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# Analysis of *Fusarium*-Common Beans Pathosystem in Aguascalientes, Mexico

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## Abstract

In Mexico, high incidences of *Fusarium* affect common bean (*Phaseolus vulgaris* L.) production, reducing grain yields due to seedling death and crop standing reductions. Production of resistant germplasm could be an appropriate strategy for grain yield increasing. Bean breeding programs need the former analysis of plant-pathogen pathosystem to perform the selection of segregating populations with improved resistance to root rot pathogens and the best agroecosystem adaptation. Here, we report our results on characterization of genetic variability patterns of *Fusarium solani* f. sp. *phaseoli* (FSP) from Aguascalientes, México; the analysis of *P. vulgaris* germplasm reactions to highly and naturally FSP-infested field and controlled conditions; and the identification of genetic basis of resistance to FSP root rot in segregating common bean populations. Significant genetic variability in FSP isolates from Aguascalientes and other regions of México was found. Also, we found high variation on reactions to FSP root rots, resistance was more frequent on black seed-coated beans, and susceptibility was common in pinto beans. Resistance to FSP in BAT 477 seedlings was associated with one quantitative trait loci (QTL).

**Keywords:** *Fusarium solani* f. sp. *phaseoli* root rots, *Phaseolus vulgaris* L., Aguascalientes, genetic diversity, root rot incidence and severity, genetic resistance, molecular markers

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## 1. Introduction

Common bean (*Phaseolus vulgaris* L.) is the second major crop in México. In 2016, approximately 1.63 million hectares were cultivated with common beans and an average grain yield

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of 690 kg ha<sup>-1</sup> was reported [1]. Grain yields of common bean in México are low since potential yields are estimated to be ≈3 t h<sup>-1</sup>. Several factors such as biotic (diseases, insect pest, weeds) and abiotic (drought, freeze, low-fertility soils, high temperatures, salinity) stresses reduce common bean production [2]. Drought stress and root rots caused by *Fusarium solani* f. sp. *phaseoli* (FSP), alone or combined, affect bean grain yield in major regions producing common beans in México. Both stresses reduce grain yields due to increase the percentages of seedling death and, consequently, reduce the crop standing (root rots) or reduce growth and development and seed production (water deficits) [3, 4].

Grain yield reductions decrease crop profits. More than 70% of common bean growers use low inputs for production, or in some cases, common bean is a subsistence crop. We consider that production of common bean germplasm with combined resistance to drought stress and diseases could be an appropriate strategy for grain yield improvement because it is a cheap, sustainable and durable strategy for grain yield stabilization [5]. The control of major root rot pathogens includes chemical, cultural and biological strategies, but most of them are not enough efficient to control pathogens or they have poor possibilities to be applied under Mexican bean grower conditions because they are expensive [6].

Mexican common bean breeding programs need the former analysis of plant-pathogen pathosystem to perform the selection of those genotypes with improved resistance to root rot pathogens and the best environmental adaptation. Another challenge is the characterization of pathogenic variability of root rot pathogen populations to identify molecular genetic factors of parasitic capability of the pathogen, since these characteristics affect the variation on reactions of common bean germplasm to the fungus. Then, the development of molecular marker technologies to improve the evaluation and selection of resistant common bean germplasm under marker-assisted selection strategy is needed [7].

This research includes three objectives: (1) to characterize the genetic variability patterns of *Fusarium* isolates from Aguascalientes and other regions of México; (2) to assess the reactions of each root rot pathogen in *Phaseolus* sp. germplasm under field and controlled conditions and (3) to define the genetic basis of resistance to each root rot pathogen in common beans.

## 2. Materials and methods

Despite the states of Aguascalientes and México, other states do not outstand as bean producers in México that three Mexican northern states (Chihuahua, Zacatecas and Durango) produce 60% of common beans at country while other four southern states (Chiapas, Oaxaca, Veracruz and Puebla) produce 20%, and both groups produce 80% of total beans in Mexico, they are considered by Mexican bean breeders as good locations for germplasm evaluation and/or selection for resistance to drought stress and root rot diseases caused by *Fusarium* sp., *Rhizoctonia solani* and *Pythium* sp., among other diseases such as common blight (*Xanthomonas axonopodis* pv. *phaseoli*) and anthracnose (*Glomerella lindemuthiana*) [8, 9].

