two markers, b) two genes, or c) between a gene and a marker locus. Association mapping refers to significant association of molecular markers with a phenotypic trait, usually performed through GWAS. Association mapping takes advantage of LD to find trait-marker associations. Association mapping is the most effective approach to utilize natural variation in the form of *ex situ* conserved crop genetic resources to discover trait-marker association (Al-Maskri et al., 2012).

The general approach of GWAS includes six steps. (i) a collection of diverse genotypes that may include, landraces, elite cultivars, wild relatives and exotic accessions, (ii) a comprehensive and precise phenotyping is performed over the traits of interest in multiple repeats and years/environments, (iii) the genotypes are then scanned with suitable molecular markers (AFLP, SSRs, SNPs), (iv) population structure and kinship are determined to avoid false positives followed by (v) quantification of LD extend using different statistics like D, D', or r^2. Finally, (vi) genotypic and phenotyping data are correlated using appropriate statistical software allowing tagging of molecular marker positioned in close proximity of gene(s) underlying a specific trait (Al-Maskri et al., 2012).

Finding markers associated with root rot complex with emphasis in FRR in common bean of Andean diversity gene pool will facilitate breeding through identification of outstanding resistant parents. GWAS method is used to find the differences in DNA (genetic variation) that explain the natural

phenotypic variation. Advances in high-throughput technologies have markedly reduced the cost per data point of molecular markers, particularly single nucleotide polymorphism (Zhu et al., 2008).GWAS links phenotypes to genotypes through adequate regression models (Yu et al., 2006). Association detection depends on genetic architecture, accurate phenotypic evaluation, and genotyping (Balding, 2006).

GWAS is a practical approach for common bean wild, domesticated and advanced populations (Chiti, 2014). It does not need any previous information on candidate genes and can test large number of markers associated with complex traits. Due to the complex population structure present in common bean and lack of information about candidate genes associated with agronomic traits, GWAS is the best approach that could be applied to study agronomic traits. The population structure and relatedness that exist in bean can lead to identify false positives.

Yu et al. (2006) and Zhang et al. (2010) developed mixed linear regression models to control population structure and relatedness. These models are flexible to deal with big amounts of data available from phenotypic family-based or population-based genotypes.Mixed linear models represent methods of choice that deals with unbalanced data across multiple trials. It shows reliable inference through the explicit modeling of correlations induced by genetic and environmental causes. Genome association and prediction integrated tool (GAPIT) package integrates principal component analysis (PCA), efficient mixed model analysis (EMMA), and mixed model (MM=PCA+EMMA) and other powerful, accurate, and computationally efficient regression models into a single R statistical package (Lipka et al., 2012).Kamfwa et al. (2015) and Cichy et al. (2015) found significant SNP markers associated with days to flower and determinacy growth habit, respectively. On the other hand, Moghaddam (2015) found SNP markers associated with seed size through GWAS.

The objectives were: 1) Identify dry bean genotypes with resistance to root rot complex in the field. 2) Find out genomic regions associated with genetic resistance to root rot using GWAS.

MATERIALS AND METHODS

Plant Material

A group of 310 genotypes was initially assembled into a panel to facilitate FRR screening. These genotypes are a subset of the ADP (Cichy et al., 2015). They were screened during the 2013 cropping season at Perham, MN, where all of them geminated, 302 flowered and 280 completed the production cycle. Therefore, FRR and halo blight were evaluated in 310 genotypes, days to flower in 302 genotypes, and plant survival, seed weight, and seed yield in 280 genotypes. During the 2014 season, 265 genotypes were selected from the previous year, based mostly on seed availability and adaptation, and planted again at Perham, MN. The 265 genotypes were split into two groups based on the results obtained the previous year: early flowering group (144 genotypes) and late flowering group (121 in genotypes). To confirm previous data, in each early and late flowering groups, 22 low scored genotypes and 22 highscored genotypes were selected, based on the FRR response and then screened again in the same location in 2015 season.

During all three seasons, five checks were used: VAX3 (Singh et al., 2001) as resistant FRR check; GTS106 (Gen-Tec Seed Co) as FRR susceptible check, Dynasty (Kuropatwa, 2013), Cabernet (Seminis/Monsanto), and Talon (Osorno et al., 2016) as FRR intermediate checks. Based on least square means (LSmeans) across the three years, a sub panel of 92 genotypes was assembled for a combined analysis of variance (ANOVA), including the five checks. Likewise, based on two years LSmeans, a sub panel of 246 genotypes was assembled for GWAS. The checks were excluded from GWAS because they have not been genotyped yet.

The 246 sub panel for GWAS included 110 landraces from Africa, 15 accessions from the CIAT Germplasm Bank, 6 accessions from the U.S. National Plant Germplasm Collection, 14 lines from Puerto Rico, one landrace from Ecuador, 15 U.S. accessions from East Africa, 8 landraces from Angola, and 77 lines and cultivars from U.S. bean breeding programs (Cychy et al., 201; USDA-FtF, 2016)

Statistical procedures

Incomplete Block Designs were used throughout the three years period. All experiments were analyzed as one-way for ANOVA using PROC MIXED and PROC GLM procedures. Replications were considered as random and genotypes as fixed effects. Fusarium root rot, halo blight, days to flower, plant

survival, seed weight, and seed yield were used in ANOVA, whereas growth habit was included in the simple linear correlation analysis among the phenotypical traits, since growth habit is a discrete trait. ANOVA tables using PROC GLM are reported in as Appendix Tables. During the 2013 season, the 310 genotypes, including five) checks were planted in 32 x 10 alpha design with two replications. Bean seeds were planted in two-row plots, 2.13 m long, 1.52 m wide (3.25 m^2 net area). In each plot, 96 seeds (230,769 seeds ha^{-1}) were planted. Higher seed density was sowed to assure seedling emergence in order to increase seed for the following years.

During the 2014 season, 144 genotypes from the early flowering group were planted in 12 x 12 square alpha lattice and 121 genotypes from the late flowering group were planted in 11 x 11 square alpha lattice. In both trials similar five checks were included. In the 2015 season, both the 49 early and 49 from late flowering groups were planted in 7 x 7 square alpha lattice, including five checks in both trials. The experimental plots in 2014 and 2015 were 3.66 m long, 1.52 m wide (5.57 m^2). In each plot 75 seeds (172,352 seeds ha^{-1}) were planted.

Individual ANOVA for each year were analyzed considering blocks and replications as random effects and genotypes as fixed effects. From the ANOVA table, statistical differences were considered at $P \leq 0.05$ level of significance. Coefficient of variation (CV%) was calculated using PROC GLM procedure.

Before doing the combined ANOVA and Pearson linear correlations, the homogeneity of variances test called “10x rule” was carried out. To do so, the highest residual value from the PROC MIXED covariance parameters was divided by the lowest residual value for each trait after computing from the five individual trials. If the difference was less than 10-fold, trials were considered homogeneous and therefore, combined analysis was performed (Patterson and Silvey, 1980).

Based on the three years LSmeans, a panel of 92 common genotypes was selected for a combined ANOVA. Years were considered as random effects and genotypes as fixed effects. Moreover, the relationship among traits was determined by Pearson’s simple correlation analysis (level of probability 0.001, 0.01, and 0.05) computed from Lsmeans across years when variances were homogenous using PROC CORR. Correlations (r) > 0.5 were considered strong, correlation (r) < 0.49 were considered weak. For GWAS, based on the two years LSmeans, a panel of 246 common genotypes was selected. An ANOVA was computed considering years as random and genotypes as fixed effects.

Location, soil characteristics, and phenotyping

The study was carried out at Perham, MN (Lat: 46.45°N; Lon: 95.21°W; Elev.: 416 m), during three consecutive years 2013, 2014, and 2015 in the field. Soil samples were taken every year from the 0 to 15 cm top layer and sent to the NDSU Soil Testing Laboratory for mechanical and chemical analyses, and Agvise Laboratories, Northwood, ND, for chemical analysis (Tables A14, A15, A16). In average, the soil contained 71% sand, 22% silt and 7% being classified as sandy-loam [(name=Sandberg; family=Entic Haplydolls; order=Mollisol (USDA-NRCS, 2016)]. According to the chemical analysis, the pH ranged from 6.2 to 7.2, organic matter content from 1.6 to 2.2, nitrate-nitrogen from 28 to 38 ppm, phosphorus 28 to 50 ppm (Olsen), potassium from 280 to 300 ppm from a soil layer 0 to 15 cm depth.

The Central Minnesota area, where Perham is located, is a leading kidney bean producer in Minnesota (Osorno et al., 2016). This location is used by the NDSU Dry Bean Breeding Program to screen mainly large-seeded breeding lines and cultivars for disease resistance, adaptation, and agronomic performance.

Since FRR phenotyping was the main objective, seeds were neither treated (with the exception of 2013) nor broadcast nitrogen was applied during the growing seasons. Additional cultural practices, such as pre-planted fertilization and irrigation were done following the farmer's common practices, weeds were eliminated manually. Previous rotational crops planted by the farmer were corn (*Zea mays* L.) in 2012, wheat (*Triticum aestivum* L.) in 2013, and potato (*Solanum tuberosum* L.) in 2014.

Infected plant samples were collected every year and sent to NDSU Plant Pathology Laboratory. Using Koch's postulates, the Laboratory identified *F. solani* f. sp. *phaseoli* associated with root rot in the Andean panel. No other root pathogen was found associated with it across three years.

Between days to flower (R6) and pod filling stage (R8), 4 plants from each plot were carefully removed with a shovel, cleaned of debris, and evaluated for FRR using the 1-9 scale (1 to 3=resistant, 4 to 6 intermediate, 7 to 9 susceptible) (CIAT, 1987). Description for each score is in Table 1.

Table 1. Description of visual disease rating scale used for FRR screening (CIAT 1987).

Score	Phenotypic description
1	No visible symptoms
3	Light discoloration either without necrotic lesions with approximately 10% of the hypocotyl and root tissues covered with lesions.
5	Approximately 25% of the hypocotyl and root tissues covered with lesions but tissues remain firm with deterioration of the root system. Heavy discoloration system may be evident.
7	Approximately 50% of the hypocotyl and root tissues covered with lesions combined with considerable softening, rooting, and reduction of the root system.
9	Approximately 75% or more of the hypocotyl and root tissues affected with advanced stages of rotting combined with a severe reduction of the root system.

Halo blight was rated using the same 1 to 9 CIAT (1987) scale between flowering (R6) and pod formation stage (R7). Description for each score is in Table 2. Inoculum from infected plants was isolated by the NDSU Plant Pathology Laboratory and race-typed using a set of eight differentials. Race 6 has been identified attacking beans in MN/ND area and to the Andean panel (K. Ghising, personal communication, 2016).

In addition to these diseases, the following agronomic traits were measured: days to flower was rated since planting date up to 50% of the plants in a plot have at least one opened flower (CIAT, 1987); growth habit 1=determinate with the main stem ending in a terminal flower bud, and 2=indeterminate, where the flower bud was not terminal (NDSU, 2013); percentage of plant survival was calculated dividing number of harvested plants by number of planted seed then multiplied by hundred; 100-seed weight, seeds were chosen randomly, weighted in grams with approximately 14% humidity; and seed yield in kg pet plot and transformed to kg ha^{-1}.

Table 2. Description of visual disease rating scale used for halo blight screening (CIAT 1987).

Score	Phenotypic description
1	No visible symptoms.
3	Approximately 2% of the leaf or pod surface area covered with round lesions. Very slight systemic chlorosis may be evident.
5	Approximately 5% of the leaf or pod surface area covered with round lesions of about 5 mm in diameter. Limited system chlorosis may be present on growing points.
7	Approximately 10% of the leaf tissues affected either by lesions or by resulting chlorosis. Limited leaf distortion is present and the pods generally show a bacterial exudation on coalescing lesions that can be about 10 mm in diameter.
9	Twenty-five percent or more of the leaf tissues affected by lesions and chlorosis. Severe leaf distortion and coalescing lesions covering large areas on pods cause deformation and empty pods.

Genotyping

A set of 5352 SNPs were obtained from the Illumina iSelect 6K Gene Chip (BARCBean6K_3; Song et al., 2015). Based on the phenotypic field data and genotypic data, 246 accessions were used for genotyping. After filtering for markers with more than 50% SNPs missing, missing data was imputed using fastPHASE 1.3 (Scheet and Stephens, 2006) and 5188 SNPs remained. Finally, the panel was filtered for minor allele frequency (5%) and monomorphic markers, resulting in 3525 SNPs for GWAS.

Population structure and trait-SNP marker association test

GWAS was done using the GAPIT package in R (Lipka et al. 2012). Multiple statistical models were tested: Naïve, PCA, MM and EMMA (Table 3). Principal component analysis was used to control for population structure; identity-by-state kinship matrix [EMMA, (Kang et al. 2008)] was used to control for family relatedness. The purpose of these models is to minimize the number of false positives which could be generated in structured populations by using genotypic information of all the markers in the genome. EMMA model (Kang et al. 2008) that controlled for both population structure and family relatedness was chosen because it most effectively reduced the number of false positives. For each trait, significant SNP

markers ($p = 1 \times 10^{-4}$) were selected from the selected best models. Manhattan plots were constructed by GAPIT package using –log10 of *P*-values against chromosome location to represent position of these markers.

Table 3. Statistical models used to test for trait-marker associations through genome association and prediction integrated tool (GAPIT) package in R (Mamidi et al., 2011).

Model	Linear regression equation	Information captured in the model
Naïve	$y = X\alpha + \varepsilon^{\dagger}$	y is related to X, without correction for structure
PCA	$y = X\alpha + P\beta + \varepsilon$	y is related to X, with correction for structure
EMMA	$y = X\alpha + Ku + \varepsilon$	y is related to X, with correction for kinship
MM	$y = X\alpha + P\beta + Ku + \varepsilon$	y is related to X, with correction structure and kinship

†y is phenotype, X is the fixed effect of the SNP; P is the fixed effect of the structure (from PCA matrix); K is the random effect of kinship; and ε is the error term.

RESULTS AND DISCUSSION

Phenotypic analysis by year and across years

Fusarium root rot

In 2013, the genotypic effect was not significant (Table 4). FRR severity averaged 4, ranging from 1 to 9, with a standard deviation of 1. In 2014, the genotypic effect was significant (*P≤0.01*) for early genotypes but not significant for late genotypes (Table 4). FRR severity averaged 5, ranging from 1 to 9, with a standard deviation of 2 in both trials. From the early genotypes VAX3 (check) ranked first with LSmeans of 2 (resistant) and GTS106 ranked last with 8 (susceptible) (Table A9).

In 2015, the genotypic effect for the early and late genotypes was significant (*P*≤0.01, *P*≤0.05, respectively) (Table 4). FRR averaged 6, ranging from 1 to 9, and the standard deviation was 2 in both trials. From early genotypes, ADP438-46_1 ranked first with LSmeans of 2 (resistant), and ADP73-Masusu ranked last with 8 (susceptible) (Table A11). From the late genotypes, VAX3 (check) ranked first with LSmeans of 2 (resistant), and GTS104 ranked last with 8 (susceptible).

All trials were homogeneous for FRR, the difference was less than 10-fold and therefore, combined ANOVA and Pearson's simple linear correlation was performed. Genotypic effect was significant (*P≤0.01*) in the combined ANOVA (Table 4). The FRR averaged 5, ranging from 2 to 8, and the standard deviation was 2. Genotypes ADP462-I527540B, ADP48-W6_6534, ADP624-Dolly, and ADP68-Soya were the top resistant and GTS106 was the most susceptible (Table 5). The checks, VAX3 confirmed its resistance, GTS106 its susceptibility, Dynasty, Cabernet, and Talon confirmed their intermediate resistance to FRR (Table A13).

The population average for FRR was 4 in 2013, 5 in 2014, and 6 in 2015 (Table 6). The yearly increase observed could be due to infected seed planted each year. *F. solani* is a seed-borne pathogen transported on the seed coat (Mahmoud et al., 2013). Seed planted in 2014 and 2015 was harvested at Perham, MN, in Fusarium infected fields.

Table 4. Population mean of five individual trials and combined analysis, range, standard deviation (SD), and P-value for six traits measured in five from Andean diversity panel grown at Perham, MN, from 2013 to 2015.

Year	Genotype No.	Parameter	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
2013	310†	Mean	4	4	47	30	44	1407
		Min	1	1	36	4	20	62
		Max	9	9	76	59	71	3960
		SD	1	2	7	11	11	818
		P-value	ns	**	**	**	**	**
2014-early	144	Mean	5	6	41	70	43	974
		Min	1	1	35	23	20	68
		Max	9	9	48	99	64	3300
		SD	2	2	4	17	9	543
		P-value	**	**	**	**	**	**
2014-late	121	Mean	5	5	49	55	39	1093
		Min	1	1	42	22	23	79
		Max	9	9	61	96	58	2880
		SD	2	2	3	14	7	617
		P-value	ns	**	**	**	**	**
2015-early	49	Mean	6	4	43	61	40	1257
		Min	1	1	36	17	22	140
		Max	9	9	52	90	58	2917
		SD	2	2	3	13	40	537
		P-value	**	**	**	ns	**	**
2015-late	49	Mean	6	3	48	60	32	813
		Min	1	1	42	38	18	115
		Max	9	9	60	91	57	3029
		SD	2	2	4	11	8	522
		P-value	*	**	**	**	**	**
Combined	92	Mean	5	4	45	52	42	1214
		Min	2	1	36	7	20	206
		Max	8	9	64	98	69	3096
		SD	2	2	5	20	10	540
		P-value	**	**	**	**	**	**

ns=not significant; *Significant at the 0.05 probability level; **Significant at the 0.01 probability level
†310 genotypes for FRR and halo blight; 302 for days to flower; 280 for plant survival, 100-seed weight and seed yield

Halo blight

Along with FRR, halo blight disease was epidemic at Perham, MN during all three years and significantly affected the Andean panel during the study period. The genotypic effect was significant

Table 5. Top five and the button genotypes for six traits from 92 combined analysis from ADP grown at Perham, MN, from 2013 to 2015.

