

Associated SNPs, heritabilities, trait correlations, and genomic breeding values for resistance in snap beans (*Phaseolus vulgaris* L.) to root rot caused by *Fusarium solani* (Mart.) f. sp. *phaseoli* (Burkholder)

Supplementary Material



Supplementary Figure 1. Aboveground biomass of five-plant samples of common bean in root rot trials in 2015 in Oregon. Scale 1-5, right-left.



Supplementary Figure 2. Protractor device used to measure root angles in the Bean CAP Snap Bean Diversity Panel. A = taproot, B = basal roots, C = adventitious roots.





Supplementary Figure 3. Biplot showing Principle Components axes 1 and 2 for the BeanCAP Snap Bean Diversity Panel genotyped with 10.6K SNPs. PCA1 explains 22% of the variation and PCA2 accounts for an additional 11%. The first PC axis separates Andean from Mesoamerican ancestry but rather than distinct groups, there is a gradient along the axis. The second PC axis primarily differentiates within the Mesoamerican group between European and American derived lines, and between ancestral and contemporary snap beans for Andean types.





Supplementary Figure 4. Histogram and normality plots for phenotypic performance for *Fusarium solani* root rot reaction and biomass of the BeanCAP Snap Bean Diversity Panel grown at the Vegetable Research Farm. Means of replicates and years combined are plotted. Rating scales of 1-5 were used for both traits. Only determinate bush type cultivars are shown for biomass. 'Black Valentine' is a root rot resistant/high biomass cultivar and 'Zodiac' is a root rot susceptible/low biomass cultivar. 'FR-266' is a moderately resistant snap bean experimental line.



Supplementary Figure 5. Box and whiskers plots based on one-way ANOVAs of SNPs associated with disease severity or biomass from a GWAS of the BeanCAP snap bean diversity panel grown and phenotyped at the OSU Vegetable Research Farm.



Supplementary Table 1. Published Quantitative Trait Loci (QTL) for root rot in common bean, including population, type of molecular marker, *Phaseolus vulgaris* chromosome, percent total genetic variation explained (R^2), LOD score and pathogen species. "-" = Data not available.

| | | | QTL | | | | | |
|------------------------------|------------|---|------------|----------------------------------|--------|------------------------|---------------------|--|
| Authors | Population | Dopulation | associated | Chrom | No. of | D ² | LOD | Root Rot |
| Authors | type | ropulation | with | | ŲΠ | Λ | LOD | ratnogen |
| Schneider et al. 2001 | biparental | Montcalm x FR-266 & Isles x FR-266 | RAPD | 01, 02, 03, 04, 05, 06, 07 | 15 | 0.05-0.31 | - | F. solani |
| Chowdhury et al. 2002 | biparental | AC Compass x NY2114-12 | RAPD | | 2 | 0.20-0.30 | 5-8 | F. solani |
| Roman-Aviles & Kelly 2005 | biparental | Red Hawk x Negro San Luis & C97407 x Negro San Luis | RAPD | 01, 05, 07, 08, 09 | 10 | 0.07-0.53 | 2.4-15.7 | F. solani |
| Navarro et al. 2008 | biparental | Eagle x Puebla 152 | RAPD | 03, 06, 07 | 5 | 0.25-0.49 | 2.6-11.3 | Pythium ultimum & Aphanomyces euteiches |
| Kamfwa et al., 2013 | biparental | K132 × MLB-49- 89A; K20 × MLB-49- 89A | SSR | 03 | 1 | 0.34 | 6.1 | F. solani |
| Hagerty et al. 2015 | biparental | OSU5446 x RR6950 | SNP | $02, 04, 06 \\ 03, 07$ | 3 2 | 0.05-0.15 0.09-0.22 | 6.7-9.3 6.2-11.5 | A. euteiches F. solani |
| Nakedde et al., 2016 | biparental | Puebla 152 x Zorro | SNP | 05 | 1 | 0.10 | 3.2 | F. solani |
| Wang et al., 2018 | biparental | CAL96 x MLB-49- 89A | SNP | 02 | 1 | 0.09-0.10 | 2.6-3.9 | F. brasiliense |
| Oladzad et al. | GWAS | Andean Diversity Panel | SNIP | 02 | 1 | 0.12 | - | Rhizoctonia |
| 2019 | GWAS | Middle American Diversity Panel | 5111 | 06, 08, 10 | 3 | 0.05-0.08 | - | solani |