Field trials included in this report were conducted in one location of the State of Aguascalientes: Sandovalés and one from the State of México: Chapingo. Sandovalés is located at 22°09'N, 102°18'W, and 2000 m above sea level and shows dry land conditions with summer rainfall. Annual average precipitations range from 350 to 400 mm, with average temperature ranges from 12 to 18°C. Chapingo is located at 19°28'N, 98°52'W; 2250 m above sea level and has a temperate climate with fresh summer and low variable temperatures (15–18°C) and the annual average precipitations range from 600 to 700 mm [10].

### 2.1. Variability of FSP isolates from Aguascalientes, México

The procedures for *Fusarium* isolates characterization by using *in vitro*, pathogenicity and AFLP genotype strategies were described when we analyzed the isolates from the State of Aguascalientes [11] and Aguascalientes, México, Guanajuato and Veracruz [4].

### 2.2. Reactions of common bean germplasm to root rot pathogens under field conditions

Previous works indicated us that soils of Chapingo and Sandovalés are highly, naturally and homogeneously infested in most cases by FSP [12, 13]. We divided the characterizations into two groups.

The first group included 6 (experiment I), 75 (experiment II) and 36 (experiment III) (**Table 1**) common bean genotypes under rainfall conditions at Sandovalés, Aguascalientes. Experiments were established on June 27 (E-I and E-II) and July 11 (E-III), 2002 under randomized complete block (RCB) design with four replications (E-I), where experimental unit was three rows 5 m-length. The germplasm of E-II was divided into three groups based on color seed coat: 25 pinto seed-type bean genotypes, 25 Flor de Mayo seed-type and 20 black seed beans. Each group of genotypes was randomized in a RCB design with three replications, and where experimental unit was two rows 6 m-length. Finally, germplasm in E-III was randomized on 6×6 lattice design with three replications and experimental unit of 2 rows 6 m in length.

In the second group of experiments, 49 common bean genotypes (**Table 1**) were evaluated under two levels of soil moisture: irrigated and rainfed conditions. Germplasm was randomized in 7 × 7 lattice design with four replications. Two replications were carried out under irrigated conditions, while the other two under rainfed conditions (irrigation was stopped when the most of germplasm initiated flowering and no irrigation was supplied until harvest). Experiments were established in Sandovalés and Chapingo, México.

In both groups of experiments, FSP root rot severity ratings were determined at 28 and 56 days after sowing. Five plants were randomly picked off from each experimental unit and damage was evaluated by using the scale described by Abawi and Pastor-Corrales [6]. The scale has nine degrees of damage (1–9) where 1 = no symptoms and 9 = more than 75% of root or stem tissues infected by the pathogen. We took the values 1–3 as a reaction of resistance, while

**Experiment I**

Early			Late		
PT Villa	PT Zapata	AZ Tapatío	Tlaxcala 62	FM M38	BY Criollo del Llano

**Experiment II**

Pintos		Flor de Mayo		Blacks	
PTD-99036	PTD-99099	FMD-99121	FMD-99009	NGD-99048	NGD-99029
PTD-99004	PTD-99057	FMD-99018	FMD-99022	NGD-99040	NG Sahuatoba
PTD-9903	PTD-99108	FMD-99035	FMD-99001	NGD-99010	NG Altiplano
PTD-99015	PTD-99092	FMD-99004	FMD-99005	NGD-99039	NG Vizcaya
PTD-99008	PTD-99044	FMD-99034	FMD-99010	NGD-99005	NG Otomí
PTD-99002	PTD-99013	FMD-99002	FMD-99007	NGD-99025	NG 8025
PTD-99107	PTD-99100	FMD-99033	FMD-99012	NGD-99028	NG San Luis
PTD-99035	PTD-99068	FMD-99006	FM Sol	NGD-99011	
PTD-99043	PT Villa	FMD-99005	FM 2000	NGD-99004	
PTD-99014	PT Mestizo	FMD-99008	FM M38	NGD-99044	
PTD-99046	PT Bayacora	FMD-99011	FJ Marcela	NGD-99023	
PTD-99034	PT Zapata	FMD-99013	FM Nura	NGD-99012	
PTD-99045		FMD-99019		NGD-99030	