Genotype	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight	Seed yield kg ha^{-1}	Growth habit[†] 1-2
			Fusarium root rot				
VAX3-resistant check	2	2	48	59	27	2450	2
ADP462-PI527540B	2	4	45	57	27	1201	2
ADP48-W6_6534	3	3	48	58	26	1201	2
ADP624-Dolly	3	3	42	50	58	2298	1
ADP68-Soya	3	4	49	52	34	1220	2
GTS104-susceptible check	7	5	44	45	49	1241	1
LSD	2						
			Halo blight				
VAX3	2	2	48	59	27	2450	2
ADP84-Kablanketi_ndefu	4	2	52	51	32	1185	2
ADP454-INIAP429	4	2	58	53	38	1694	2
ADP55-Kabuku	4	2	48	52	33	1493	2
ADP122-Kranskop	4	2	52	48	39	1093	2
ADP242-G9013	4	8	38	77	49	1735	1
LSD		2					
			Days to flower				
ADP676-CELRK	6	7	37	57	50	862	1
ADP242-G9013	4	8	38	77	49	1735	1
ADP644-FoxFire	5	4	38	67	48	1650	1
ADP5-Kabuku	5	4	38	59	41	1392	1
ADP648-RedKloud	4	5	38	65	49	1686	1
ADP621-JaloEEP558	4	3	58	57	30	715	2
LSD			3				
			Plant survival				
ADP242-G9013	4	8	38	77	49	1735	1
ADP172	4	3	41	69	26	2038	2
ADP644-FoxFire	5	4	38	67	48	1650	1
ADP648-RedKloud	4	5	38	65	49	1686	1
ADP680-Clouseau	4	6	40	63	59	1675	1
ADP646-Myasi	5	5	42	27	32	521	1
LSD				18			

Table 5. Top five and one last genotypes for six traits from 92 combined analysis from ADP grown at Perham, MN, from 2013 to 2015 (continued).

Genotype	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight	Seed yield kg ha^{-1}	Growth habit 1-2
			Seed weight				
ADP649-Kamiakin	5	3	43	61	59	2091	1
ADP680-Clouseau	4	6	40	63	59	1675	1
ADP616-OAC_Lyrick	6	6	38	57	58	1025	1
ADP624-Dolly	3	3	42	50	58	2298	1
ADP225-G6415	5	3	42	56	57	1489	1
ADP93-Moro	4	3	50	48	25	627	2
LSD					6		
			Seed yield				
VAX3	2	2	48	59	27	2450	2
ADP624-Dolly	3	3	42	50	58	2298	1
ADP649-Kamiakin	5	3	43	61	59	2091	1
ADP172	4	3	41	69	26	2038	2
ADP614-Rosie	4	3	43	59	49	1924	1
ADP646-Myasi	5	5	42	27	32	521	1
LSD						657	

†1=determinate; 2=indeterminate

($P \leq 0.01$) in each individual year (Table 4). The average during 2013 for 310 genotypes was 4. During 2014, the average for 144 early genotypes was 6 and for 121 late genotypes was 5; during 2015, the average for 49 early genotypes was 4 and for 49 late genotypes was 3. In all trials the disease scores ranged from 1 to 9, standard deviation was 2.

The early upright genotypes tend to be more susceptible to halo blight probably due to smaller canopy area compared larger canopy to late-climbing genotypes. Late genotypes recovered from early infections through new canopy formation since most of them have indeterminate growth habit. Schwartz (1989) stated that, in general, older plants are more resistant to infection.

All trials were homogeneous for halo blight, the difference was less than 10-fold and therefore, combined ANOVA and Pearson's simple linear correlation was performed. In the combined ANOVA, the genotypic effect was significant ($P \leq 0.01$) (Table 4). The FRR averaged 5, ranging from 1 to 9, and the standard deviation was 2. From the genotypes tested, VAX3, ADP84-Kablanketi_ndefu, DP454-INIAP429, ADP55-Kabuku, and ADP122-Kranskop were the top resistant and ADP242-G9013 was the

most susceptible (Table 5). All top resistant had indeterminate growth habit and the susceptible genotype indeterminate. Among the checks, VAX3 was resistant, Cabernet susceptible, Dynasty, GTS104, and Talon intermediate resistant.

Halo blight and FRR diseases were not correlated (r=0.20) (Table 7). Thus each disease seems like is governed by independent genes. However, the genotypes VAX3, ADP48-W6_6534, ADP624-Dolly, and ADP438-46_1 were resistant to both diseases. From the three genotypes, ADP624-Dolly had determinate growth habit (Table A13).

Disease severity of halo blight in 2013 started with 3, raised to 5 in 2014, and was 3 in 2015 (Table 6). Increased infection in 2014 was due to higher plant population (plant survival 65%) and canopy development compared to the other two years. Moreover, favorable weather conditions promoted halo blight attack (Markell and Pasche, 2014). Halo blight was negatively correlated with growth habit (r=-0.54***) (Table 7). Halo blight symptoms increased in determinate growth habit genotypes and decreased in indeterminate as has been suggested by Schwartz (1989).

Days to flower

The genotypic effect was significant ($P \leq 0.01$) in each individual trials (Table 4). In 2013, for 302 genotypes the average was 47 days, ranged from 36 to 76, and standard deviation was 7. In 2014, for 144 early genotypes, the average was 41 days, and for 121 late genotypes 49 days. In 2015, for 49 early genotypes the average was 43 days, and for 49 late genotypes was 48 days.

All trials were homogeneous for days to flower, the difference was less than 10-fold and therefore, combined ANOVA and Pearson's simple linear correlation was performed. In the combined ANOVA across years, the genotypic effect was significant ($P \leq 0.01$) (Table 4), the average was 45, ranged from 36 to 64, and the standard deviation was 5. From the genotypes tested, ADP676-CELRK, ADP242-G9013, ADP644-Foxfire, ADP5-Kabuku, and ADP648-Redkloud were among the earliest with 38 days after planting and ADP621-JaloEEP558 was the latest with 55 days average after planting. All five earliest had determinate growth habit and all ADP621-JaloEEP558 indeterminate growth habit (Table 5). Among the checks, Cabernet flowered at 41 days, Dynasty at 42 days, Talon at 43 days, GTS104 at 44 days, and VAX3 at 48 days after planting (Table A13). Population average for days to flower across years ranged from 45 to 46 days after planting (Table 6) being the most stable trait.

Days to flower was positively correlated with growth habit (r=0.56***) and negatively correlated with seed weight (r=-0.60***) (Table 7). Early genotypes were mostly determinate growth habit with high 100-seed weight at Perham, MN. This correlation agrees with Kelly et al. (1998b) and Kornegay et al. (1992) findings.

Table 6. Means of six traits measured on the 92 common genotypes grown across three years at Perham, MN, from 2013 to 2015.

Year	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
2013	4	3	46	29	46	1465
2014	5	5	45	65	44	1174
2015	6	3	46	60	35	1002

Growth habit

Growth habit was evaluated as discrete variable (determinate/indeterminate), and consequently it was not used for ANOVA. Instead, it was used for correlation purposes. Growth habit was negatively correlated with seed weight (r=-0.50***) (Table 7). From 92 genotypes, 52 genotypes had determinate growth habit, 40 indeterminate (Table A13). Most Andean genotypes from Nueva Granada race usually have determinate growth habit and larger seed than Mesoamerican races (Kornegay et al., 1992). Among the checks, VAX3 was indeterminate, whereas Cabernet, Dynasty, GTS104, and Talon had determinate growth habit.

Plant survival

The genotypic effect was significant ($P \leq 0.01$) for all trials, except for the 2015 early trial (Table 4). In 2013, for 280 genotypes the average was 30%, ranged from 4 to 59%, and standard deviation was 11. In 2014, for 144 early genotypes, the average was 70%, ranged from 23 to 99%, and standard deviation was 17; for 121 late genotypes 55%, ranged from 22 to 96%, standard deviation was 14. In 2015, for 49 early genotypes the average was 61%, ranged from 17 to 90%, standard deviation was 13 and for late genotypes the average was 6%, ranged from 38 to 91%, standard deviation was 11.

All trials were homogeneous, the difference was less than 10-fold for plant survival, therefore combined ANOVA and Pearson's simple linear correlation was performed. In the combined ANOVA, the genotypic effect was significant ($P \leq 0.01$) (Table 4). The average was 52%, ranged from 7 to 98%, and the standard deviation was 20. From the genotypes tested, ADP242-G9013, ADP172, ADP644-Foxfire, ADP648-Redkloud, and ADP680-Clouseau had the top plant survival with 70% average and ADP646-Myasi had the lowest plant survival with 27% average (Table 5). Among checks, VAX3 had 59%, Cabernet 52%, Dynasty 51%, Talon 48%, and GTS104 45% plant survival (Table A13).

From the yearly mean population, in 2013, plant survival average was the lowest with 30%, increased to 65% in 2014 and to 60% in 2015 (Table 6). Low plant survival was due to low seedling emergence after heavy rainfall in 2013, even though seed was treated. In 2014 and 2015, low plant survival was due to seed-borne fungi *F. solani* and *P. syringae* attack and poor adaptation of some introduced Andean genotypes. Plant survival was positively correlated with seed yield (r=0.61***) (Table 7), Thus, higher plant survival produced higher seed as expected.

Seed weight

The genotypic effect was significant (*P*≤0.01) (Table 4) in all trials. In 2013, the average for 280 genotypes was 44 g, ranged from 20 to 71, standard deviation was 11. In 2014, the average was 43 g, ranged from 20 to 64 g, standard deviation was 9 for early trial; and the average 39 g, ranged from 23 to 58 g, standard deviation was 7 for late trial. In 2015, the average 40 g, raged from 22 to 58, standard deviation was 40 g for early trial; and average 32 g, ranged from 18 to 57 g, standard deviation was 8 for late trial.

All trials were homogeneous seed weight, the difference was less than 10-fold and therefore, combined ANOVA and Pearson's simple linear correlation was performed. In the combined analysis the genotypic effect was significant (*P≤0.01*) (Table 4). The average was 42 g, ranged from 20 g to 69 g, and the standard deviation was 10 g. From the genotypes, ADP649-Kamiakin, ADP680-Clouseau, ADP616-OAC_Lyrick, ADP624-Dolly, and ADP225-G6415 had the highest seed weight with 58 g average, and ADP93-Moro had the lowest seed weight with 25 g average (Table 5). Among checks, Dynasty 57 g, Cabernet, GTS104, and Talon 49 g each, and VAX3 29 g per seed weight (Table A13). From yearly population mean, in 2013, seed weight average was 44 g, in 2014 was 46 g, and in 2015 was 35 g (Table 6). In 2015 harvested plots were harvested with reduced moisture content in the seed.

Seed yield

The genotypic effect was significant (*P*≤0.01) for all trials (Table 4). In 2013, the average was 1407 kg ha^{-1}, ranged from 62 to 3960 kg, standard deviation was 818; in 2014, for early the average was 974 kg ha^{-1}, ranged from 68 to 3300 kg, standard deviation was 543, and for late was 1093 kg ha^{-1}, ranged from 79 to 2880 kg, standard deviation was 617. In 2015, for early the average was 1257 kg ha^{-1},

ranged from 140 to 2917 kg, standard deviation was 537, and for late trial the average was 813 kg ha^{-1}; ranged from 115 to 3029 kg, standard deviation was 522.

All trials were homogeneous for seed yield, the difference was less than 10-fold and therefore, combined ANOVA and Pearson's simple linear correlation was performed. In the combined analysis the genotypic effect was significant ($P \leq 0.01$) (Table 4). The average was 1214 kg ha^{-1}, ranged from 206 to 3096, and standard deviation was 540 kg ha^{-1}. From the genotypes tested, VAX3, ADP624-Dolly, ADP649-Kamiakin, ADP172, and ADP614-Rosie had the highest seed yield with 2160 kg ha^{-1} average, and ADP646-Myasi had the lowest seed yield with 521 kg ha^{-1} average (Table 5). Among checks, VAX3 2450 kg, Talon 1659 kg, Dynasty1607, Cabernet 1268, and GTS104 kg ha^{-1} (Table A13).

Seed yield of 1214 kg ha^{-1} averaged across three years was (Table 4) low compared to 2185 kg ha^{-1} Minnesota seed yield average (Lofthus and Byrne, 2015). It was due to FRR and halo blight infection, poor adaptation and late maturity of some introduced genotypes included in the Andean panel.

Seed yield was positively correlated with plant survival as expected (r=0.61***) (Table 7). Likewise, FRR and halo blight affected negatively slight affected seed yield (r=-024*). On the other hand, late-indeterminate-small-seeded genotypes usually have higher seed yield than early-determinate-large-seeded genotypes (Kelly et al., 1998b; Schneider et al., 2001), although the short cropping season, 105 days, at Perham, MN, did not allow to express all seed yield potential to late-indeterminate-small-seeded genotypes.

Table 7. Pearson correlation coefficients among seven traits measured on 92 genotypes grown at Perham, MN, from 2013 to 2015.

Trait	Halo blight 1-9	Days to flower No.	Growth habit	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
Fusarium root rot	0.20	-0.22*	-0.28**	-0.27**	0.38***	-0.24*
Halo blight		-0.43***	-0.54***	0.00	0.30***	-0.24*
Days to flower			0.56***	-0.40***	-0.60***	-0.37***
Growth habit				-0.08	-0.50***	-0.04
Plant survival					0.11	0.61***
100-seed weight						0.32***

*Significant at the 0.05 probability level; ** Significant at the 0.01 probability level;
*** Significant at the 0.001 probability level

Genome-wide association study

Population structure

Using two years data an ANOVA was computed (Table A7). With the exception of plant survival, significant ($P \leq 0.05$) genotypic differences for FRR, halo blight, days to flower, seed weight, and seed yield were found. For GWAS, Lsmeans from all traits, including determinacy growth habit, is in Table A14.

For 246 genotypes, 3525 SNP markers were used to evaluate population structure via principal component analysis using a correlation matrix on GAPIT package. SNP markers were plotted in two-dimension graphs using principal component approach. For 246 Andean panel, the first principal component (PC1) comprised ADP in two sub populations, which correspond to the two gene pools: Andean and Mesoamerican. The second PC2 separated Andean panel in a sub set groups, probably corresponding to admixtures among the two gene pools (Figure 1). Similar two subpopulations and subset groups described Cichy et al. (2015) for 374 accessions from ADP and 3385 SNP markers using the software STRUCTURE. Likewise Kamfwa et al. (2015), also using STRUCTURE, described two subpopulations within 237 accessions from ADP and 4850 SNP markers, one big subpopulation from Andean gene pool and one small subpopulation from Mesoamerica gene pool.

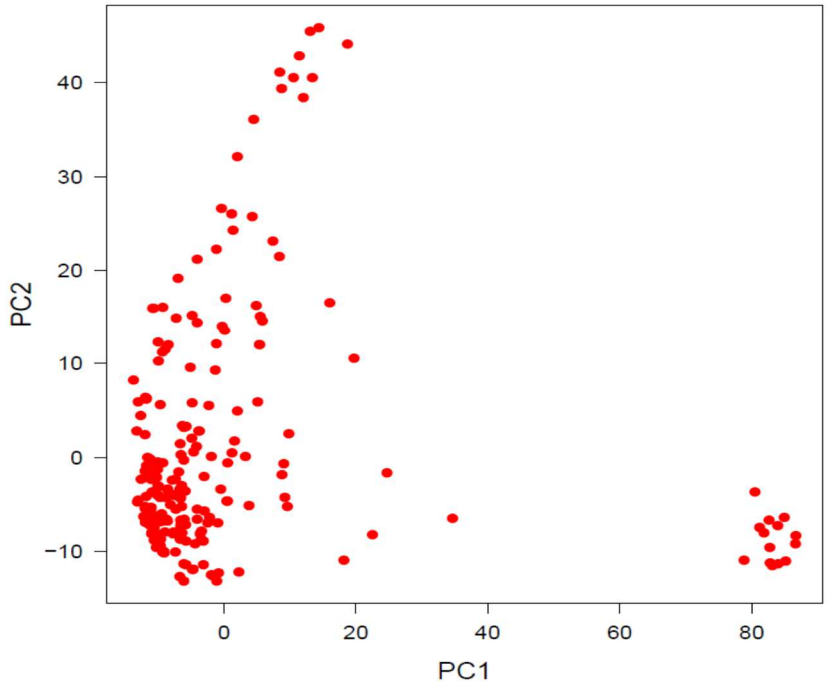

Figure 1. Principal component analysis of 246 genotypes determined by 3525 SNP markers. The x-axis represents the eigenvalue for principal component 1 (PC1) and the y-axis represents the eigenvalue for principal component 2 (PC2).