| | Population | | QTL associated | | No. of | | | Root Rot | |
|----------------------------------|------------|------------------------------------|-------------------|-------------------------------------|--------|----------------|-----|--------------|--|
| Authors | type | Population | with | Chrom. | QTL | R ² | LOD | Pathogen | |
| Dramadri et al., 2020 | GWAS | Andean Diversity Panel | SNP | 01, 02, 04, 05, 09 | 16 | 0.29-0.39 | - | P. ultimum | |
| Zitnick-Anderson et al., 2020 | GWAS | Andean Diversity Panel | SNP | 01 02, 03, 04, 07, 08, 09, 11 | 16 | 0.09-0.15 | - | F. solani | |
| | | Middle American Diversity Panel | | 01, 03, 04, 07, 08 | 7 | 0.07-0.10 | - | | |
| Paulino et al., 2021 | GWAS | Middle American Diversity Panel | SNP | 01, 03, 04, 05, 07, 10, 11 | 2 | 0.09-0.64 | - | F. oxysporum | |

Supplementary Table 2. Extent of linkage disequilibrium (LD) around SNPs associated with *Fusarium solani* disease reaction or biomass of a diversity panel of snap beans. Cutoff for LD based on a D' or R^2 of 0.8 and $P \le 0.01$.

| | | | | | D' | | \mathbf{R}^2 | | | | |
|---------|-------------|------------|------------|------------|------------|------------|----------------|------------|------------|--|--|
| | | | | | | Size of LD | | | Size of LD | | |
| Trait | SS ID No. | Chromosome | Position | Proximal | Distal | block | Proximal | Distal | block | | |
| | | _ | | | | bp | | | | | |
| Disease | ss715647578 | Pv03 | 12,661,037 | 11,799,126 | 32,624,773 | 20,825,647 | 12,640,644 | 13,319,393 | 678,749 | | |
| Disease | ss715646526 | Pv07 | 34,296,485 | 28,548,135 | 35,840,739 | 7,292,604 | 34,080,347 | 34,296,485 | 216,138 | | |
| Disease | ss715639797 | Pv08 | 32,951,182 | 18,361,451 | 54,388,710 | 36,027,259 | - | - | 0 | | |
| Biomass | ss715649390 | Pv10 | 5,677,538 | 4,962,514 | 7,431,711 | 2,469,197 | 5,495,323 | 5,916,721 | 421,398 | | |
| Disease | ss715649485 | Pv10 | 7,910,750 | 6,170,351 | 8,060,803 | 1,890,452 | 7,910,750 | 8,060,803 | 150,053 | | |
| Disease | ss715646318 | Pv10 | 40,686,027 | 38,845,021 | 41,217,646 | 2,372,625 | - | - | 0 | | |
| Biomass | ss715645486 | Pv11 | 766,814 | 716,937 | 766,814 | 49,877 | - | - | 0 | | |

Supplementary Table 3. Mean and standard deviation (SD) for predictive ability (r) at four ratios of training to testing populations compared to observed and predicted correlation for the entire population for seven root and *Fusarium* root rot traits of the BeanCAP Snap Bean Diversity Panel.

| Adventitious | | | | Basal root | | Disease | | | | Shallo | w root | Tap root | | |
|----------------|-------|-------|---------------|------------|-------|-------------|-------|-----------------|-------|--------|--------|----------|-------|-------|
| Training | roots | | Biomass diame | | neter | er severity | | Deep root angle | | angle | | diameter | | |
| population (%) | Mean | SD | Mean | SD | Mean | SD | Mean | SD | Mean | SD | Mean | SD | Mean | SD |
| 60 | 0.295 | 0.098 | 0.483 | 0.082 | 0.202 | 0.091 | 0.497 | 0.062 | 0.554 | 0.046 | 0.301 | 0.082 | 0.329 | 0.077 |
| 70 | 0.308 | 0.090 | 0.480 | 0.087 | 0.225 | 0.077 | 0.543 | 0.062 | 0.606 | 0.071 | 0.376 | 0.070 | 0.387 | 0.118 |
| 80 | 0.308 | 0.162 | 0.473 | 0.089 | 0.222 | 0.079 | 0.583 | 0.114 | 0.511 | 0.106 | 0.290 | 0.133 | 0.461 | 0.145 |
| 90 | 0.345 | 0.348 | 0.565 | 0.197 | 0.242 | 0.309 | 0.590 | 0.113 | 0.650 | 0.148 | 0.309 | 0.244 | 0.481 | 0.170 |
| 100 | 0.720 | - | 0.900 | - | 0.680 | - | 0.780 | - | 0.810 | - | 0.640 | - | 0.730 | - |