**Experiment III**

RAB-608	RJB	SEA 17	SEA 23	G 40068	Tío Canela 75
RAB-609	RAB-632	SEA 18	INB 35	G 40159	DOR 390
RAB-618	RAB-650	SEA 19	INB 36	G 21212	PT Villa
RAB-636	RAB-651	SEA 20	INB 37	G 1977	Apetito
RAB-619	SEA 15	SEA 21	INB 38	SEA 5	FM Sol
RAB-620	SEA16	SEA 22	INB 39	BAT 477	FM 2000

**Irrigated-Rainfed Experiment**

G 17427	G 13637	G 842	97RS110	PT Zapata	AZ Namiquipa
G 14645	G 19012	G 4258	DON35	MD 23–24	ICA Quimbaya
G 22923	G 19953A	G 801	DON38	VAX 2	NG Veracruz
G 1836	G 2774	G 18147	BY San Luis	SEA 5	Black Jack
G 17666	G 16054	G 4364	97RS101	TLP 19	NG Huasteco 81
G 1354	G 16054	G 3386	NG Durango	MC 6	
G 6762	G 21137	G 1977	NG 8025	B98111	
G 1688	G 2846	G 3107	G 4523	NG INIFAP	
G 14538	G 847	SEA10	PT Villa		

Prefix indicates seed coat color or commercial type: PT = 'Pinto', AZ = 'Azufrado' (Yellow), FM = 'Flor de Mayo', BY = 'Bayo' (Cream or beige), FJ = 'Flor de Junio' and NG = Black.

**Table 1.** Germplasm included on field experiments at Sandoval and Chapingo, México.

values of 4–9 indicated susceptibility. Plants were analyzed at laboratory in order to ratify the infection by FSP [11]. Days to flowering and to maturity were registered in each experimental unit in all experiments, and grain yield ( $\text{kg h}^{-1}$ ) registered after physiological maturity.

Data were subjected to analysis of variance (ANOVA). When ANOVA detected significant ( $P < 0.05$ ) differences among treatments, Tukey significant difference values (Tukey LSD,  $P = 0.05$ ) were calculated for mean comparisons. Statistical analysis was performed using Statistical Analysis System version 6.12 and Statistica version 6.0 for Windows.

### 2.3. Genetic basis of resistance to root rot pathogens in selected common bean cultivars

We selected two common bean genotypes based on their contrasting reaction to FSP under both controlled and field conditions: BAT 477 (resistant) and Pinto UI-114 (susceptible). Crosses between the two parents were carried out under greenhouse conditions at Chapingo, México during 2002.  $F_1$  to  $F_8$  seeds were obtained in successive sowings in different locations of México. Reactions to a highly virulent isolate of FSP were measured in  $F_{9:10}$  recombinant inbred lines [3]. A genetic linkage map was built with genotypic data obtained with 30 + 3/+3 AFLP. QTLs associated with resistance to FSP were identified using R software ver. 2.10.1 [14, 15].

## 3. Results

### 3.1. Variability of FSP isolates from Aguascalientes, México

Nineteen isolates of *Fusarium* were obtained from different locations of Aguascalientes, although most of them were collected in Pabellón. Ten isolates were FSP and the other nine were *F. oxysporum* f. sp. *phaseoli* (FOP). As controls, isolates from Guanajuato, México and Veracruz were included. FSP and FOP isolates showed a great variability on morphology (**Figure 1**). Most of the isolates showed radial growth of colony, purple color of colony and variation on mycelial production and conidia size and shapes (**Table 2**). Most of the common bean cultivars were susceptible to most of FSP isolates, mainly those from Mesoamerican genetic race. AFLP molecular markers clearly separated FSP isolates from FOP isolates, but pathogenicity patterns were not associated with *Fusarium* species (**Table 3**) [11].

Significant differences were found in morphology, pathogenicity and AFLP genotype among isolates. Isolates from Veracruz, Guanajuato and Aguascalientes grew faster *in vitro* than those from México and showed the largest conidia. The most pathogenic isolates were from Aguascalientes and Mexico. Bean cultivars with Flor de Mayo (Jalisco race) and Pinto (Durango race) seed coat showed the highest frequencies of resistance to the most of FSP isolates (**Table 2**). Isolates from the State of Mexico were genetically different from the other isolates with genetic dissimilarity of >9% [4].