Fitting the best trait-marker regression model

Using FRR phenotypic data from the 246 Andean panel and their corresponding 3525 SPNs in order to select the best statistical approach, four linear regression models using QQ-plots (quantile-quantile plots) were analyzed. QQ-plots were generated by plotting observed –log10 *P*-values against expected –log10 *P*-values GAPIT package (Lipka et al., 2012).

From the four QQ-plots, the Naïve model is far from the regression line with the higher amount of *P*-values far from the regression line (Figure 2a); whereas PCA, EMMA and MM are closer to the regression line (Figure 2b, 2c, 2d). However, EMMA model fits better the regression line for FRR (Figure 2d), halo blight, days to flower, growth habit, and plant survival (Figures not shown). Moreover, EMMA model produced more redundant markers. The *P*-value distribution for the full model follows the expected distribution under the null hypothesis of independence between the SNPs and the trait.

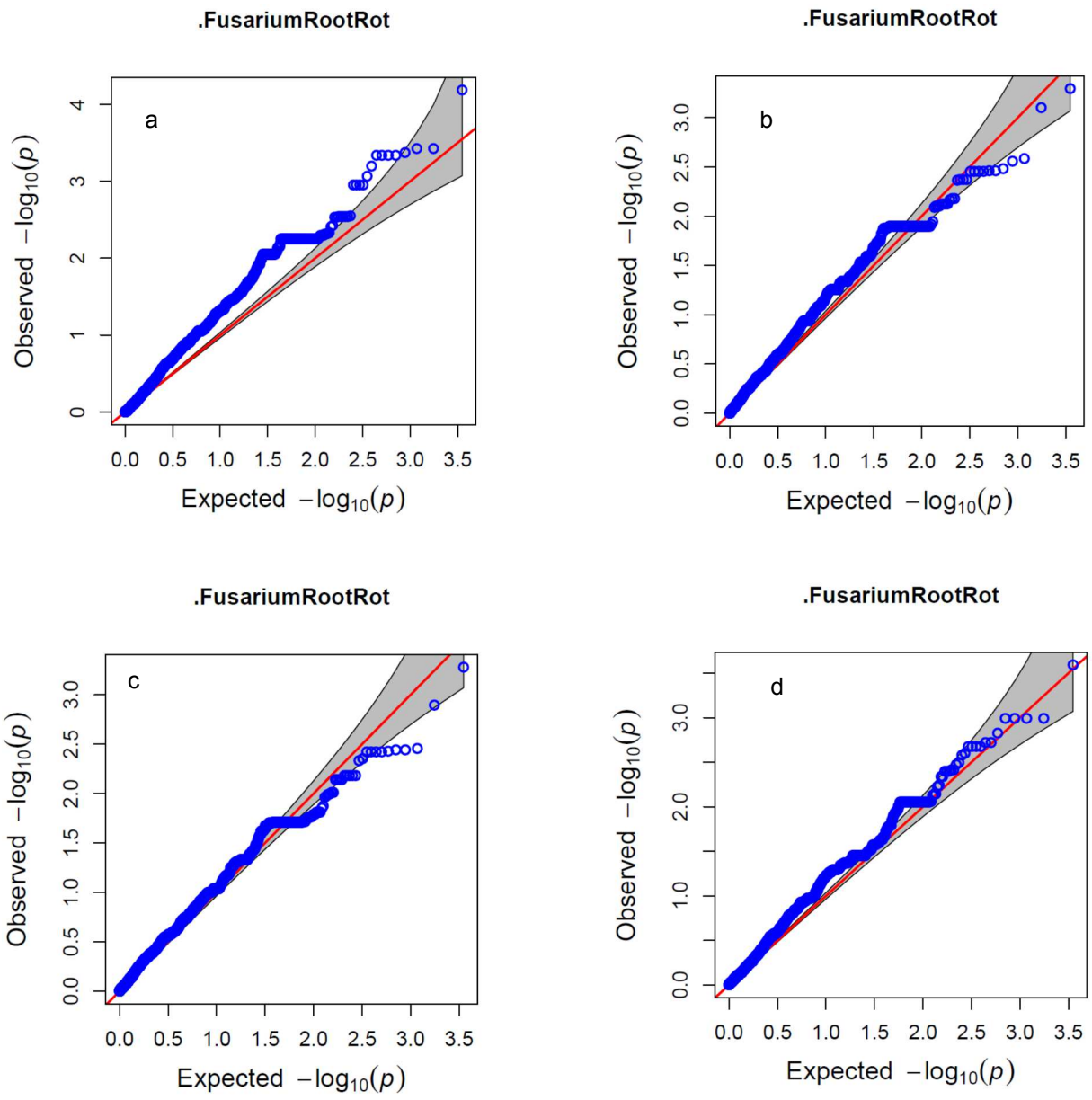

Figure 2. QQ-plots from 246 phenotypic data from Andean panel associated with 3525 SNP markers using FRR score: a) Naïve, b) Principal component analysis (PCA), c) Mixed model (MM=PCA+EMMA), d) Efficient mixed model analysis (EMMA).

Trait-marker associations

Significant associations were found for FRR, halo blight, days to flower, growth habit, and plant survival ($P \leq 0.001$) (Table 8). There were no significant associations for seed weight and seed yield. Manhattan plots were drawn from EMMA model to represent the chromosomal position of outstanding

markers. Plots were built using -log10 of transformed *P*-values on the Y axes against the physical positions of the SNPs on chromosome location on the X axes.

Table 8. Top three SNPs, chromosome, position and significant *P*-values (*P*≤0.001=-log10 (*P*) ≥3.0) for seven traits measured on 246 genotypes in the Andean diversity panel grown at Perham, MN, in 2013 and 2014.

Traits	SNP	Chromosome	Position Mb	-log10
Fusarium root rot (1-9)	m1545	4	3,3	3.6
	m2129	5	13,4	3.0
	m2172	5	17,9	3.0
Halo blight (1-9)	m2368	5	38,8	3.4
	m2372	5	38,9	3.2
	m2373	5	38,9	3.2
Days to flower (No.)	m373	1	48,3	6.2
	m333	1	43,6	3.6
	m19	1	3,0	2.8
Growth habit (determinate/indeterminate)	m333	1	43,6	3.8
	m1566	4	3,8	3.6
	m339	1	45,2	3.6
Plant survival (%)	m373	1	48,3	3.8
	m1701	4	19,2	3.0
	m1347	3	42,8	2.7
Seed weight (g)	m1939	5	1.0	2.7
	m333	1	43,6	2.7
	m4601	10	40,6	2.4
Seed yield (kg ha-1)	m1328	3	39,8	2.9
	m824	2	31,7	2.8
	m4544	10	38,4	2.7

Fusarium root rot

A clear peak on Pv04/3.3 Mb was associated with FRR (Table 8, Figure 3) in this study. Schneider et al. (2001) found markers associated with FRR on Pv02, Pv03; Roman-Aviles and Kelly (2005) on Pv02 and Pv05; Navarro et al. (2008) on Pv06 by using RAPDs; Kamfwa et al. (2013), using SSR markers, on Pv03; Hagerty et al. (2015), using SNP markers, on Pv03 and Pv07 and Bello et al. (2014) found significant marker associated with FRR on chromosome Pv09.

One SNP marker, within the genomic region, found on Pv04 was significantly associated with FRR in this study. However, caution should be taken before making definite conclusions. GWAS depends

on regression model, software used, population size, population structure, and cut-off *P*-value. Consequently, data should be validated before making recommendation. Besides, FRR has complex inheritance, and the pathogen interact with other soil-borne pathogens making more difficult to identify

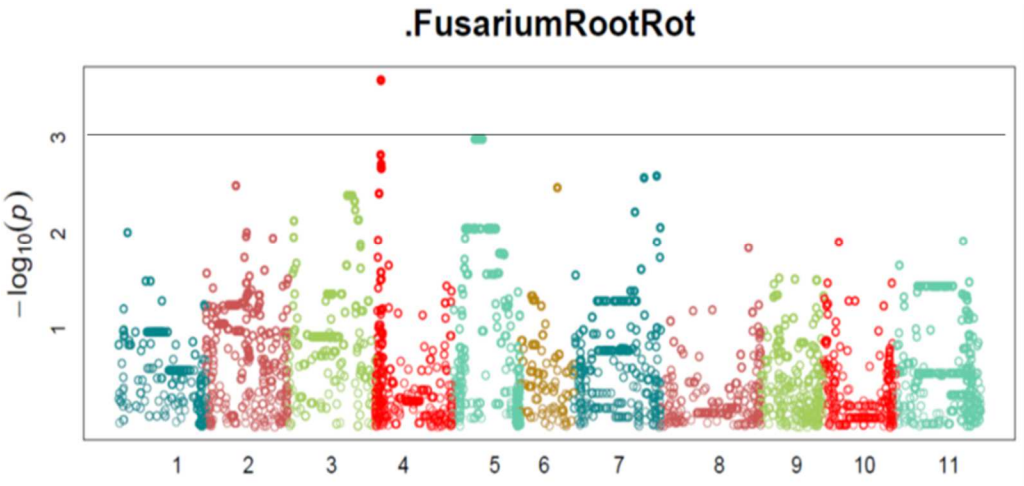

Figure 3. Manhattan plots drawn using EMMA model for Fusarium root rot. Different colors represent different chromosomes.

Halo blight

Halo blight Race 6 has been identified attacking common bean in MN/ND region in 2015 (K. Ghising, personal communication, 2016). One clear peak on Pv05/3.8 to 3.9 Mb was associated with halo blight resistance (Table 8, Figure 4). Ariyarathne et al. (1999), working with recombinant inbred lines derived from cross Neb-RR-1/A55 reported significant effect for halo blight resistance associated with one chromosomal region of Pv5 conferring resistance to two strains used. In other study, Robast et al. (2010) found one SSR marker on Pv04 closely linked to a major QTL involved in halo blight resistance. This marker was found in the 188 F_7-derived lines from a cross between Magister x Clovis and is being used in a marker assisted selection (MAS) programs. Unfortunately these authors did not report race specific resistance.

Evaluation with differential lines confirmed the monogenic inheritance of halo blight. The genes conditioning resistance to 1 to 9 Psp races are Pse-1, Pse-2, Pse-3, Pse-4, Pse5 (Singh and Schwartz, 2010). Genes Pse1, Pse2, Pse4, and Pse5 are located on Pv10 conditioning resistance to Races 1, 3, 4, 5, 7, 8, 9, whereas gene Pse3 on chromosome Pv02 conferring resistance to Races 2, 3, 4, 5, 7, 8 and 9

(Singh and Schwartz, 2010). A new gene, Pse-6, was reported by Miklas et al. (2014), working with 76 F9–derived lines from a cross Neb-RR-1/A55. The gene is located on Pv04 conditioning resistance to Races 1, 5, 7 and 9.

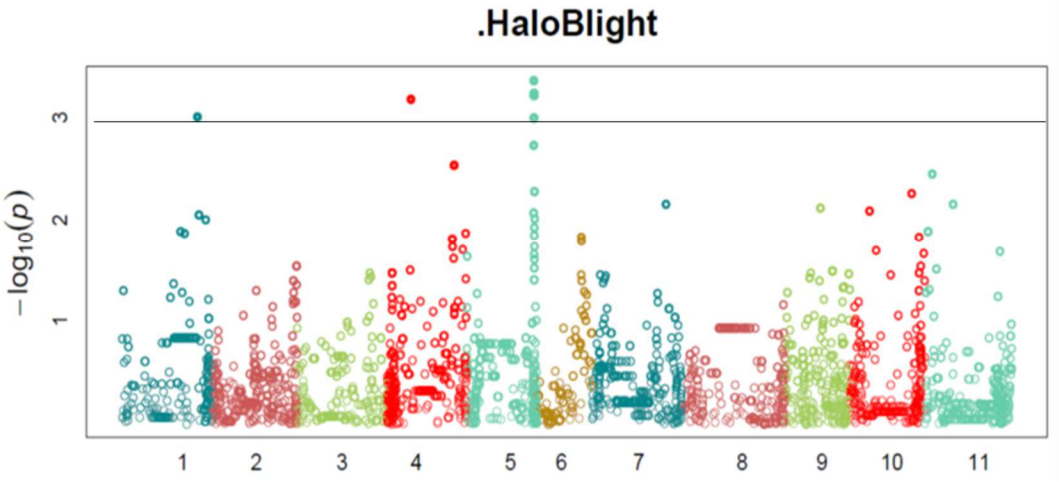

Figure 4. Manhattan plots drawn using EMMA model for halo blight. Different colors represent different chromosomes.

In other study, Duncan et al. (2014) found resistance to Race 6 on cultivar US14HBR6 but molecular characterization of the resistant gene and chromosome localization is not reported. However, Trabanco et al. (2014), working with 110 F_7-derived lines from the cross Xana\Cornell 49242 found one RAPD marker on Pv4 and one on Pv6, conferring tolerance to Race 6.

Major R genes are implicated in resistance to Psp, however, specific bean genotypes exhibit a quantitative mode of inheritance of resistance to Psp (Trabanco et al., 2014). Accordingly, Miklas and Fourie (2015) stated that none of the R genes condition resistance to the most prevalent Race 6 but some lines like CAL 143, PI150414, and GN #1 sel 27, have quantitative resistance to this race. The QTL for resistance to Race 6 in CAL 143 resides within a large R gene cluster toward the proximal end of Pv04. US14 pinto has resistance to Race 6 conferred by two independent recessive resistance genes.

The genomic regions found in this study on Pv05 and significant marker on Pv04 should be validated to assure that they are related to resistant factors located on these chromosomes conferring resistance to Race 6 before using as MAS in the breeding programs.

Days to flower

Two significant genomic regions were identified associated with days to flower on Pv01/43.7 Mb and Pv10148.3 Mb (Table 8, Figure 5). Kamfwa et al. (2015), working with 237 genotypes from Andean panel, found one SNP marker associated with days to flower on Pv01 using GWAS. Likewise, Moghaddam (2015), found one SNP marker (m32210) on Pv01 and one (m2535) on Pv03 associated with days to flower in 280 genotypes from the Mesoamerica diversity panel through GWAS. Consequently, this study confirmed the existence of genes on Pv01 determining the period from planting to flowering in the Andean panel. Genomic region on Pv1 also was associated with growth habit in this study.

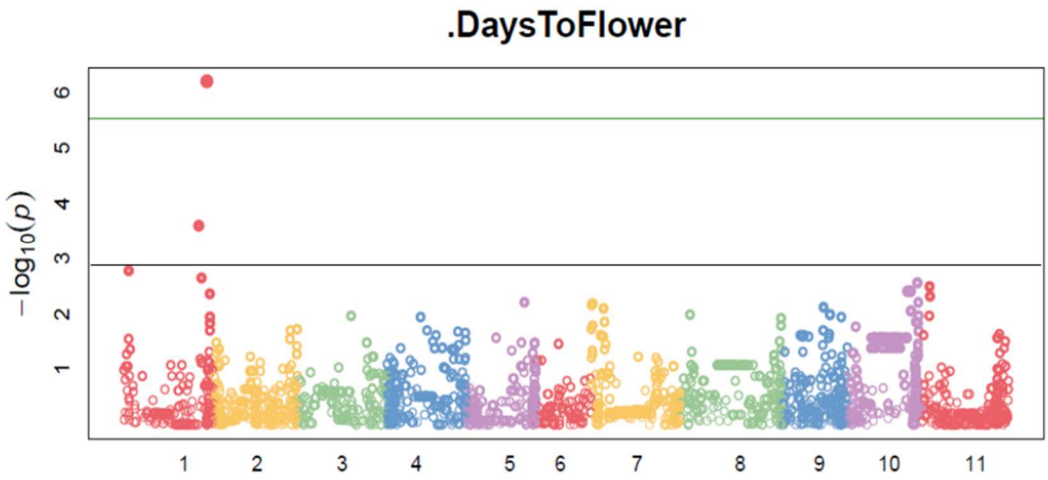

Figure 5. Manhattan plots drawn using EMMA model for days to flower. Different colors represent different chromosomes.

Growth habit

A region composed by significant markers on Pv01/45.2 Mb and Pv01/43.7 Mb was linked to determinacy growth habit (Table 8, Figure 6). A major signal on Pv01 was detected by Moghaddam (2015) working with 280 genotypes from Mesoamerica panel. Similarly, Cichy et al. (2015), working with 374 genotypes from Andean panel, found a significant region associated with determinacy on Pv01. Kwak et al. (2008) identified *Fin* locus for determinacy co-segregating with *TFL1* locus for terminal flower on Pv01. The genomic region on Pv01 associated with determinacy growth habit overlapped with genomic

region for days to flower. Kwak et al. (2008) stated that determinacy causes early flowering, thus selecting for one trait also the other trait is being selected, since they close linked.

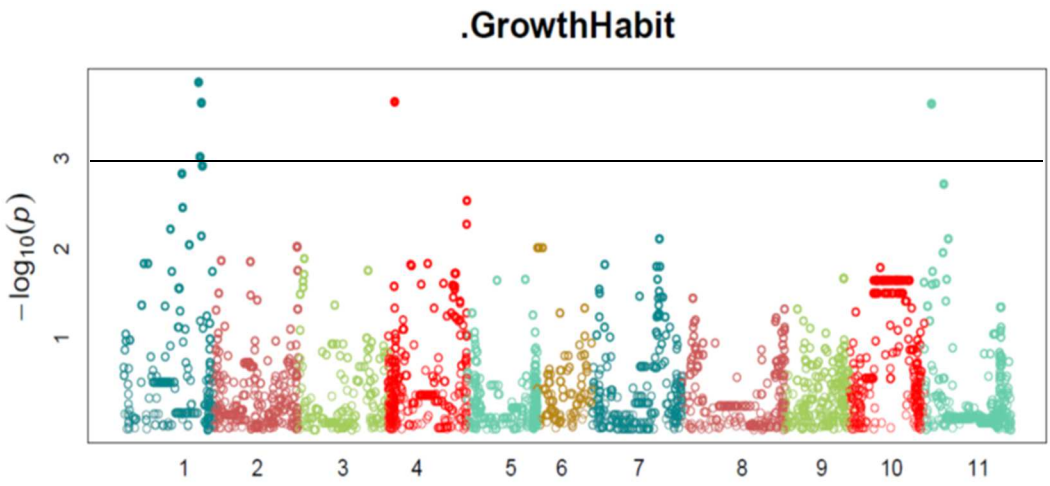

Figure 6. Manhattan plots drawn using EMMA model for growth habit. Different colors represent different chromosomes.

Plant survival

One marker on Pv01/48.3 Mb was the unique significant SNP marker associated with percentage of plant survival (Table 8, Figure 7). However, a genomic region on Pv04/19.2 Mb (Figure 3.5) was associated to plant survival. Since plant survival and FRR are close to each other, genes associated with both traits could be involved. Otherwise, plant survival has not been studied yet, thus It should be validated in further studies since it is an important trait correlated with seed yield.

Seed weight

Seed weight was not significantly associated with any SNP marker in this study (Table 8, Figure 8), probable due to low amount of small-seeded genotypes from Mesoamerican origin within the 246 Andean panel. However, Moghaddam (2015) confirmed three SNP markers on Pv07 by employing GWAS in 280 genotypes from Mesoamerica gene pool. Other major peaks residing on Pv010, Pv06, and Pv03 were found by the same author in the same Mesoamerica panel. High seed weight correlated with large seed size is important in societies than consume beans in physiological stage. This character is

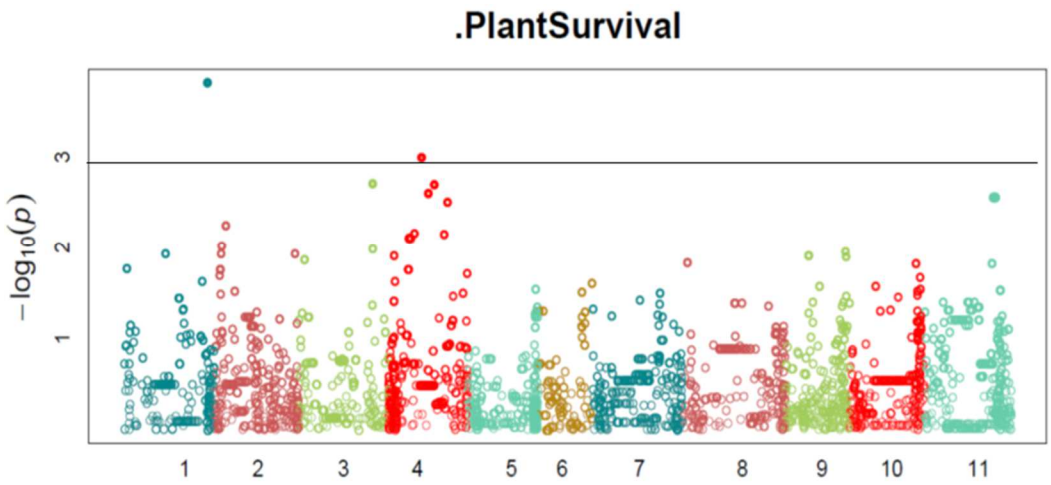

Figure 7. Manhattan plots drawn using EMMA model for percentage of plant survival. Different colors represent different chromosomes.

important in Nueva Granada race that invariably should be taken in account in bean breeding programs working for this type of seed market preferences.

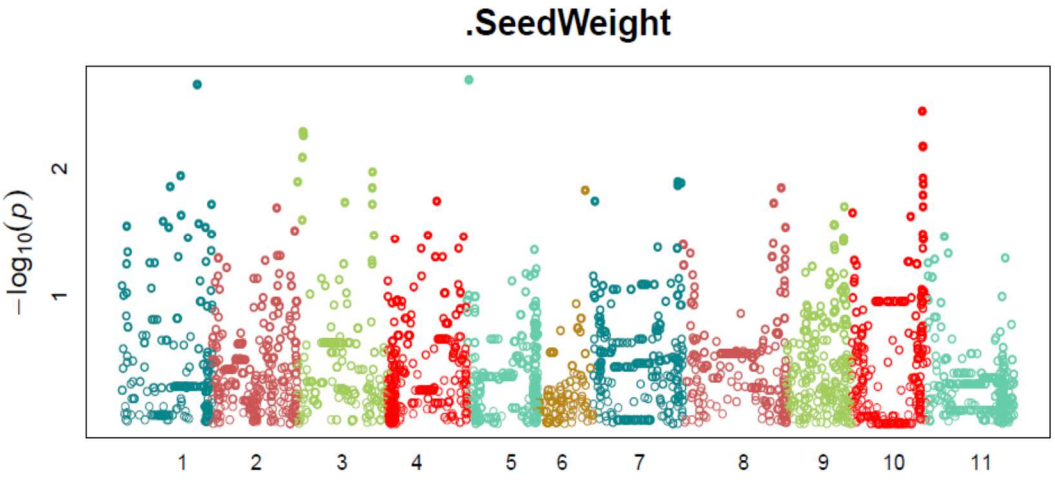

Figure 8. Manhattan plots drawn using EMMA model for 100-seed weight. Different colors represent different chromosomes.

Seed yield

Seed yield was not significantly associated with any SNP marker in this study (Table 8, Figure 9). However, Kamfwa et al. (2015) found SNP markers associated with seed yield on Pv03 and Pv09 through GWAS by employing 237 genotypes from the ADP. In other study, using Mesoamerican panel,

Moghaddam (2015) found significant genomic region on Pv03 and Pv06 associated with seed weight and seed yield. Linares-Ramirez (2013) working with 335 $F_{5.9}$ derived lines from a cross between Buster/Ser22 found a mayor QTL on Pv03. Since, a consistent genomic region affected seed weight and seed yield on Pv03, although not detected in this research, this region should be validated to use in bean breeding programs.

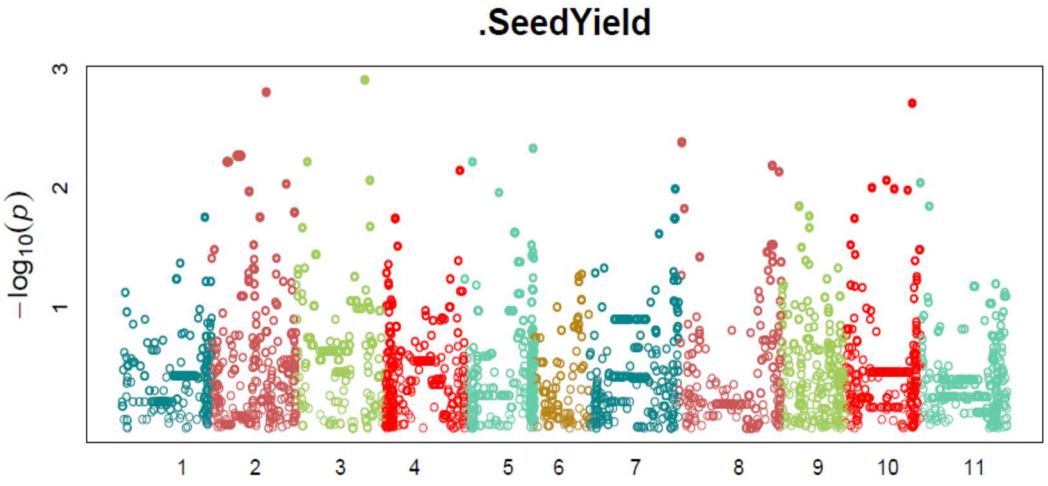

Figure 9. Manhattan plots drawn using EMMA model for seed yield. Different colors represent different chromosomes.

SUMMARY AND CONCLUSIONS

It is important to be cautious when interpreting GWAS data, peaks can change depending on population structure, environment, sample size, and evaluation criteria. GWAS analyses can produce both false positive and false negatives. False negatives might not only be due to the nature of regression analysis but also the significant cutoff value to control for experiment-wide error rate that is chosen. Repeatability, validation, unified phenotyping criteria, sample size, molecular techniques employed are key points before making conclusions about makers involved in or close to the genes associated with the trait of interest.

Fusarium root rot, halo blight, days to flower, determinacy growth habit, plant survival, seed weight are significant traits related to seed yield. Phenotyping under natural field conditions helped identifying resistant and susceptible genotypes to the prevalent diseases and characterize for valuable agronomic traits. Discovering the genetic architecture of these traits was done thought GWAS using a set of genotypes from Andean pool. GWAS takes advantage of the historic recombination that exist in the population to find trait-markers associations. The availability of whole genome sequence data in Andean panel helped to accomplish the genomic study. Marker-assisted selection has been proposed as a means of identifying markers linked to important traits that follow a quantitative inheritance. However, this utility will depend on how reliable trait-marker associations are for predicting the phenotype based on the genotype. Ideally, a genomic region or SNP marker should invariably express the trait without being be greatly affected by the environment. Up-to-date only major genes/markers have been used successfully in MAS breeding programs.

Fusarium root rot, caused by Fsp, along with halo blight, caused by Psp, were found to be the most significant biotic constraints in beans at Perham, MN, for three years. The genotypes VAX3 (check), ADP48-W6_6534, ADP624-Dolly, and ADP438-46_1 were resistant to both diseases. These genotypes can be used as parents in the bean breeding programs.

ADP676-CELRK, ADP242-G9013, ADP644-Foxfire, ADP648-Redkloud, ADP5-Kabuku, and ADP616-OAC_Lyric were the earliest days to flower genotypes with 38 days average, whereas ADP621-JaloEEP558 and ADP454-INIAP429 were the latest with 58 days. The earliest flowering group had determinate growth habit, the latest flowering group were indeterminate growth habit.

On plant survival ADP242-G9013, ADP172, ADP644-Foxfire, and ADP648-Redkloud presented the highest plant survival, whereas ADP514-Mantegaamarela, ADP269-G13092, ADP105-Sewani_97 and ADP646-Myasi presented the lowest percentage of plant survival.

For seed weight, ADP680-Clouseau, ADP649-Kamiakin, ADP616-OAC_Lyrick, and ADP624-Dolly presented the highest weight with 59 g average, whereas ADP172, ADP465-PI321094D, ADP48-W6_6534, and ADP93-Moro presented the lowest seed weight with 26 g average. Since this second group had small seed, most probably it belongs to Mesoamerican gene pool.

For seed yield, ADP624-Dolly, ADP649-Kamiakin, ADP172, ADP614-Rosie, ADP647-Redkanner, ADP75-Mabuku, ADP242-G9013, ADP454INIAP-429, ADP648-Redkloud, and ADP636-Montcalm had the highest seed yield with 1885 kg ha^{-1}, whereas ADP514-Mantegaamarela, ADP652-Lisa, ADP269-G13092, and ADP646-Myasi were the lowest seed yield genotypes with 560 kg ha^{-1}. From the top ten high-seed-yield genotypes, six are U.S inbreeded cultivars. ADP624-Dolly is cranberry seed type; ADP649-Kamiakin, ADP614-Rosie, ADP647-RedKanner, and ADP636-Montcalm are red kidney type.

The outstanding genotypes were ADP624-Dolly with resistance to FRR, high seed weight, and high seed yield; ADP649-Kamiakin with high seed weight and high seed yield; ADP648-Redkloud with early flowering, high plant survival and high seed yield; ADP172 with high plant survival and high seed yield; and ADP242-G9013 with early flowering, high plant survival and high seed yield, although susceptible to halo blight. Fusarium root rot and halo blight affected seed yield, whereas plant survival benefited.

GWAS provided significant markers and genomic regions associated with five out of seven traits in 246 Andean panel. After regression analysis, two genomic regions on Pv04 were linked to FRR and plant survival, one genomic region on Pv05 to halo blight, and two genomic regions on Pv01 linked to days to flower and growth habit. Genomic regions that were identified to be significantly associated with more than one trait should be validated before using in MAS. Most probably there are independent genes affecting each trait localized within the same DNA segment. Thus phenotyping cultivars and landraces, correlating to available annotated Andean panel though GWAS and estimating significant markers associated with traits of interest could help to select better parents to develop progenies in more efficient

way and in short time period. However, caution should be taken when the inheritance is polygenic such as in FRR.

Consequently, resistant genotypes can promptly be used as parents in bean breeding programs. However, markers conferring resistance to FRR and/or halo blight, the two prevalent disease in kidney beans in Minnesota, needs to be validated before using as molecular markers.

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APPENDIX

Table A1. Mean squares, F-tests, and percent coefficients of variation (CV%) from the analyses of variance of six agronomic traits measured on 310, 302, and 280 genotypes grown at Perham, MN, in 2013.

SOV	df	Fusarium root rot 1-9	Halo blight 1-9	df	Days to flower No.	df	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
Rep	1	0.4	19.9**	1	25.6	1	2762**	259**	262026**
Blk(rep)	18	2.8	13.2**	18	9.2	18	262**	23**	13813218**
Genotype	309	2.0	3.7**	301	129.9**	279	152**	164**	1966887**
Error	291	1.7	1.5	283	8.2	254	54	11	877010
CV%		36.3	35.6		6.0		25	8	36

Table A2. Mean squares, F-tests, and percent coefficients of variation (CV%) from the analyses of variance of six agronomic traits measured on 144 early genotypes grown at Perham, MN, in 2014.

SOV	df	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
Rep	1	9.8**	0.5	7.4	986**	13**	77061
Blk(rep)	22	1.4	1.6	2.1	240**	16*	211347**
Genotype	143	3.1**	5.2**	21.6**	418**	119**	411055**
Error	121	2.1	1.1	2.0	134	9	108929
CV%		28.6	16.8	3.4	17	7	34

Table A3. Mean squares, F-tests, and percent coefficients of variation (CV%) from the analyses of variance of six agronomic traits measured on 121 late genotypes grown at Perham, MN, in 2014.

SOV	df	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
Rep	1	3.0	9.1**	0.0	458*	6	1359600**
Blk(rep)	20	2.0	1.1	3.2	249**	22**	726418**
Genotype	121	4.9	4.1**	11.7**	242**	81**	473534**
Error	100	3.9	0.9	1.9	86	5	117292
CV%		36.3	19.0	2.8	17	6	31

Table A4. Mean squares, F-tests, and percent coefficients of variation (CV%) from the analyses of variance of six agronomic traits measured on 49 early genotypes grown at Perham, MN, in 2015.

SOV	df	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
Rep	1	0.5	0.8	10.5	420	57**	851512**
Blk(rep)	12	1.7	1.1	4.1	156	6	200433*
Genotype	48	5.2**	9.5**	12.0**	180	104**	318000**
Error	36	1.9	0.9	2.7	142	4	96220
CV%		24.1	26.0	3.8	20	5	25

Table A5. Mean squares, F-tests, and percent coefficients of variation (CV%) from the analyses of variance of six agronomic traits measured on 49 late genotypes grown at Perham, MN, in 2015.

SOV	df	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
Rep	1	0.7	0.1	34.2**	22	0	330020**
Blk(rep)	12	4.2*	1.6**	5.2	248**	7	145392**
Genotype	48	4.0*	6.4**	25.5**	148**	89**	276136**
Error	36	1.8	0.6	2.8	50	4	30509
CV%		22.8	28.8	3.4	12	6	21

Table A6. Mean squares, F-tests, and percent coefficients of variation (CV%) from the combined analyses of variance of six agronomic traits measured on 92 common genotypes grown at Perham, MN, from 2013 to 2015.

SOV	df	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha-1
Year	2	121.1**	144.5**	34.9**	34308**	2996**	4676428**
Genotype	91	2.7**	6.9**	63.1**	183**	228**	492954**
Error	182	1.6	1.3	4.2	120	15	166499
CV%		26.4	28.8	4.5	21	9	34

Table A7. Mean squares, F-tests, and percent coefficients of variation (CV%) from the combined analyses of variance of six agronomic traits measured on 246 common genotypes grown at Perham, MN, in 2013 and 2014.

SOV	df	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
Year	1	241.9**	447.1**	98.4**	13.2.9**	973.3**	25012009**
Genotypes	245	1.7**	4.2**	52.5**	161.7	154.9**	369007**
Error	245	1.2	1.2	3.8	133.2	17.5	268951.0
CV%		25.8	24.3	4.3	24.7	9.8	41.7

Table A8. LSmeans for six traits measured on 310 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013.