Figure 1. *In vitro* variation of *F. solani* f. sp. *phaseoli* isolates from Aguascalientes, México.

Isolate	Origin	Growth pattern	Color of colony	Conidia ( $\mu\text{m}$ )			Aerial mycelium
				Length	Width	L/W	
AGS01	Sta. Rosa	Radial	Pink	1.42	0.48	2.97	+
AGS02	Pabellón	"	Purple	1.49	0.55	2.72	—
AGS03	El Novillo	"	"	1.31	0.53	2.48	+
AGS04	Pabellón	"	"	0.73	0.33	2.20	—
AGS05	Sta. Rosa	"	White	1.32	0.40	3.31	+
AGS06	Pabellón	"	"	1.92	0.91	2.11	+
AGS07	Pabellón	"	Purple	1.22	0.34	3.62	+
AGS08	Sta.Rosa/Loreto	"	White	1.38	0.52	2.68	+
AGS09	"	"	Dark purple	1.26	0.37	3.45	—
AGS10	Pabellón	Irregular	Pink	1.19	0.46	2.61	+
AGS11	Pabellón	Radial	Purple	1.43	0.34	4.19	+
AGS12	El Molino	"	Dark purple	2.41	0.64	3.81	—
AGS13	Pabellón	"	Purple	1.33	0.32	4.23	—
AGS14	Pabellón	"	White	1.20	0.45	2.67	+
AGS15	Pabellón	"	Pink	1.33	0.40	3.35	+
AGS16	La Luz	"	White	0.86	0.32	2.60	+
<b>Mean</b>				<b>1.48</b>	<b>0.46</b>	<b>2.89</b>	

Isolate	Origin	Growth pattern	Color of colony	Conidia (µm)			Aerial mycelium
				Length	Width	L/W	
VER01	Cotaxtla	Radial	White	1.94	0.72	2.69	+
GTO01	Irapuato	Radial	"	1.27	0.48	2.65	+
MEX01	Texcoco	Irregular	Yellow	1.28	0.47	2.72	+
<b>Mean</b>				<b>1.50</b>	<b>0.56</b>	<b>2.69</b>	

**Table 2.** Morphological *in vitro* characteristics of *F. solani* f. sp. *phaseoli* isolates from Aguascalientes, México.

### 3.2. Reactions of common bean germplasm to root rot pathogens under field conditions

**Experiment I.** The greatest root rot severity was found in Flor de Mayo M38, Pinto Zapata, and Azufrado Tapatío, while Pinto Villa, Tlaxcala 62 and Bayo Criollo del Llano showed the low severity. Tlaxcala 62, Bayo Criollo del Llano and Flor de Mayo M38 were more later than Pinto Villa, Azufrado Tapatío and Pinto Zapata. Pinto Villa, Azufrado Tapatío and Pinto Zapata exhibited the best agronomic characteristics (**Table 4**). A negative association between seed yield and root rot severity at vegetative and reproductive stages was found. Seed yield was negatively associated to days to flowering and days to maturity, while phenology was positively related to harvest index. Harvest index was found to be negatively associated to days to flowering and days to maturity. A positive relationship between root rot severity at vegetative and reproductive stage was found (**Table 5**).

Germplasm seed coat color/type (genotypes)	Genetic race	Resistance (%)	Susceptibility (%)
<b>48 Mexican FSP isolates</b>			
Flor de Mayo (FM Sol, FM Bajío, FM M38)	Jalisco	47	53
Pintos (PT Villa, PT Mestizo, PT Zapata)	Durango	47	53
Bayos (BY Zacatecas, BY Madero, BY Criollo del Llano)	Durango	29	71
Black/Yellow (NG Altiplano, NG Vizcaya, Tlaxcala 62)	Durango/ Mesoamérica/Jalisco	7	12
<b>10 Aguascalientes FSP isolates</b>			
Mesoamérica (BAT 477, TLP 19, SEQ 12, NG 8025, Río Tibagí)	Mesoamérica	32	78
Durango (BY Durango, PT Villa, PT UI-114)	Durango	13	87
Jalisco (BY Mecentral, AZ Tapatío)	Jalisco	10	90

**Table 3.** Resistance/susceptibility percentages in common bean germplasm classified by genetic races in response to inoculation with *F. solani* f. sp. *phaseoli* isolates.