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-ssed weight g	Seed yield kg ha^{-1}
1	ADP1ROZI_KOKO	4	3	47	34	40	632
2	ADP2W6_16444	5	3	41	30	53	947
3	ADP3KIDUNGU	5	3	39	8	47	847
4	ADP4KILOMBERO	4	7	48	34	37	289
5	ADP5KABUKU	3	5	38	19	46	1587
6	ADP6W6_16465	4	3	43	34	54	1564
7	ADP7BUKOBA	3	3	39	21	43	1038
8	ADP8Nyayo	3	3	73	.	.	.
9	ADP9Maalasa	4	3	71	.	.	.
10	ADP10CANADA	3	6	42	21	57	1024
11	ADP11KIBOROLONI	5	6	39	37	45	2053
12	ADP12W6_16489	5	4	43	26	52	1257
13	ADP13KIBUMBULA	4	6	53	32	32	141
14	ADP14KIANGWE	3	4	49	38	44	1346
15	ADP15W6_16495	4	4	44	36	47	1148
16	ADP16GOLOLI	3	5	38	27	47	2117
17	ADP17W6_16529	2	5	44	37	54	1850
18	ADP18SODAN	3	4	46	35	48	1652
19	ADP19KASUKANYWELE	4	7	41	25	50	699
20	ADP20KIGOMA	3	7	38	36	51	2491
21	ADP21MBULAMTWE	4	5	40	17	48	417
22	ADP22KISAPURI	4	6	39	31	44	2043
23	ADP23MSHORONYLONI	6	3	40	43	43	2499
24	ADP24YELLOW	3	2	48	34	45	619
25	ADP25RUHONDELA	5	4	42	46	34	1658
26	ADP26Black_Wonder	4	6	38	38	46	1901
27	ADP27Incomparable	3	3	46	27	44	1380
28	ADP28Sisi	4	6	37	33	48	2020
29	ADP29RH2	4	3	52	39	44	1480
30	ADP30RH6	5	3	41	45	33	1033
31	ADP31RH11	4	4	45	27	41	619
32	ADP32RH21	3	3	46	27	45	1574
33	ADP33KIJIVU	6	3	41	23	53	1463
34	ADP34KIJIVU	3	2	42	33	52	1525
35	ADP35Kokola	3	3	69	.	.	.
36	ADP36Lyamungu85	3	2	69	.	.	.
37	ADP37W6_16488	3	5	54	36	42	947
38	ADP38Moono	4	4	44	17	60	652

Table A8. LSmeans for six traits measured on 310 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-ssed weight g	Seed yield kg ha^{-1}
39	ADP39RoziKoko	3	2	47	40	42	969
40	ADP40KATWELA	1	3	48	36	23	1075
41	ADP41MRONDO	3	2	54	42	34	1487
42	ADP42MKOKOLA	2	1	52	32	33	813
43	ADP43Bwana_shamba	4	4	45	31	40	1209
44	ADP44KIJIVU	4	3	48	37	44	1659
45	ADP45RH12	4	2	49	37	41	2064
46	ADP46RH4	5	2	50	38	42	911
47	ADP47MSOLINI	5	2	40	31	56	2493
48	ADP48W6_6534	2	2	50	38	29	797
49	ADP49W6_16546	3	4	48	28	45	947
50	ADP50SALUNDE	5	2	54	29	40	1087
51	ADP51RH3	4	3	51	30	39	1428
52	ADP52RH9	3	2	52	29	35	1864
53	ADP53Maharage_makubwa	4	3	56	33	41	784
54	ADP54W6_16447	5	2	50	21	37	1026
55	ADP55KABUKU	2	2	48	41	37	1925
56	ADP56SOYA	5	2	45	31	39	2448
57	ADP57KIJIVU	3	3	52	31	44	1126
58	ADP58CANADA	4	3	54	39	37	1264
59	ADP59Poto	3	2	51	25	38	1340
60	ADP60CANADA	6	2	62	38	32	784
61	ADP61Maulasi	4	2	52	35	36	1608
62	ADP62MAULASI	4	2	46	42	39	2736
63	ADP63Soya	3	3	51	33	39	1481
64	ADP64W6_16500	3	3	57	31	29	1107
65	ADP65W6_16501	4	3	46	31	43	2541
66	ADP66NJANO	3	5	54	30	33	1099
67	ADP67NJANO	4	4	43	30	36	1272
68	ADP68Soya	3	4	48	38	37	2013
69	ADP69SOYA	4	2	51	39	41	1391
70	ADP70Msafiri	3	4	53	35	31	647
71	ADP71NJANO_DOLEA	5	1	53	39	39	1530
72	ADP72MASUSU	4	2	45	22	41	1051
73	ADP73MASUSU	5	3	41	37	55	2426
74	ADP74KABLANKETI	3	2	47	35	33	1648
75	ADP75MABUKU	3	2	39	33	52	2741
76	ADP76KABLANKETI	3	2	49	31	36	1484
77	ADP78W6_16535	4	2	54	34	34	697
78	ADP79LUNGEMBA	3	2	56	37	31	735

Table A8. LSmeans for six traits measured on 310 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-ssed weight g	Seed yield kg ha^{-1}
79	ADP80KABLANKETI	3	3	48	30	33	2016
80	ADP81KABLANKETI	3	2	51	22	37	1173
81	ADP82KABLANKETI	5	3	51	32	37	714
82	ADP83W6_16547	4	2	56	21	45	777
83	ADP84Kablanketi_ndefu	3	1	52	39	29	1366
84	ADP85KABLANKETI	4	3	46	33	31	1095
85	ADP86Nyamhonga_mwekundu	3	2	52	33	40	809
86	ADP87KABLANKETI	3	3	49	18	37	741
87	ADP88KABLANKETI	5	1	50	27	38	1548
88	ADP89KABLANKETI	2	2	50	32	37	1122
89	ADP90Kasukanywele	3	2	44	22	59	767
90	ADP91W6_16560	3	3	53	48	21	650
91	ADP92MORO	3	3	46	33	29	548
92	ADP93MORO	2	3	51	28	26	595
93	ADP94LUSHALA	3	2	51	35	31	906
94	ADP95CANADA	3	3	45	17	60	1251
95	ADP96Rojo	3	4	43	36	38	1077
96	ADP97Bilfa4	2	4	45	42	34	3135
97	ADP98Selian97	3	4	52	20	43	420
98	ADP99BwanaShamba	3	3	45	30	54	1344
99	ADP100EG21	3	3	41	31	29	1223
100	ADP101Witrood	3	3	43	15	38	357
101	ADP102Jesca	3	3	41	27	50	1730
102	ADP103Pesa	4	4	42	31	36	1299
103	ADP105Sewani_97	4	5	62	17	35	598
104	ADP106Zawadi	4	5	36	40	36	2616
105	ADP107Mishindi	3	5	40	37	32	1059
106	ADP108Njano	5	2	44	40	35	1921
107	ADP109Kablanketi	4	2	49	31	39	1572
108	ADP110SUG131	5	2	60	35	40	1309
109	ADP111Uyole98	3	2	41	18	44	2108
110	ADP112Uyole96	5	3	43	23	49	1862
111	ADP113OPSRS4	4	3	52	36	40	755
112	ADP114OPS_RS1	4	2	49	38	45	2018
113	ADP115Bonus	5	2	59	35	33	1154
114	ADP116A800	4	2	45	30	35	3338
115	ADP117A483	2	2	57	40	35	1676
116	ADP118Werna	3	2	49	33	37	1781
117	ADP119A193	5	3	67	35	38	896
118	ADP120Tygerberg	4	2	62	30	33	1019

Table A8. LSmeans for six traits measured on 310 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-ssed weight g	Seed yield kg ha^{-1}
119	ADP121KranskopHR1	3	2	54	35	32	718
120	ADP122Kranskop	3	2	52	30	41	1350
121	ADP123Jenny	4	4	53	.	.	.
122	ADP124Maini	3	3	62	19	27	714
123	ADP126SELIAN_05	4	3	.	.	.	.
124	ADP127SELIAN_06	5	3	.	.	.	.
125	ADP166NABE4	3	2	72	.	.	.
126	ADP168Kanyebwa	3	3	40	28	45	2065
127	ADP172	3	3	42	45	28	2166
128	ADP183G994	4	3	60	33	53	907
129	ADP186G1368	4	3	60	12	36	164
130	ADP192G2377	5	1	.	.	.	.
131	ADP199G3452	5	2	.	.	.	.
132	ADP204G4474	4	2	.	.	.	.
133	ADP205G4494	6	3	51	34	48	470
134	ADP207G4564	2	4	48	33	52	1410
135	ADP211G4780	5	3	72	.	.	.
136	ADP212G4970	3	4	47	29	42	632
137	ADP213G5034	5	5	44	27	36	541
138	ADP214G5087	3	2	69	29	34	951
139	ADP225G6415	3	2	43	30	66	1568
140	ADP232G7930	6	4	48	10	44	93
141	ADP238G8897	5	1	.	.	.	.
142	ADP242G9013	4	5	39	50	58	3063
143	ADP247G9975	2	3	49	12	47	631
144	ADP255G10994	6	1	53	.	.	.
145	ADP269G13092	3	5	46	35	50	578
146	ADP276G13654	3	2	.	.	.	.
147	ADP277G13778	4	2	43	42	43	1545
148	ADP303G17913	3	5	43	46	64	2424
149	ADP310G18356	4	6	36	32	59	2102
150	ADP324G20729	4	2	45	24	49	742
151	ADP337G21303	5	2	49	28	51	1263
152	ADP346G22246	5	2	57	32	42	1712
153	ADP351G22420	4	2	40	45	27	2105
154	ADP355G22513	5	4	47	24	42	2058
155	ADP367G23086	2	3	60	18	38	340
156	ADP368G23093	3	2	68	18	37	799
157	ADP376PI189408	2	6	44	18	52	505
158	ADP379PI203934	4	1	.	.	.	.

Table A8. LSmeans for six traits measured on 310 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-ssed weight g	Seed yield kg ha^{-1}
159	ADP383PI209486	3	4	54	34	31	788
160	ADP390PI307808	3	6	50	30	40	472
161	ADP391PI308894	3	6	44	31	49	1154
162	ADP392PI309701	2	2	48	19	43	1056
163	ADP417PI451906	3	5	44	19	54	931
164	ADP427Badillo	4	3	51	37	44	1554
165	ADP428ColoradodelPais	3	2	39	43	37	2810
166	ADP429PR9920_171	3	2	47	43	41	2657
167	ADP430PR1013_3	3	2	53	26	41	2059
168	ADP431Gurabo5	4	5	39	42	31	2474
169	ADP432PR0637_134	3	3	70	37	29	537
170	ADP433PR9745_232	2	2	44	36	34	1638
171	ADP434PR0737_1	2	2	60	8	31	82
172	ADP435RM_05_07	3	1	42	30	36	1468
173	ADP436JB178	4	3	67	30	39	268
174	ADP437PC50	3	2	47	33	40	918
175	ADP43846_1	4	4	41	33	31	2135
176	ADP439754_3	3	2	50	.	.	.
177	ADP44049_2	3	3	43	34	26	675
178	ADP44191_1	2	3	51	45	24	896
179	ADP443Vazon7	3	5	41	36	31	1955
180	ADP444HondoValle25	3	4	49	12	27	544
181	ADP445Chijar	5	4	45	19	25	2065
182	ADP446Raz25	3	3	53	28	34	651
183	ADP447INIAP414	4	4	72	28	49	361
184	ADP449INIAP420	2	2	63	.	.	.
185	ADP450INIAP422	5	2	74	.	.	.
186	ADP451INIAP424	3	4	72	.	.	.
187	ADP452INIAP425	3	6	62	.	.	.
188	ADP453INIAP428	3	2	66	.	.	.
189	ADP454INIAP429	2	2	64	37	36	2178
190	ADP455INIAP430	2	5	73	.	.	.
191	ADP456INIAP480	3	3	73	.	.	.
192	ADP457INIAP481	3	4	68	45	35	1576
193	ADP458INIAP483	3	5	71	.	.	.
194	ADP460PI331356B	4	5	47	34	40	1355
195	ADP461PI527540A	2	2	42	.	.	.
196	ADP462PI527540B	2	3	45	36	28	1019
197	ADP464PI353534B	2	4	41	37	32	607
198	ADP465PI321094D	4	5	47	30	28	1387

Table A8. LSmeans for six traits measured on 310 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-ssed weight g	Seed yield kg ha^{-1}
199	ADP467PI209808	5	5	40	36	49	1751
200	ADP468PI527538	3	4	41	32	46	1631
201	ADP470PI527508	4	6	41	36	40	1862
202	ADP471PI527537C	3	3	42	25	39	1237
203	ADP472PI527537B	3	3	51	.	.	.
204	ADP474PI527519	4	5	47	22	30	1342
205	ADP475PI319706	3	4	41	40	41	1319
206	ADP476Heirloom	3	3	43	19	38	1270
207	ADP477PI527512	3	3	43	45	39	1408
208	ADP478PI353536	4	4	39	27	44	806
209	ADP481PI449428	3	4	46	35	47	687
210	ADP483PI209815	4	2	46	29	36	1246
211	ADP508Calembe	3	3	65	25	28	541
212	ADP509Fernando	2	5	46	31	38	531
213	ADP510Ohliodeperdiz	3	2	68	39	35	703
214	ADP511Canario	6	2	55	16	31	838
215	ADP513Canario	4	3	53	13	28	648
216	ADP514MantegaAmarela	3	3	55	13	29	873
217	ADP515KatarinaKibala	4	5	44	35	36	627
218	ADP516MantegaKibala	3	3	48	17	37	363
219	ADP517CariocaKibala	2	4	48	39	26	2235
220	ADP518MantegablancaKibala	3	4	52	12	36	174
221	ADP519KatarinaCela	4	4	39	13	34	771
222	ADP520ChumboCela	3	1	65	.	.	.
223	ADP521CeboCela	3	2	58	.	.	.
224	ADP522AmareloCela	3	1	69	.	.	.
225	ADP523CanarioCela	6	2	55	16	33	843
226	ADP598Charlevoix	3	6	43	32	55	1208
227	ADP600K07921	6	4	45	26	51	735
228	ADP601Camelot	4	4	43	15	55	879
229	ADP602Sacramento	4	5	37	41	58	2430
230	ADP603Wallace773_V98	3	6	40	29	48	2139
231	ADP6041062_V98	4	5	39	33	55	1549
232	ADP6051132_V96	3	2	44	8	55	902
233	ADP607NY105	3	4	39	26	62	1537
234	ADP608UI_51	3	3	40	13	60	733
235	ADP610G122	4	5	43	36	38	944
236	ADP611PompadourB	3	6	45	26	38	941
237	ADP612ICAQuimbaya	4	6	44	26	48	1254
238	ADP61302_385_14	7	6	40	34	52	1616

Table A8. LSmeans for six traits measured on 310 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-ssed weight g	Seed yield kg ha^{-1}
239	ADP614Rosie	5	3	43	31	50	2193
240	ADP615Litekid	3	4	43	24	46	1239
241	ADP616OAC_Lyrick	6	6	38	16	68	913
242	ADP617RedRider	2	4	43	31	56	3109
243	ADP618AC_Elk	2	5	39	13	56	1229
244	ADP619UCD0906	3	6	48	29	52	1295
245	ADP620UCD0405	4	7	40	31	51	2623
246	ADP621JaloEEP558	4	2	62	40	29	557
247	ADP622UCD0701	4	5	40	31	58	2381
248	ADP623Drake	5	7	41	37	52	1873
249	ADP624Dolly	3	2	42	24	61	2920
250	ADP625Micran	3	2	48	13	47	1937
251	ADP626Badillo	6	2	51	29	43	1261
252	ADP627H9659_21_1	5	3	49	14	48	816
253	ADP628H9659_27_7	3	3	46	23	50	1673
254	ADP629H9659_27_10	6	2	47	34	48	1824
255	ADP630H9659_23_1	4	3	45	20	45	1578
256	ADP631OAC_Inferno	3	3	46	28	47	1372
257	ADP633TARS_HT2	5	4	45	27	53	1785
258	ADP634UC_RedKidney	4	7	46	27	47	740
259	ADP636Montcalm	7	4	41	29	57	2228
260	ADP637Isabella	5	6	38	38	55	2080
261	ADP638RedHawk	3	6	41	50	52	1853
262	ADP639Chinook2000	4	6	43	36	53	2024
263	ADP640Beluga	2	6	42	30	47	1477
264	ADP641Capri	5	4	39	25	63	1654
265	ADP642TaylorHort	4	3	44	16	50	1155
266	ADP643Cardinal	4	3	39	20	63	1971
267	ADP644FoxFire	4	1	38	46	56	2932
268	ADP646Myasi	4	5	43	8	39	521
269	ADP647RedKanner	5	2	42	34	53	2645
270	ADP648RedKloud	4	6	38	54	55	2494
271	ADP649Kamiakin	3	3	44	34	65	3037
272	ADP650K42	3	5	46	36	46	1536
273	ADP651K59	2	4	46	31	58	1795
274	ADP652Lisa	3	5	46	33	49	588
275	ADP653USDK_CBB_15	4	4	40	41	51	2670
276	ADP654USDK4	5	4	43	35	57	2583
277	ADP655Fiero	3	6	43	33	61	2680
278	ADP656RoyalRed	4	6	44	37	49	1674

Table A8. LSmeans for six traits measured on 310 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-ssed weight g	Seed yield kg ha^{-1}
279	ADP657Kardinal	4	7	46	36	39	905
280	ADP658Blush	3	3	45	34	57	2138
281	ADP659USLK1	4	5	38	38	64	2651
282	ADP660Krimson	2	4	38	24	63	2256
283	ADP661USCR7	2	5	39	16	55	1499
284	ADP662USCR9	3	6	38	39	56	2085
285	ADP663USCR_CBB_20	3	4	38	32	50	2229
286	ADP664SilverCloud	4	6	43	32	64	1569
287	ADP665USWK_CBB17	4	2	40	29	49	1918
288	ADP666USWK6	3	5	44	17	62	1331
289	ADP667VA19	3	4	43	28	50	1810
290	ADP670AC_Calmont	3	3	44	26	58	1540
291	ADP672CDRK	2	6	45	30	55	1752
292	ADP673UC_Nichols	4	5	44	29	50	1366
293	ADP674UCD0704	4	5	46	26	40	594
294	ADP675UCD0801	3	4	48	24	49	1267
295	ADP676CELRK	4	4	37	21	62	1388
296	ADP677Etna	3	4	39	23	61	1738
297	ADP678Hooter	3	3	44	14	61	1502
298	ADP679RedRover	5	7	45	24	57	1017
299	ADP680Clouseau	4	4	40	17	68	1638
300	ADP681Belagio	7	1	46	9	52	909
301	ADP683IJR	3	2	48	38	39	1771
302	ADP684Majesty	5	4	47	19	63	1429
303	ADP685Chianti	4	2	45	13	63	1372
304	ADP686UCD707	3	4	46	15	47	872
305	ADP687PinkPanther	3	6	38	43	50	3037
306	VAX3	2	1	46	43	29	2081
307	GTS104	5	4	43	19	55	1415
308	Talon	4	4	43	22	51	1829
309	Cabernet	3	5	41	34	59	2469
310	Dynasty	4	2	42	19	62	1787
	LSD	ns	2	6	14	7	1021

Table A9. LSmeans for six traits measured on 144 early flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014.

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
1	ADP2W6_16444	5	4	41	83	48	1650
2	ADP3KIDUNGU	5	7	36	96	41	1383
3	ADP5KABUKU	5	7	37	87	42	1315
4	ADP6W6_16465	5	5	45	55	52	1530
5	ADP7BUKOBA	3	5	39	80	35	2005
6	ADP10CANADA	4	6	40	57	49	1025
7	ADP11KIBOROLONI	5	9	37	96	40	1083
8	ADP12W6_16489	4	6	44	55	53	1580
9	ADP15W6_16495	3	7	46	57	45	1302
10	ADP16GOLOLI	5	8	36	82	40	1331
11	ADP17W6_16529	5	5	44	62	50	1381
12	ADP19KASUKANYWELE	5	5	43	53	52	814
13	ADP20KIGOMA	5	8	38	58	35	267
14	ADP22KISAPURI	5	7	36	83	38	898
15	ADP23MSHORONYLONI	5	6	38	74	35	894
16	ADP25RUHONDELA	6	4	45	66	35	756
17	ADP26Black_Wonder	6	9	39	92	32	468
18	ADP28Sisi	5	8	37	82	37	1207
19	ADP30RH6	5	6	40	51	32	724
20	ADP31RH11	5	6	46	57	39	802
21	ADP33KIJIVU	4	5	41	71	47	953
22	ADP34KIJIVU	5	5	42	73	47	1133
23	ADP38Moono	5	6	46	57	53	811
24	ADP43BWANA_SHAMBA	4	3	48	74	39	1670
25	ADP47MSOLINI	5	6	37	88	49	1120
26	ADP56SOYA	5	5	41	74	36	907
27	ADP67NJANO	6	4	44	56	34	588
28	ADP72MASUSU	5	5	38	49	43	681
29	ADP73MASUSU	7	6	36	81	46	879
30	ADP75MABUKU	3	6	37	89	45	1102
31	ADP90KASUKANYWELE	5	5	42	45	57	728
32	ADP95CANADA	8	5	41	47	60	588
33	ADP96Rojo	6	4	44	73	45	1616
34	ADP99BwanaShamba	6	5	45	56	50	951
35	ADP100EG21	4	4	44	70	35	1311
36	ADP102Jesca	7	5	41	73	44	1377
37	ADP103Pesa	6	5	44	56	47	968
38	ADP106Zawadi	5	7	37	81	30	582
39	ADP107Mishindi	7	4	45	67	31	815

Table A9. LSmeans for six traits measured on 144 early flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
40	ADP108Njano	6	4	47	60	38	1065
41	ADP111Uyole98	8	5	41	57	34	552
42	ADP112Uyole96	4	4	46	51	46	1338
43	ADP116A800	3	3	42	87	37	2346
44	ADP168KANYEBWA	5	5	38	69	46	877
45	ADP172	4	6	40	87	25	1768
46	ADP213G5034	6	4	44	52	34	398
47	ADP225G6415	7	5	39	80	56	1748
48	ADP242G9013	5	9	37	98	50	1116
49	ADP277G13778	5	7	44	61	37	795
50	ADP303G17913	6	6	40	92	52	894
51	ADP310G18356	7	7	42	56	42	166
52	ADP324G20729	6	5	45	69	55	1352
53	ADP351G22420	3	5	40	86	24	1231
54	ADP376PI189408	4	9	43	43	40	366
55	ADP391PI308894	4	8	46	63	45	554
56	ADP417PI451906	6	7	42	57	39	476
57	ADP428ColoradodelPais	7	8	37	92	28	1002
58	ADP431Gurabo5	4	7	37	80	22	683
59	ADP433PR9745_232	4	5	45	96	30	811
60	ADP435RM_05_07	5	7	39	85	29	638
61	ADP43846_1	4	5	42	94	31	1384
62	ADP44049_2	5	7	44	91	24	1045
63	ADP443Vazon7	5	7	39	75	28	495
64	ADP445Chijar	5	5	48	70	27	1774
65	ADP462PI527540B	3	5	45	74	32	1936
66	ADP464PI353534B	4	4	43	57	34	682
67	ADP467PI209808	4	6	42	78	43	1220
68	ADP468PI527538	6	5	42	76	44	887
69	ADP470PI527508	4	7	40	84	37	1124
70	ADP471PI527537C	7	8	39	69	34	485
71	ADP475PI319706	5	6	40	69	36	486
72	ADP476Heirloom	3	6	42	80	34	1084
73	ADP477PI527512	4	4	45	76	44	1434
74	ADP478PI353536	5	7	37	58	38	591
75	ADP515KatarinaKibala	5	4	45	57	38	983
76	ADP519KatarinaCela	5	7	37	62	29	480
77	ADP598Charlevoix	6	9	45	56	49	470
78	ADP600K07921	7	8	44	50	48	697
79	ADP601Camelot	8	9	41	58	45	626

Table A9. LSmeans for six traits measured on 144 early flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
80	ADP602Sacramento	6	9	36	73	48	605
81	ADP603Wallace773_V98	4	9	38	75	38	333
82	ADP6041062_V98	4	9	38	48	42	189
83	ADP6051132_V96	6	6	43	83	57	1262
84	ADP607NY105	7	9	38	54	45	139
85	ADP608UI_51	4	6	38	83	54	1156
86	ADP610G122	4	5	45	69	35	713
87	ADP611PompadourB	7	8	46	47	36	329
88	ADP612ICAQuimbaya	6	5	47	48	48	677
89	ADP61302_385_14	7	7	40	57	41	498
90	ADP614Rosie	4	3	42	79	54	2075
91	ADP615Litekid	6	5	42	89	46	1842
92	ADP616OAC_Lyrick	5	8	36	96	52	801
93	ADP617RedRider	7	7	44	68	49	892
94	ADP618AC_Elk	6	8	36	59	51	733
95	ADP620UCD0405	5	8	37	82	48	921
96	ADP622UCD0701	7	8	40	45	47	624
97	ADP623Drake	5	9	41	57	46	596
98	ADP624Dolly	3	4	42	60	61	1661
99	ADP630H9659_23_1	3	5	47	91	38	976
100	ADP633TARS_HT2	8	4	46	74	49	1074
101	ADP637Isabella	5	8	37	82	42	490
102	ADP638RedHawk	7	7	41	65	46	486
103	ADP639Chinook2000	6	5	42	74	48	1389
104	ADP640Beluga	4	7	42	74	48	1585
105	ADP641Capri	5	8	37	77	50	556
106	ADP642TaylorHort	5	7	42	68	40	557
107	ADP643Cardinal	6	7	37	88	52	917
108	ADP644FoxFire	5	8	37	86	46	1002
109	ADP646Myasi	4	7	39	51	30	781
110	ADP647RedKanner	4	4	43	76	50	1876
111	ADP648RedKloud	4	8	37	74	46	854
112	ADP649Kamiakin	5	4	43	78	60	1519
113	ADP650K42	6	7	47	54	46	638
114	ADP653USDK_CBB_15	6	5	44	63	50	1472
115	ADP654USDK4	7	7	43	69	51	1142
116	ADP655Fiero	5	7	41	85	49	684
117	ADP656RoyalRed	8	8	48	32	44	185
118	ADP658Blush	5	6	44	73	55	1177
119	ADP659USLK1	6	9	36	58	47	286

Table A9. LSmeans for six traits measured on 144 early flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
120	ADP660Krimson	6	6	37	73	53	1179
121	ADP661USCR7	4	7	39	75	49	1129
122	ADP662USCR9	6	9	39	28	39	183
123	ADP663USCR_CBB_20	4	7	38	82	41	675
124	ADP664SilverCloud	7	7	44	53	63	932
125	ADP665USWK_CBB17	6	4	38	58	43	437
126	ADP666USWK6	7	6	42	63	56	1105
127	ADP667VA19	6	6	43	69	47	1275
128	ADP670AC_Calmont	8	8	43	64	48	841
129	ADP672CDRK	6	9	47	41	46	424
130	ADP673UC_Nichols	7	8	47	42	44	301
131	ADP676CELRK	7	9	36	81	43	513
132	ADP677Etna	5	9	38	92	47	888
133	ADP678Hooter	5	3	43	58	50	1159
134	ADP679RedRover	5	6	42	70	45	979
135	ADP680Clouseau	4	7	38	96	59	1662
136	ADP681Belagio	5	6	43	62	55	787
137	ADP685Chianti	6	4	43	74	51	1205
138	ADP687PinkPanther	6	7	37	89	49	863
139	ADP636Montcalm	6	5	43	69	48	1003
140	VAX3	2	1	47	81	29	3048
141	GTS104	8	6	43	65	51	1338
142	Talon	5	5	43	76	49	1301
143	Cabernet	7	9	40	76	41	471
144	Dynasty	5	5	42	70	56	1619
	LSD	3	2	3	23	6	653

Table A10. LSmeans for six traits measured on 121 late flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014.

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
1	ADP1ROZI_KOKO	6	4	48	50	46	1214
2	ADP14KIANGWE	6	5	47	56	37	1285
3	ADP18SODAN	6	6	46	49	46	736
4	ADP24YELLOW	6	7	46	49	43	887
5	ADP27Incomparable	6	5	46	69	41	1408
6	ADP29RH2	6	5	49	41	42	653
7	ADP32RH21	5	4	47	66	43	1902
8	ADP37W6_16488	4	6	48	59	49	1390
9	ADP39RoziKoko	5	3	49	58	39	771
10	ADP40KATWELA	2	4	49	56	26	1503
11	ADP41MRONDO	6	3	51	56	28	735
12	ADP42MKOKOLA	6	4	51	58	32	516
13	ADP44KIJIVU	6	5	47	66	42	1152
14	ADP45RH12	3	5	49	52	40	639
15	ADP46RH4	4	5	51	45	39	721
16	ADP48W6_6534	1	5	48	64	28	1942
17	ADP49W6_16546	4	3	51	67	43	1085
18	ADP50SALUNDE	3	3	51	59	47	1464
19	ADP51RH3	4	5	49	60	43	1150
20	ADP52RH9	6	5	49	57	40	1212
21	ADP53Maharage_makubwa	6	6	50	38	32	396
22	ADP54W6_16447	4	3	49	69	36	1577
23	ADP55KABUKU	3	3	49	53	36	1249
24	ADP57KIJIVU	5	4	49	60	34	1505
25	ADP58CANADA	4	5	49	57	34	1406
26	ADP59Poto	5	6	51	46	39	694
27	ADP60CANADA	5	4	53	49	27	964
28	ADP61Maulasi	5	5	48	58	35	1497
29	ADP62MAULASI	5	4	47	54	36	1100
30	ADP63Soya	5	5	49	61	41	788
31	ADP64W6_16500	4	5	51	59	31	837
32	ADP65W6_16501	5	6	47	69	38	1240
33	ADP66NJANO	5	5	50	44	29	507
34	ADP68Soya	4	6	50	53	40	1103
35	ADP69SOYA	5	6	50	52	39	826
36	ADP70Msafiri	2	5	49	57	31	522
37	ADP71Njano_dolea	5	4	49	82	46	1812
38	ADP74KABLANKETI	5	5	49	49	34	1031
39	ADP76KABLANKETI	7	7	49	44	39	589
40	ADP78W6_16535	3	4	53	46	32	382

Table A10. LSmeans for six traits measured on 121 late flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
41	ADP79LUNGEMBA	5	5	56	46	41	362
42	ADP80KABLANKETI	3	4	51	45	35	784
43	ADP81KABLANKETI	4	6	49	62	40	926
44	ADP82KABLANKETI	5	5	50	56	41	818
45	ADP83W6_16547	6	4	51	31	45	417
46	ADP84Kablanketi_ndefu	3	3	51	65	38	1449
47	ADP85KABLANKETI	7	5	49	66	32	1013
48	ADP86Nyamhonga_mwekundu	7	4	52	39	40	950
49	ADP87KABLANKETI	5	6	50	54	37	792
50	ADP88KABLANKETI	5	7	50	52	41	1210
51	ADP89KABLANKETI	6	4	49	50	42	1135
52	ADP91W6_16560	2	4	48	72	23	2102
53	ADP92MORO	6	6	45	49	31	888
54	ADP93MORO	3	6	50	63	29	1031
55	ADP94LUSHALA	4	6	50	59	31	1153
56	ADP97Bilfa4	7	5	45	65	30	1778
57	ADP105Sewani_97	3	4	50	55	41	1182
58	ADP109Kablanketi	5	5	49	61	40	1357
59	ADP110SUG131	6	4	50	68	43	1177
60	ADP113OPSRS4	6	3	54	70	43	782
61	ADP114OPS_RS1	5	3	52	60	48	1294
62	ADP115Bonus	6	3	58	48	28	559
63	ADP117A483	4	3	50	59	34	2682
64	ADP118Werna	4	3	51	60	42	2066
65	ADP120Tygerberg	6	3	57	42	48	896
66	ADP121KranskopHR1	5	4	54	53	34	807
67	ADP122Kranskop	3	3	51	68	44	1384
68	ADP124Maini	4	3	51	55	32	547
69	ADP183G994	4	6	51	40	49	681
70	ADP205G4494	5	4	47	50	49	887
71	ADP207G4564	6	9	45	46	37	108
72	ADP212G4970	6	6	48	61	43	458
73	ADP247G9975	4	8	50	43	41	400
74	ADP269G13092	3	9	47	35	43	396
75	ADP337G21303	5	5	50	47	48	932
76	ADP346G22246	5	5	51	55	48	660
77	ADP355G22513	5	5	49	51	36	1320
78	ADP383PI209486	4	5	51	59	35	1126
79	ADP390PI307808	4	8	48	39	38	450
80	ADP392PI309701	5	6	53	44	45	988

Table A10. LSmeans for six traits measured on 121 late flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
81	ADP429PR9920_171	5	7	48	73	33	1255
82	ADP430PR1013_3	6	3	49	71	40	1566
83	ADP437PC50	4	4	46	46	41	743
84	ADP44191_1	3	5	49	54	24	1760
85	ADP444HondoValle25	3	7	49	40	29	1191
86	ADP446Raz25	3	5	53	52	28	1575
87	ADP454INIAP429	4	3	54	65	45	1981
88	ADP460PI331356B	5	7	46	69	43	1367
89	ADP465PI321094D	2	7	47	49	28	1065
90	ADP474PI527519	3	7	47	65	34	1357
91	ADP481PI449428	4	5	45	66	47	1527
92	ADP483PI209815	4	5	49	66	44	1062
93	ADP509Fernando	4	7	46	63	39	1279
94	ADP511Canario	7	4	48	46	33	775
95	ADP513Canario	6	5	48	37	31	575
96	ADP514MantegaAmarela	7	5	50	48	34	625
97	ADP517CariocaKibala	1	3	48	71	26	2861
98	ADP523CanarioCela	5	3	48	60	39	1314
99	ADP619UCD0906	8	6	46	53	46	870
100	ADP621JaloEEP558	2	4	52	75	35	1382
101	ADP625Micran	5	4	46	56	49	1313
102	ADP626Badillo	5	3	50	61	48	1368
103	ADP627H9659_21_1	5	4	47	47	48	1042
104	ADP628H9659_27_7	3	5	47	73	44	1584
105	ADP629H9659_27_10	4	7	47	87	43	1040
106	ADP631OAC_Inferno	4	7	43	50	48	1166
107	ADP634UC_RedKidney	6	8	46	37	47	579
108	ADP651K59	6	6	47	58	52	1079
109	ADP652Lisa	5	7	49	43	44	672
110	ADP657Kardinal	6	7	50	32	45	339
111	ADP674UCD0704	5	7	48	37	37	812
112	ADP675UCD0801	5	8	47	53	42	1026
113	ADP683IJR	4	5	48	83	38	1885
114	ADP684Majesty	7	7	47	58	53	1042
115	ADP686UCD707	5	8	47	24	43	320
116	ADP636Montcalm	7	5	42	46	50	1254
117	VAX3	2	2	48	62	29	2966
118	GTS104	7	7	45	38	46	663
119	Talon	5	6	46	48	51	1510
120	Cabernet	7	8	42	47	43	729

Table A10. LSmeans for six traits measured on 121 late flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight g	Seed yield kg ha^{-1}
121	Dynasty	6	7	42	52	55	1410
	LSD	ns	2	3	18	4	679

Table A11. LSmeans for six traits measured on 49 early flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014.