Experiment	Classification	Genotype	Days to flowering	Days to maturity	Seed yield (kg h <sup>-1</sup> )	Root rot severity
I	Early	PT Villa	44	89	778	4.9
		PT Zapata	42	86	703	6.6
		AZ Tapatío	43	89	719	6.2
		<b>Mean</b>	<b>43</b>	<b>88</b>	<b>733</b>	<b>5.9</b>
	Late	FM M38	56	98	547	6.9
		Tlaxcala 62	56	109	597	5.0
		BY Criollo del Llano	56	100	546	5.0
		<b>Mean</b>	<b>56</b>	<b>102</b>	<b>563</b>	<b>5.6</b>
		Tukey (P = 0.05)	1	1	218	0.9
II	Pinto-Resistant	PTD-99057	50	97	782	3.5
		PTD-99092	36	88	739	3.5
		PTD-99004	46	96	871	3.6
		<b>Mean</b>	<b>44</b>	<b>94</b>	<b>797</b>	<b>3.5</b>
	Pinto-Susceptible	PT Mestizo	38	88	877	5.8
		PTD-99008	43	96	1056	5.8
		PT Zapata	36	88	705	5.7
		<b>Mean</b>	<b>41</b>	<b>91</b>	<b>879</b>	<b>5.8</b>
	Flor de Mayo-Resistant	FMD-99033	40	91	594	3.3
		FMD-99019	42	97	747	3.7
		FMD-99004	44	88	884	3.7
		<b>Mean</b>	<b>42</b>	<b>92</b>	<b>742</b>	<b>3.6</b>
	Flor de Mayo-Susceptible	FMD-99022	44	92	810	6.0
		FMD-99013	40	88	825	5.9
		FMD-99002	39	90	768	5.9
		<b>Mean</b>	<b>41</b>	<b>90</b>	<b>801</b>	<b>5.9</b>
	Black-Resistant	NG Otomí	43	98	1000	2.3
		NG 8025	54	96	855	2.4
		NGD-99023	50	97	1003	2.6
		<b>Mean</b>	<b>49</b>	<b>97</b>	<b>953</b>	<b>2.4</b>
Black-Susceptible	NG Altiplano	51	97	848	3.9	
	NGD-99040	46	100	1055	3.9	
	NGD-99028	44	99	963	3.8	
	<b>Mean</b>	<b>47</b>	<b>99</b>	<b>955</b>	<b>3.9</b>	
	Tukey (P = 0.05)	3	2	290	1.5	



Experiment	Classification	Genotype	Days to flowering	Days to maturity	Seed yield (kg h <sup>-1</sup> )	Root rot severity
III	Resistant	SEA 20	46	93	798	1.6
		RAB 636	43	91	689	2.6
		BAT 477	47	95	1052	2.6
		<b>Mean</b>	<b>45</b>	<b>93</b>	<b>846</b>	<b>2.3</b>
	Susceptible	FM 2000	47	101	862	9.0
		SEA 16	43	91	780	5.3
		SEA 15	43	91	688	4.9
		<b>Mean</b>	<b>44</b>	<b>94</b>	<b>777</b>	<b>6.4</b>
	Tukey (P = 0.05)	4	5	504	3	

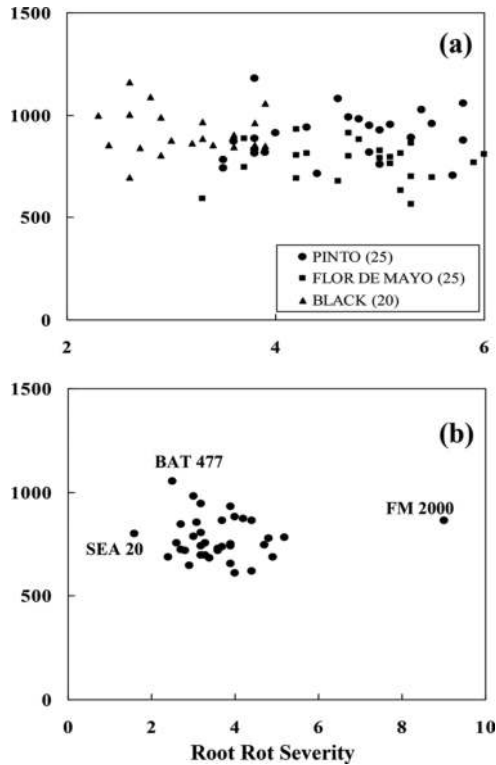
**Table 4.** Phenology, seed yield and root rot severity in common bean germplasm grown in Aguascalientes, México.