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight	Seed yield kg ha^{-1}
1	ADP2W6_16444	7	3	40	60	37	1024
2	ADP3KIDUNGU	6	4	41	67	40	1476
3	ADP5KABUKU	7	2	40	71	36	1273
4	ADP6W6_16465	4	2	47	61	33	1134
5	ADP10CANADA	6	9	43	63	34	929
6	ADP12W6_16489	5	3	45	67	30	1279
7	ADP15W6_16495	4	5	44	56	27	940
8	ADP73MASUSU	8	2	43	45	43	1444
9	ADP75MABUKU	7	2	44	66	45	1549
10	ADP90KASUKANYWELE	7	2	44	54	40	784
11	ADP95CANADA	6	2	45	59	40	1231
12	ADP102Jesca	8	3	45	47	34	870
13	ADP112Uyole96	8	2	44	58	32	1093
14	ADP168KANYEBWA	5	2	41	68	38	1465
15	ADP172	5	2	42	74	25	2180
16	ADP225G6415	6	2	43	58	49	1152
17	ADP242G9013	4	9	37	82	40	1026
18	ADP391PI308894	7	7	43	57	37	615
19	ADP43846_1	2	2	45	53	22	961
20	ADP462PI527540B	2	2	46	63	22	649
21	ADP467PI209808	8	2	45	76	36	880
22	ADP477PI527512	8	1	44	68	33	610
23	ADP600K07921	5	6	45	64	43	1117
24	ADP601Camelot	8	3	39	54	40	1066
25	ADP608UI_51	7	1	43	43	49	909
26	ADP610G122	6	5	44	58	27	746
27	ADP614Rosie	4	2	44	66	42	1505
28	ADP615Litekid	7	3	45	61	39	1674
29	ADP616OAC_Lyrick	6	4	41	60	55	1361
30	ADP624Dolly	3	2	43	65	53	2312
31	ADP630H9659_23_1	4	1	46	66	37	1807
32	ADP638RedHawk	7	7	40	55	41	841
33	ADP640Beluga	6	6	42	65	38	1136
34	ADP644FoxFire	7	3	39	70	42	1017
35	ADP646Myasi	8	4	43	23	28	261
36	ADP647RedKanner	6	3	44	61	41	1198
37	ADP648RedKloud	4	3	40	66	45	1711
38	ADP649Kamiakin	7	3	43	72	53	1717
39	ADP661USCR7	7	2	46	42	50	1367

Table A11. LSmeans for six traits measured on 49 early flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight	Seed yield kg ha^{-1}
40	ADP670AC_Calmont	7	7	43	49	45	1388
41	ADP676CELRK	7	9	39	68	44	684
42	ADP677Etna	6	9	39	68	46	1567
43	ADP680Clouseau	3	5	41	77	50	1726
44	ADP636Montcalm	7	2	42	61	48	1741
45	VAX3	2	2	51	55	24	2082
46	GTS104	7	3	43	70	43	1492
47	Talon	6	4	43	56	47	2115
48	Cabernet	8	8	41	59	47	962
49	Dynasty	7	4	43	57	54	1549
	LSD	3	2	3	ns	4	629

Table A12. LSmeans for six traits measured on 49 late flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014.

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight	Seed yield kg ha^{-1}
1	ADP1ROZI_KOKO	6	2	46	66	32	787
2	ADP14KIANGWE	7	5	46	57	28	935
3	ADP24YELLOW	6	3	43	61	32	332
4	ADP29RH2	4	2	49	59	28	500
5	ADP45RH12	4	2	48	80	30	921
6	ADP46RH4	5	3	52	50	27	566
7	ADP48W6_6534	5	2	46	72	20	865
8	ADP50SALUNDE	6	2	51	63	31	418
9	ADP51RH3	5	2	48	69	27	516
10	ADP55KABUKU	8	1	46	62	27	1306
11	ADP58CANADA	7	2	50	58	22	312
12	ADP68Soya	3	1	49	66	26	545
13	ADP80KABLANKETI	7	1	53	61	24	570
14	ADP81KABLANKETI	5	1	48	60	25	503
15	ADP84Kablanketi_ndefu	7	1	53	49	30	741
16	ADP87KABLANKETI	6	1	50	57	26	432
17	ADP93MORO	7	1	50	52	20	256
18	ADP105Sewani_97	6	2	48	44	26	662
19	ADP122Kranskop	7	1	53	46	32	546
20	ADP183G994	7	2	51	48	32	347
21	ADP269G13092	5	9	46	50	34	672
22	ADP383PI209486	5	2	55	50	23	550
23	ADP437PC50	5	3	47	63	26	706
24	ADP454INIAP429	5	1	56	58	34	922
25	ADP465PI321094D	8	2	54	63	23	863
26	ADP474PI527519	6	2	46	56	26	1264
27	ADP481PI449428	7	2	44	74	33	1188
28	ADP483PI209815	4	2	50	61	29	773
29	ADP509Fernando	6	4	44	67	27	500
30	ADP511Canario	8	2	48	59	26	708
31	ADP514MantegaAmarela	6	1	52	59	23	249
32	ADP523CanarioCela	6	2	50	58	26	759
33	ADP619UCD0906	6	5	46	50	33	340
34	ADP621JaloEEP558	5	2	60	55	27	206
35	ADP625Micran	7	1	46	78	41	1470
36	ADP626Badillo	7	2	50	55	39	1302
37	ADP628H9659_27_7	6	4	47	68	44	1135
38	ADP629H9659_27_10	8	1	45	64	39	872

Table A12. LSmeans for six traits measured on 49 late flowering common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Plant survival %	100-seed weight	Seed yield kg ha^{-1}
39	ADP631OAC_Inferno	7	1	44	63	44	1029
40	ADP652Lisa	7	8	46	52	35	486
41	ADP657Kardinal	7	6	45	59	40	992
42	ADP683IJR	6	3	53	49	30	913
43	ADP684Majesty	3	5	47	54	54	1316
44	ADP636Montcalm	7	3	43	49	44	1619
45	VAX3	2	2	52	69	23	2444
46	GTS104	8	4	44	62	43	1124
47	Talon	6	4	43	64	46	1369
48	Cabernet	8	8	42	66	42	509
49	Dynasty	5	5	43	91	51	1486
	LSD	3	2	3	14	4	354

Table A13. LSmeans for seven agronomic traits measured on 92 common bean genotypes in the Andean diversity panel grown at Perham, MN, from 2013 to 2015.

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-2	Plant survival %	100-seed weight	Seed weight kg ha^{-1}
1	ADP1ROZI_KOKO	5	3	47	1	50	39	878
2	ADP2W6_16444	6	3	41	1	58	46	1207
3	ADP3KIDUNGU	5	4	39	1	57	43	1235
4	ADP5KABUKU	5	4	38	1	59	41	1392
5	ADP6W6_16465	4	3	45	1	50	46	1409
6	ADP10CANADA	4	7	42	1	47	47	993
7	ADP12W6_16489	5	4	44	1	49	45	1372
8	ADP14KIANGWE	5	5	47	1	50	36	1189
9	ADP15W6_16495	4	5	45	1	50	40	1130
10	ADP24YELLOW	5	4	46	1	48	40	613
11	ADP29RH2	5	3	50	2	46	38	878
12	ADP45RH12	4	3	49	2	56	37	1208
13	ADP46RH4	5	3	51	2	44	36	733
14	ADP48W6_6534	3	3	48	2	58	26	1201
15	ADP50SALUNDE	5	2	52	2	50	39	990
16	ADP51RH3	4	3	49	2	53	36	1031
17	ADP55KABUKU	4	2	48	2	52	33	1493
18	ADP58CANADA	5	3	51	2	51	31	994
19	ADP68Soya	3	4	49	2	52	34	1220
20	ADP73MASUSU	7	3	40	2	54	48	1583
21	ADP75MABUKU	4	3	40	2	63	47	1797
22	ADP80KABLANKETI	4	3	51	2	45	31	1123
23	ADP81KABLANKETI	4	3	49	2	48	34	867
24	ADP84KABLANKETI_NDEFU	4	2	52	2	51	32	1185
25	ADP87KABLANKETI	5	3	50	2	43	33	655
26	ADP90KASUKANYWELE	5	3	43	2	40	52	760
27	ADP93MORO	4	3	50	2	48	25	627
28	ADP95CANADA	6	3	44	2	41	53	1023
29	ADP102Jesca	6	4	42	1	49	43	1326
30	ADP105Sewani_97	4	4	53	1	39	34	814
31	ADP112Uyole96	6	3	44	2	44	42	1431
32	ADP122Kranskop	4	2	52	2	48	39	1093
33	ADP168KANYEBWA	4	3	40	2	55	43	1469
34	ADP172	4	3	41	2	69	26	2038
35	ADP183G994	5	4	54	2	40	45	645
36	ADP225G6415	5	3	42	1	56	57	1489
37	ADP242G9013	4	8	38	1	77	49	1735
38	ADP269G13092	4	8	46	1	40	42	549
39	ADP383PI209486	4	4	53	2	48	30	821
40	ADP391PI308894	5	7	44	1	50	44	774

Table A13. LSmeans for seven agronomic traits measured on 92 common bean genotypes in the Andean diversity panel grown at Perham, MN, from 2013 to 2015 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-2	Plant survival %	100-seed weight	Seed weight kg ha^{-1}
41	ADP437PC50	4	3	47	1	47	36	789
42	ADP43846_1	3	3	43	2	60	28	1493
43	ADP454INIAP429	4	2	58	2	53	38	1694
44	ADP462PI527540B	2	4	45	2	57	27	1201
45	ADP465PI321094D	5	5	49	2	47	26	1105
46	ADP467PI209808	6	4	42	1	63	43	1284
47	ADP474PI527519	4	5	47	2	48	30	1321
48	ADP477PI527512	5	3	44	1	63	39	1151
49	ADP481PI449428	5	4	45	1	58	42	1134
50	ADP483PI209815	4	3	48	2	52	36	1027
51	ADP509Fernando	4	5	45	1	54	35	770
52	ADP511Canario	7	3	50	2	40	30	774
53	ADP514MantegaAmarela	5	3	52	2	40	29	582
54	ADP523CanarioCela	6	2	51	1	45	33	972
55	ADP600K07921	6	6	45	1	47	47	850
56	ADP601Camelot	7	5	41	1	42	47	857
57	ADP608UI_51	5	3	40	1	46	54	933
58	ADP610G122	5	6	44	1	54	33	801
59	ADP614Rosie	4	3	43	1	59	49	1924
60	ADP615Litekid	5	4	43	1	58	44	1585
61	ADP616OAC_Lyrick	6	6	38	1	57	58	1025
62	ADP619UCD0906	6	6	47	1	44	44	835
63	ADP621JaloEEP558	4	3	58	2	57	30	715
64	ADP624Dolly	3	3	42	1	50	58	2298
65	ADP625Micran	5	2	47	2	49	46	1573
66	ADP626Badillo	6	2	50	2	49	43	1310
67	ADP628H9659_27_7	4	4	47	2	55	46	1464
68	ADP629H9659_27_10	6	3	46	2	62	43	1245
69	ADP630H9659_23_1	4	3	46	2	59	40	1454
70	ADP631OAC_Inferno	5	4	44	1	47	46	1189
71	ADP636Montcalm	7	4	42	1	47	51	1679
72	ADP638RedHawk	6	7	41	1	57	46	1060
73	ADP640Beluga	4	6	42	1	56	44	1399
74	ADP644FoxFire	5	4	38	1	67	48	1650
75	ADP646Myasi	5	5	42	1	27	32	521
76	ADP647RedKanner	5	3	43	1	57	48	1906
77	ADP648RedKloud	4	5	38	1	65	49	1686
78	ADP649Kamiakin	5	3	43	1	61	59	2091
79	ADP652Lisa	5	7	47	1	42	43	582

Table A13. LSmeans for seven agronomic traits measured on 92 common bean genotypes in the Andean diversity panel grown at Perham, MN, from 2013 to 2015 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-2	Plant survival %	100-seed weight	Seed weight kg ha-1
80	ADP657Kardinal	6	7	47	1	42	41	745
81	ADP661USCR7	4	4	41	1	44	51	1332
82	ADP670AC_Calmont	6	6	43	1	46	50	1256
83	ADP676CELRK	6	7	37	1	57	50	862
84	ADP677Etna	5	7	39	1	61	51	1398
85	ADP680Clouseau	4	6	40	1	63	59	1675
86	ADP683IJR	4	3	50	1	57	36	1523
87	ADP684Majesty	5	5	47	2	44	57	1262
88	VAX3	2	2	48	2	59	27	2450
89	GTS104	7	5	44	1	45	49	1241
90	Talon	5	4	43	1	48	49	1659
91	Cabernet	6	7	41	1	52	49	1268
92	Dynasty	5	4	42	1	51	57	1607
	LSD	2	2	3		18	6	657

Table A14. LSmeans for seven traits measured on 246 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 and 2014.

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-9	Plant survival %	100-seed weight	Seed Yield kg ha^{-1}
1	ADP1ROZI_KOKO	5	4	48	1	42	43	859
2	ADP2W6_16444	5	4	42	1	57	51	1300
3	ADP3KIDUNGU	5	4	38	1	52	44	1450
4	ADP5KABUKU	4	5	38	1	53	44	1614
5	ADP6W6_16465	5	3	44	1	45	53	1499
6	ADP7BUKOBA	3	4	40	1	50	39	1671
7	ADP10CANADA	4	6	42	1	39	53	1164
8	ADP11KIBOROLONI	5	6	39	1	67	42	1469
9	ADP12W6_16489	5	4	44	1	40	53	1488
10	ADP14KIANGWE	5	5	48	1	47	41	1206
11	ADP15W6_16495	4	6	45	1	47	46	1129
12	ADP16GOLOLI	4	6	38	1	54	44	1782
13	ADP17W6_16529	4	5	44	1	50	52	1519
14	ADP18SODAN	5	5	46	1	42	47	1118
15	ADP19KASUKANYWELE	5	7	42	1	39	51	840
16	ADP20KIGOMA	4	7	39	1	47	43	1300
17	ADP22KISAPURI	5	6	38	1	57	41	1461
18	ADP23MSHORONYLONI	6	3	40	1	58	39	1516
19	ADP24YELLOW	5	5	47	1	41	44	711
20	ADP25RUHONDELA	6	4	44	1	56	35	972
21	ADP26Black_Wonder	5	7	39	1	65	39	1071
22	ADP27Incomparable	5	4	47	1	48	42	1439
23	ADP28Sisi	5	7	37	1	58	43	1573
24	ADP29RH2	5	4	51	2	40	43	946
25	ADP30RH6	5	4	41	1	48	33	654
26	ADP31RH11	5	5	46	1	42	40	761
27	ADP32RH21	4	4	47	1	46	44	1791
28	ADP33KIJIVU	5	4	41	1	47	50	1315
29	ADP34KIJIVU	4	3	42	1	53	50	1294
30	ADP37W6_16488	4	6	51	1	47	46	1084
31	ADP38Moono	5	6	45	1	38	57	917
32	ADP39RoziKoko	4	3	48	1	49	41	725
33	ADP40KATWELA	2	4	49	2	47	25	1188
34	ADP41MRONDO	5	3	53	2	48	31	938
35	ADP42MKOKOLA	4	3	52	2	45	33	634
36	ADP43Bwana_shamba	4	4	47	2	53	40	1429
37	ADP44KIJIVU	5	4	48	2	52	44	1303
38	ADP45RH12	4	4	49	2	45	41	1248
39	ADP47MSOLINI	5	4	39	2	60	52	1797
40	ADP48W6_6534	2	4	49	2	51	29	1259