Characteristic	Root rot severity (56 d after sowing)	Days to flowering
<b>Experiment I</b>		
Seed yield	-0.25NS	-0.54**
Days to flowering	-0.17NS	
<b>Experiment II</b>		
Seed yield	-0.11NS	0.29**
Days to flowering	-0.10NS	
<b>Experiment III</b>		
Seed yield	-0.07NS	0.02NS
Days to flowering	-0.09NS	
<b>Combined irrigated-rainfed experiment</b>		
Seed yield	-0.25**	0.18**
Days to flowering	0.12*	

\*(p≤0.05); \*\*(p≤0.01).

**Table 5.** Pearson's correlation coefficients (r) among characteristics of common bean grown in experiments conducted at Sandoval and Chapingo, México.

**Experiment II.** No clear relationship between root rot severity and seed yield was found (Figure 2a; Table 5). Grain yields ranged from 500 to 1250 kg h<sup>-1</sup>, but we found a clear differentiation among cultivars by reaction to root rots on the basis of seed coat color. Resistance was more frequent in black beans while intermediate reactions were found in Flor de Mayo germplasm and susceptibility was found in pinto beans. No differences on grain yield were detected between resistant and susceptible genotypes in any seed color type. Resistance was common in bred cultivars, as can be seen in pinto or Flor de Mayo bean types (Table 4).



**Figure 2.** Relationship between root rot severity caused by *F. solani* f. sp. *phaseoli* and grain yield in common beans: (a) experiment II and (b) experiment III.

**Experiment III.** As found in E-II, no clear relationship between root rot severity and seed yield was detected in this experiment (**Figure 2b**; **Table 5**). All 36 genotypes showed grain yields ranged from 550 to 1100 kg h<sup>-1</sup>. Here, we found that most of germplasm showed a root rot severity ranged from 2 to 5.5 (intermediate), while grain yield ranged from 550 to 1000 hg h<sup>-1</sup>. Only three cultivars were clearly different from all other cultivars: BAT 477 (that showed the highest seed yields), SEA 20 (that exhibited the lowest root rot severity) and Flor de Mayo 2000 (that showed the highest root rot severity). No differences can be appreciated on days to flowering or days to maturity or seed yield between resistant and susceptible cultivars (**Table 4**).

**Rainfed-irrigated experiment.** In Chapingo, germplasm showed later biological cycle and greater seed yields and root rot severity than at Sandoval. In both locations, rainfed conditions reduced seed yields and increased root rot severity (**Table 6**). In this experiment, negative relationship between seed yield and root rot severity was more clear than other experiments and a positive association was found between seed yield and days to flowering and flowering and root rot severity (**Table 5**). The relationship between root rot severity and grain yield exhibited different patterns across locations. In Sandoval, we found a greater variation on root rot severity on the germplasm, while an opposite response was found at Chapingo.

	Days to flowering	Seed yield (kg ha <sup>-1</sup> )	Root rot severity (56 d after sowing)
<b>Experiment Sandovalés</b>			
Rainfed	49	622	5.7
Irrigated	48	1141	4.6
<b>Experiment Chapingo</b>			
Rainfed	53	940	6.3
Irrigated	54	1730	5.4
Tukey (P = 0.05)	1	109	0.7
<b>Resistant genotypes</b>			
G 2494	53	982	4.0
G 4258	44	1015	4.1
97RS101	52	1273	4.3
NG 8025	54	1303	4.6
PT Zapata	44	1303	4.6
<b>Mean</b>	<b>49</b>	<b>1175</b>	<b>4.3</b>
<b>Susceptible genotypes</b>			
G 801	52	947	8.1
SEA 5	51	588	7.7
G 14538	58	653	7.1
G 4523	48	1094	7.0
G 14645	46	763	6.7
<b>Mean</b>	<b>51</b>	<b>809</b>	<b>7.3</b>
Tukey (P = 0.05)	2	556	2.4

**Table 6.** Agronomical characteristics on common bean germplasm under rainfed-irrigated conditions in two locations of México.