Table A14. LSmeans for seven traits measured on 246 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 and 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-9	Plant survival %	100-seed weight	Seed Yield kg ha^{-1}
41	ADP49W6_16546	4	4	50	2	48	44	1036
42	ADP50SALUNDE	4	3	53	2	44	43	1283
43	ADP51RH3	4	4	50	2	44	41	1302
44	ADP52RH9	5	4	51	2	44	37	1546
45	ADP53Maharage_makubwa	5	5	53	2	35	37	545
46	ADP54W6_16447	5	3	50	2	45	37	1435
47	ADP55KABUKU	3	3	49	2	47	37	1422
48	ADP56SOYA	5	3	43	2	52	38	1663
49	ADP57KIJIVU	4	4	51	2	46	39	1299
50	ADP58CANADA	4	4	52	2	48	36	1206
51	ADP59Poto	4	4	51	2	36	39	1080
52	ADP60CANADA	6	3	58	2	44	30	753
53	ADP61Maulasi	5	4	50	2	47	36	1470
54	ADP62MAULASI	5	3	47	2	48	38	1737
55	ADP63Soya	4	4	50	2	47	40	1084
56	ADP64W6_16500	4	4	54	2	45	30	954
57	ADP65W6_16501	5	5	47	2	50	41	1872
58	ADP66NJANO	4	5	52	2	37	31	808
59	ADP67NJANO	5	4	43	2	43	36	930
60	ADP68Soya	5	5	49	2	46	39	1442
61	ADP69SOYA	5	4	51	2	46	40	975
62	ADP70Msafiri	3	5	51	2	46	31	507
63	ADP71Njano_dolea	5	3	51	2	61	43	1527
64	ADP72MASUSU	5	3	42	2	36	42	981
65	ADP73MASUSU	6	4	39	2	60	51	1540
66	ADP74KABLANKETI	4	4	48	2	43	34	1257
67	ADP75MABUKU	3	4	38	2	61	49	1872
68	ADP76KABLANKETI	5	5	49	2	38	38	1022
69	ADP79LUNGEMBA	4	4	56	2	42	36	434
70	ADP80KABLANKETI	3	4	50	2	38	34	1392
71	ADP81KABLANKETI	4	4	50	2	42	39	1174
72	ADP82KABLANKETI	5	4	52	2	44	39	730
73	ADP83W6_16547	5	3	54	2	26	46	726
74	ADP84Kablanketi_ndefu	3	2	52	2	52	33	1273
75	ADP85KABLANKETI	6	4	48	2	50	32	1011
76	ADP86Nyamhonga_mwekund	5	3	52	2	36	40	836
77	ADP87KABLANKETI	4	5	50	2	36	37	954
78	ADP88KABLANKETI	5	4	50	2	40	40	1425

Table A14. LSmeans for seven traits measured on 246 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 and 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-9	Plant survival %	100-seed weight	Seed Yield kg ha^{-1}
79	ADP89KABLANKETI	4	3	50	2	41	40	1094
80	ADP90KASUKANYWELE	4	3	43	2	34	58	866
81	ADP91W6_16560	3	4	50	2	60	22	1105
82	ADP92MORO	5	5	46	2	42	30	665
83	ADP93MORO	3	5	51	2	46	28	849
84	ADP94LUSHALA	4	4	51	2	48	31	944
85	ADP95CANADA	6	4	43	2	32	60	1113
86	ADP96Rojo	5	4	44	1	55	41	1253
87	ADP97Bilfa4	5	5	45	1	54	32	2271
88	ADP99BwanaShamba	5	4	45	1	43	52	1140
89	ADP100EG21	4	3	43	1	51	32	1243
90	ADP102Jesca	5	4	41	1	51	47	1589
91	ADP103Pesa	5	4	43	1	44	42	1115
92	ADP105Sewani_97	4	5	56	1	36	38	1082
93	ADP106Zawadi	4	6	37	1	61	33	1455
94	ADP107Mishindi	5	4	43	1	53	31	822
95	ADP108Njano	6	3	46	2	51	36	1338
96	ADP109Kablanketi	5	4	49	2	46	40	1438
97	ADP110SUG131	6	3	55	2	52	42	1173
98	ADP111Uyole98	6	4	41	2	38	39	1498
99	ADP112Uyole96	5	3	45	2	37	48	1708
100	ADP113OPSRS4	5	3	53	2	53	42	673
101	ADP114OPS_RS1	5	3	50	2	49	47	1521
102	ADP115Bonus	6	3	59	2	42	31	777
103	ADP116A800	4	3	44	2	59	36	2836
104	ADP117A483	3	3	54	2	50	35	2024
105	ADP118Werna	4	3	50	2	47	40	1875
106	ADP120Tygerberg	5	3	60	2	36	41	959
107	ADP121KranskopHR1	4	3	54	2	44	33	684
108	ADP122Kranskop	3	3	52	2	49	43	1360
109	ADP124Maini	4	3	57	2	37	30	798
110	ADP168KANYEBWA	4	4	39	2	49	46	1500
111	ADP205G4494	6	4	49	2	42	49	620
112	ADP207G4564	4	7	47	1	40	45	714
113	ADP212G4970	5	5	48	1	45	43	555
114	ADP213G5034	6	5	44	2	40	36	510
115	ADP225G6415	5	3	41	1	55	62	1671
116	ADP242G9013	5	7	38	1	74	54	1800
117	ADP247G9975	3	6	50	2	28	44	775
118	ADP269G13092	3	7	47	1	35	47	422

Table A14. LSmeans for seven traits measured on 246 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 and 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-9	Plant survival %	100-seed weight	Seed Yield kg ha^{-1}
119	ADP277G13778	4	5	43	1	51	40	1006
120	ADP303G17913	5	6	42	1	70	58	1415
121	ADP310G18356	5	7	39	1	44	51	1106
122	ADP324G20729	5	4	45	2	47	52	1135
123	ADP346G22246	5	4	54	2	44	46	1164
124	ADP351G22420	4	3	40	1	66	26	1452
125	ADP355G22513	5	5	48	2	38	40	1789
126	ADP376PI189408	3	8	44	2	31	46	610
127	ADP383PI209486	4	5	53	2	47	33	901
128	ADP390PI307808	4	7	49	1	35	39	459
129	ADP391PI308894	4	7	45	1	47	47	841
130	ADP392PI309701	4	4	51	2	31	44	1194
131	ADP417PI451906	5	7	43	1	39	46	861
132	ADP428ColoradodelPais	5	5	38	1	68	33	1704
133	ADP429PR9920_171	4	5	48	1	58	37	1765
134	ADP430PR1013_3	5	3	51	2	49	41	1867
135	ADP431Gurabo5	4	6	39	1	61	27	1404
136	ADP433PR9745_232	3	3	45	1	66	32	1137
137	ADP435RM_05_07	4	4	41	1	58	33	1042
138	ADP437PC50	4	3	47	1	40	41	786
139	ADP43846_1	4	4	42	2	64	31	1712
140	ADP44049_2	4	5	44	2	63	25	802
141	ADP44191_1	3	4	50	2	50	24	1106
142	ADP443Vazon7	4	5	41	2	56	30	1122
143	ADP444HondoValle25	4	6	50	2	26	28	1129
144	ADP445Chijar	5	4	47	2	45	26	2075
145	ADP446Raz25	3	4	53	2	40	31	1141
146	ADP454INIAP429	3	3	59	2	51	41	1984
147	ADP460PI331356B	5	6	47	1	52	42	1306
148	ADP462PI527540B	3	5	45	2	55	30	1393
149	ADP464PI353534B	4	4	42	1	47	34	543
150	ADP465PI321094D	3	6	47	2	40	28	1229
151	ADP467PI209808	5	5	41	1	57	46	1389
152	ADP468PI527538	5	5	42	1	54	45	1236
153	ADP470PI527508	4	7	41	2	60	39	1405
154	ADP471PI527537C	6	6	41	2	47	37	933
155	ADP474PI527519	4	6	47	2	44	32	1471
156	ADP475PI319706	4	5	41	2	55	39	756
157	ADP476Heirloom	3	4	43	2	50	36	1337
158	ADP477PI527512	4	4	44	1	61	42	1191

Table A14. LSmeans for seven traits measured on 246 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 and 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-9	Plant survival %	100-seed weight	Seed Yield kg ha^{-1}
159	ADP478PI353536	5	5	38	2	43	41	751
160	ADP481PI449428	4	5	46	1	51	47	1037
161	ADP483PI209815	4	4	48	2	48	40	1158
162	ADP509Fernando	3	6	46	1	47	38	889
163	ADP511Canario	7	3	52	2	31	32	1012
164	ADP513Canario	5	4	51	2	25	30	862
165	ADP514MantegaAmarela	5	4	53	2	31	32	989
166	ADP515KatarinaKibala	5	5	44	1	46	37	724
167	ADP517CariocaKibala	2	4	49	2	55	26	2423
168	ADP519KatarinaCela	5	6	38	1	37	32	873
169	ADP523CanarioCela	6	3	52	2	38	36	1287
170	ADP598Charlevoix	5	8	44	1	44	52	810
171	ADP600K07921	7	6	45	1	38	50	765
172	ADP601Camelot	6	6	42	1	37	50	978
173	ADP602Sacramento	5	7	37	1	57	53	1359
174	ADP603Wallace773_V98	4	7	39	1	52	43	1247
175	ADP6041062_V98	4	7	38	1	41	49	821
176	ADP6051132_V96	5	4	44	1	45	56	1409
177	ADP607NY105	5	7	39	1	40	53	894
178	ADP608UI_51	4	4	39	1	48	57	1199
179	ADP610G122	4	6	44	1	53	36	746
180	ADP611PompadourB	5	8	46	1	36	37	701
181	ADP612ICAQuimbaya	5	5	46	1	37	48	1024
182	ADP61302_385_14	7	7	40	1	46	47	987
183	ADP614Rosie	5	3	43	1	55	52	2115
184	ADP615Litekid	5	5	43	1	56	46	1621
185	ADP616OAC_Lyrick	6	7	37	1	56	60	1072
186	ADP617RedRider	5	6	44	1	50	53	1997
187	ADP618AC_Elk	4	7	37	1	36	54	1228
188	ADP619UCD0906	6	6	48	1	41	49	1099
189	ADP620UCD0405	5	8	39	1	57	50	1751
190	ADP621JaloEEP558	3	3	57	2	57	32	832
191	ADP622UCD0701	6	7	40	1	38	53	1477
192	ADP623Drake	5	8	41	1	47	49	1120
193	ADP624Dolly	3	4	42	1	42	61	2379
194	ADP625Micran	4	3	47	2	35	48	1871
195	ADP626Badillo	6	3	51	2	45	45	1330
196	ADP627H9659_21_1	5	4	48	2	31	48	1161
197	ADP628H9659_27_7	3	4	47	2	48	47	1726
198	ADP629H9659_27_10	5	5	47	2	61	45	1372

Table A14. LSmeans for seven traits measured on 246 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 and 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-9	Plant survival %	100-seed weight	Seed Yield kg ha^{-1}
199	ADP630H9659_23_1	4	4	46	2	56	42	1416
200	ADP631OAC_Inferno	4	5	45	1	39	48	1292
201	ADP633TARS_HT2	7	4	46	1	51	52	1466
202	ADP634UC_RedKidney	5	8	46	1	32	47	698
203	ADP636Montcalm	7	5	42	1	43	53	1692
204	ADP637Isabella	5	7	38	1	61	49	1155
205	ADP638RedHawk	5	8	41	1	58	49	870
206	ADP639Chinook2000	5	6	43	1	55	51	1614
207	ADP640Beluga	3	7	42	1	52	48	1519
208	ADP641Capri	5	6	38	1	51	56	1180
209	ADP642TaylorHort	5	6	43	1	42	45	1068
210	ADP643Cardinal	5	4	38	1	54	58	1591
211	ADP644FoxFire	5	4	38	1	66	51	1733
212	ADP646Myasi	4	6	41	1	29	35	975
213	ADP647RedKanner	5	3	43	1	55	51	2197
214	ADP648RedKloud	4	7	37	1	64	51	1317
215	ADP649Kamiakin	4	4	44	1	56	62	2212
216	ADP650K42	5	6	46	1	46	46	988
217	ADP651K59	4	5	47	1	45	55	1414
218	ADP652Lisa	4	6	48	1	38	46	590
219	ADP653USDK_CBB_15	5	5	42	1	52	50	1908
220	ADP654USDK4	6	5	43	1	52	54	1781
221	ADP655Fiero	4	6	42	1	59	55	1631
222	ADP656RoyalRed	6	7	46	1	35	46	824
223	ADP657Kardinal	5	7	48	1	34	42	528
224	ADP658Blush	4	5	45	1	54	56	1596
225	ADP659USLK1	5	7	37	1	48	56	1344
226	ADP660Krimson	4	5	38	1	49	59	1795
227	ADP661USCR7	3	6	39	1	46	52	1513
228	ADP662USCR9	5	8	39	1	34	48	985
229	ADP663USCR_CBB_20	4	6	38	1	57	46	1404
230	ADP664SilverCloud	6	7	44	1	43	64	1217
231	ADP665USWK_CBB17	5	4	39	1	44	46	1179
232	ADP666USWK6	5	6	45	1	40	59	1416
233	ADP667VA19	5	5	43	1	49	49	1562
234	ADP670AC_Calmont	6	6	44	1	46	53	1237
235	ADP672CDRK	4	8	46	1	36	51	1075
236	ADP673UC_Nichols	6	7	46	1	36	48	830
237	ADP674UCD0704	4	7	47	1	32	39	765
238	ADP675UCD0801	4	7	47	1	39	46	1235

Table A14. LSmeans for seven traits measured on 246 common bean genotypes in the Andean diversity panel grown at Perham, MN, in 2013 and 2014 (continued).

No.	Identification	Fusarium root rot 1-9	Halo blight 1-9	Days to flower No.	Growth habit 1-9	Plant survival %	100-seed weight	Seed Yield kg ha^{-1}
239	ADP676CELRK	6	7	37	1	52	53	1066
240	ADP677Etna	4	7	39	1	58	55	1410
241	ADP678Hooter	4	4	44	1	37	56	1558
242	ADP679RedRover	5	7	44	1	47	51	1074
243	ADP680Clouseau	4	6	39	1	57	64	1830
244	ADP681Bellagio	6	3	45	2	36	54	1142
245	ADP683IJR	4	4	48	2	61	39	1706
246	ADP684Majesty	6	6	47	2	39	58	1386
	LSD	2	2	4		23	8	1022

Table A15. Soil mechanical and chemical analysis done by Soil Testing Laboratory, NDSU. Perham, MN, in 2013.

Misc. Laboratory No.	Sample I.D. #	Depth (inches)	Percent sand	Percent silt	Percent clay	Soil texture
20	Perham	0-6	65.9	27.2	6.9	Sandy-loam

Mechanical Analysis by Hydrometer Method.

Laboratory No.	Sample I.D.	Depth inches	NO_3-N lb/A	P ppm	K ppm	pH	EC mmhos/cm	OM %	S lb/A	Zn ppm	Fe ppm	Mn ppm	Cu ppm	Cl lb/A
232	Perham	6	34	36	300	7.2	0.15	2.2	8	6.8	36	14	4.8	6.7

pH in water; NO_3-N (lb/acre) extracted with water; OM (%) by ignition; P=Phosphorus; P(ppm) by Olson procedure; K(ppm) by 1N ammonium acetate; soluble salts (EC-mmhos/cm) in 1:1 soil: water; Zn, Fe, Mn, and Cu by DTPA; SO4-S (lb/acre) extracted with 500 ppm P as monobasic calcium phosphate; Cl (lb/acre) extracted with .01M Ca(NO3)2; Ca.

Table A16. Soil mechanical and chemical analysis done by Soil Testing Laboratory, NDSU. Perham, MN, in 2014.

Misc. Laboratory No.	Sample I.D.	Depth (inches)	Percent sand	Percent silt	Percent clay	Soil texture
233	1	0-12	76.1	18.2	5.7	Loamy sand

Mechanical Analysis by Hydrometer Method.

Laboratory No.	Sample I.D.	Depth inches	NO_3-N lb/A	P ppm	K ppm	pH	EC mmhos/cm	OM %	S lb/A	Zn ppm	Fe ppm	Mn ppm	Cu ppm	Cl lb/A
10149	1	0-12	6	28	280	7.2	0.11	1.6	6	3.7	21	8	0.3	35

pH in water; NO3-N (lb/acre) extracted with water; OM (%) by ignition; P=Phosphorus; P(ppm) by Olson procedure; K(ppm) by 1N ammonium acetate; soluble salts (EC-mmhos/cm) in 1:1 soil: water; Zn, Fe, Mn, and Cu by DTPA; SO4-S (lb/acre) extracted with 500 ppm P as monobasic calcium phosphate; Cl (lb/acre) extracted with .01M Ca(NO3)2; Ca.

Table A17. Soil chemical analysis done by Agvise Laboratory. Perham, MN, in 2015.

Laboratory No.	Sample I.D.	Depth inches	NO_3-N lb/A	P ppm	K ppm	pH	EC mmhos/cm	OM %	S lb/A	Zn ppm	Fe ppm	Mn ppm	Cu ppm
175960	534	6	25	50	299	6.2	0.22	1.9	20	6.41	20.7	8.5	3.04