An opposite pattern was found in grain yield because higher seed yields were found at Chapingo (50–1880 kg h<sup>-1</sup> under rainfed conditions and 230–3300 kg h<sup>-1</sup> under irrigated conditions) than Sandovalés (150–1150 under rainfed and 500–2300 kg h<sup>-1</sup> under irrigated conditions) (**Figure 3a and b**). No differences on days to flowering are detected between the two groups of genotypes, but resistant germplasm exhibited greater seed yields than susceptible cultivars (**Table 4**).

### 3.3. Genetic basis of resistance to root rot pathogens in selected common bean cultivars

Genetic analysis identified one QTL significantly associated with resistance to FSP in BAT 477 growing under controlled conditions. This QTL explained 2.7% of variation in response to the disease and the marker was found at LG 5 [16].

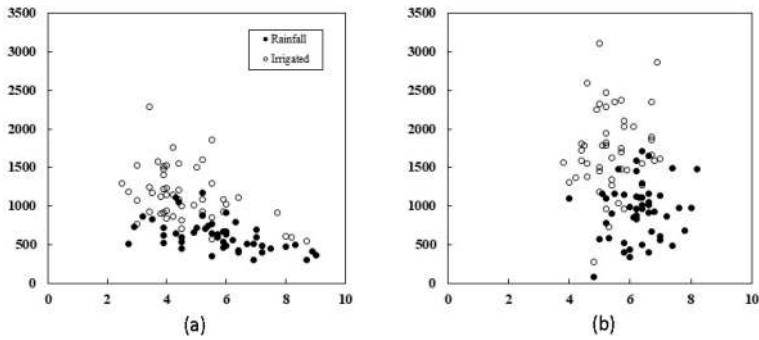


Figure 3. Relationship between root rot severity caused by *F. solani* f. sp. *phaseoli* and grain yield in 49 common bean genotypes under two soil moisture regimes: (a) Sandoval, Aguascalientes and (b) Chapingo, State of México, México.

## 4. Discussion

### 4.1. Variability of *Fusarium solani* f. sp. *phaseoli* from Aguascalientes, México

A high morphologic, pathogenic and genetic variability was found in FSP isolates from Aguascalientes, despite the identical host (common beans) and geographical origin. In addition, no relationship among morphology, pathogenicity and genotype was found. Our results indicated the high values of genetic variability in the species due to the presence of heterokaryosis and parasexualism as genetic exchange mechanisms between vegetative compatible isolates. Single members of the same vegetative compatibility group (VCGs) are genetically similar and they are related on basis of genetic lineages [17]. The characterization of VCGs on *Fusarium* isolates from Aguascalientes and other regions of México could clarify the association among *Fusarium* populations and genetic lineages. This research confirmed the diverse and heterogeneous nature on the genus. Host specialization could be useful to establish artificial taxonomic divisions and to perform pathogenic groups and *formae speciales*. However, the host plays an important biological role in selection pressure to the fungus. In addition, the genetic exchange between isolates is supported by the development of VCGs or other strategies for DNA transmission. The evolution of pathogenicity and VCGs contribute to increase in molecular variability. Further research that includes traditional and molecular methodologies will improve the knowledge and understanding of *Fusarium* biodiversity.

The most of common bean cultivars were susceptible to most of FSP isolates, and all isolates were pathogenic to common beans. This result is opposite to Cramer et al. [18]. Most of the resistant germplasm belonged to Mesoamerica of Jalisco genetic races, while susceptible cultivars are classified as Durango race. High frequencies of resistance to other root rot pathogen (*Macrophomina phaseolina*) of common beans were found in Mesoamerican beans [19].

Results suggest that resistance to root rot pathogens in common beans could be operating as a resistance gene cluster that controls similar strategies to defend roots and stems against root rot fungi. Further research could confirm this suggestion. No clear association between host and fungus genotypes was found; this relation was reported in *M. phaseolina*-common beans [20] in contrast with other biotrophic pathogens of common bean as *Colletotrichum lindemuthianum* [21], where a clear formation of genetic lineages based on geographical origin was found.

#### **4.2. Reactions of common bean germplasm to *F. solani* f. sp. *phaseoli* under field conditions**

A high variation on reactions to FSP was found in both locations and no immunity was found, while no immunity to root rot pathogens in common bean germplasm was detected previously [8, 22, 23] in Pabellón de Arteaga, Aguascalientes and Chapingo, State of México. No clear association between root rot severity and seed yield or phenology was found in all experiments. However, results indicated that resistance to FSP was more frequent on black beans, while susceptibility was common on pinto beans, which has been found in previous works [20, 22]. Results suggest that black beans from Mesoamerican race could provide resistance to FSP in México. Under rainfed conditions, genotypes as BAT 477 and SEA 20 stood out for their high seed yields and resistance to root rot pathogens. BAT 477 has showed a consistent resistance to root rot pathogens such as *Fusarium*, *Rhizoctonia* and *Macrophomina* [20, 22, 24].

In both locations, rainfed conditions reduced seed yields and increased root rot severity in common bean germplasm. Navarrete-Maya et al. [23] reported a positive relationship between rain precipitation and *Fusarium* severity in Chapingo. We suggest that low water availability increased physiological stress in the host. Therefore, host defense mechanisms are not efficient to arrest fungal infection or for slow pathogenesis. The relationship between root rot severity and grain yield exhibited different patterns, since a broad variation on root rot severity on the germplasm (Sandoval) or an opposite response (Chapingo). Opposite patterns in grain yields were found, the highest seed yields were found in Chapingo and the lowest in Sandoval. Our data suggested that climate and fungi conditions of Sandoval are more appropriate for common bean germplasm screening for resistance to root rot pathogens under field conditions than Chapingo.

#### **4.3. Genetics of resistance to *Fusarium solani* f. sp. *phaseoli* in common bean cv. BAT 477**

Genetic analysis identified one QTL significantly associated with resistance to FSP in BAT 477 growing under controlled conditions. This QTL explained 2.7% of variation in response to the disease and the marker was found at LG 5 [16]. Identification of few QTLs with high effects on explanation of phenotypic variation is important and promising to simplify the

introgression of resistance genes to susceptible germplasm. However, our results indicated a low genetic effect of the QTL detected in BAT 477. Therefore, a more intensive searching of significant QTLs is needed. Genetic map development allows identification and use of genes and genomic regions (QTLs) with economic interest and then develops marker-assisted selection (MAS) strategies [25]. Vallejos et al. [26] performed the first gene map of common beans using morphologic, isozymes and RFLP markers. Then, Schneider et al. [27] identified 16 QTLs associated with *F. solani* f. sp. *phaseoli* resistance in  $F_{4,6}$  RILs derived from Montcalm (susceptible) × FR266 (resistant). These QTLs were mainly found on LGs 2 and 5, and seven QTLs explained 64% of disease resistance. Chowdhury et al. [28] identified two QTLs associated with FSP resistance and explaining 50% of phenotypic variance using  $F_{2,6}$  RILs from AC Compass (susceptible) × NY2114–12 (resistant), while Román-Avilés et al. [29] identified nine QTLs associated with resistance to FSP in  $F_{4,5}$  inbred backcross populations from Red Hawk (susceptible) × NG San Luis (Resistant) and C97407 (susceptible) × NG San Luis, which explained from 5 to 53% of phenotype variation and located mainly at LGs 1 and 7.

## 5. Conclusions

We found significant genetic variability in FSP isolates from Aguascalientes and other regions of México although no clear association among morphology, pathogenicity or AFLP genotype was detected.

Under field conditions, we found high variation on reactions to FSP root rots; resistance was more frequent on black seed-coated beans, while susceptibility was common in pinto beans. We found a greater variation on root rot severity disease in Aguascalientes when compared with State of México, while an opposite response on grain yields was found across locations.

One QTL with low variance explanation of FSP resistance in BAT 477 was found; therefore, more intensive searching of significant QTLs is needed to improve marker-assisted selection strategies in common beans for México.

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