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Hellenic Plant Protection Journal **14:** 14-23, 2021
DOI 10.2478/hppj-2021-0002

Infections of bean plant and field soil are linked to region, root rot pathogen and agro-ecosystem

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Summary Understanding pathogen-agrosystem interaction is particularly essential when applying a control method to minimize pathogen prevalence prior to plant infection. To meet this requirement, frequency of major root rot pathogens isolated from bean root and seed, and their soil populations were examined in farmers' fields. Multivariate analyses evidenced more frequent isolations of *Fusarium solani* and *Rhizoctonia solani* from root and seed compared to *Macrophomina phaseolina* and *Fusarium oxysporum*. Two Fusarium species had denser soil populations than *R. solani* and *M. phaseolina*. More frequent isolations of pathogens were detected in root and seed collected from Abhar and Khodabandeh compared to Kheirabad region. Agronomic and soil variables corresponded less closely to root infections compared to soil infestation and seed infections. Bean market class, herbicide application, and planting depth were linked to root, seed and soil infestations. Such information provides a basis for increased confidence in choosing appropriate control strategies for a pathogen and region in sustainable agriculture.

Additional keywords: Fungus, Legume, *Phaseolus vulgaris,* principal component analysis, soil-borne

Introduction

Common or dry bean (*Phaseolus vulgaris* L.) is considered as an essential legume food crop in Iran where more than 116,000 ha of bean crops are planted annually (Anonymous, 2014). Under various soil and environmental conditions, soil-borne pathogens may infect beans in any possible combination and cause root-rot-disease complexes (Abawi and Pastor Corrales, 1990; Naseri and Hemmati, 2017).

Our earlier findings based on assessing commercial bean fields demonstrated that the most prevalent of root rot pathogens are: *Fusarium solani* (Mart.) Saec. f. sp. *phaseoli* (Burk.) Snyd. and Hans, *Rhizoctonia solani* Kuhn, *Macrophomina phaseolina* (Tassi) Goid., and *F. oxysporum* Schlechtend:Fr. Moreover, reductions in Zanjan's bean production due to root rots could be estimated as high as 65% (Naseri, 2008). Later and shallower planting, irrigating at 6-9 days intervals, herbicide and manure use, higher soil organic matter and rhizobial nodulation, manual seeding, proper plant density, and sprinkler irrigation lowered root rot diseases and crop damage by these pathogens (Naseri and Tabande, 2017). Furthermore, growing beans after maize and seed treatment with fungicide lowered Fusarium root rot caused by *F. solani* and improved bean productivity (Naseri and Marefat, 2011; Naseri, 2014a; Naseri *et al*., 2016). Growing beans after potato and tomato decreased Rhizoctonia root rot caused by *R. solani* (Naseri and Moradi, 2015). High soil pH and sand use, and growing beans following legumes or cereals use intensified charcoal root rot caused by *M. phaseolina* (Naseri, 2014b). Cultivation in sandy soil with neutral pH reduced Fusarium wilt caused by *F. oxysporum* (Naseri, 2014c).

Although the above-mentioned studies focused on measuring disease symptoms in interaction with agro-ecological conditions, associations of agro-ecosystem with pathogens populations in bean root and

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seed, and field soil is little understood. Naseri and Mousavi (2015) examined interrelationships among development of root rots, bean yield and populations of pathogens isolated from root, seed and soil, which revealed that the intensity and spread of bean root rots are linked to high soil populations of *R. solani* and *F. solani* (Naseri and Mousavi, 2015). Hence, a better epidemiological understanding of agro-ecological indicators of pathogens populations in the plant and soil affecting this disease complex deserves more consideration. Moreover, based on our multi-point assessments over the bean growing season (Naseri and Mousavi, 2015), fungal species and experimental sites affected isolations of *F. solani*, *R. solani*, *M. phaseolina* and *F. oxysporum* from seed, soil and root. Based on this research, it would be interesting to compare these soil-borne pathogens for their potential to infect root, seed and soil in the bean-root-rot pathosystem. Furthermore, information on association of the region and cropping system with infections of the root, seed and soil by root rot pathogens would assist in identifying the importance of inoculum sources for each pathogen and region under commercial production conditions to improve experimental designs for disease control and sustainable agronomy purposes. Thus, the objectives of this investigation were to: (1) evaluate the effect of pathogen on frequencies of *F. solani*, *R. solani*, *M. phaseolina* and *F. oxysporum* isolated from root, seed and soil samples, (2) determine the influence of region on infections of root, seed and soil by the pathogens, and (3) compare the correspondences of pathogens infecting either root, seed or soil with 14 agronomic and soil descriptors.

Materials and Methods

Experimental site assessment

The present study area was estimated at 6149 ha in a North-Western part of Iran, Zanjan, with a cold semi-arid climate, hot and dry summer season from June to September. Zanjan province has 315.4 mm and 11.7°C mean annual rainfall and temperature, respectively. To assess soil populations of major root rot pathogens, 13 producers' fields were randomly selected from the main bean growing region as representative experimental sites. Agronomic and soil characteristics of the fields are represented in Table 1.

The methodology of collecting plant, seed and soil samples, fungal isolation, identification and pathogenicity confirmation have been reported earlier (Naseri and Mousavi, 2015). Briefly, monosporic isolates of *Fusarium* spp. isolated from root, seed and soil samples were transferred to carnation leaf agar and identified to species level according to key characteristics provided by Nelson *et al.* (1983). Isolates of *F. solani* f. sp. *phaseoli* were specified according to the greenhouse studies followed by specific molecular detection (Khodagholi *et al.,* 2013).

The following samples were collected at pod maturity stage of bean growth from either of three observations per field: (1) two to four symptomatic plants (wilt and yellowing along with cankered and discolored roots); (2) seeds of 50 bean plants; (3) four samples (*ca* 1 kg in total) from the soil surrounding bean roots.

Laboratory assessment

Concisely, four pieces per symptomatic root were surface sterilized (for 2 min in 1% NaOCl) and then cultured on potato dextrose agar (PDA, Difco, Detroit, MI, USA). After identification, isolation frequencies of *F. solani*, *R. solani*, *M. phaseolina* and *F. oxysporum* were defined as the total number of isolations of each fungal pathogen from all root segments (four 1 mm^3 pieces per root) per root sample expressed as percentage (Naseri, 2008).

A subsample of 12 seeds (48 seeds in total per field) from each seed sample, were surface sterilized, rinsed in sterile distilled water, and then placed onto PDA amended with 30 mg l^{-1} streptomycin (streptomycin sulfate, Sigma, St Louis, MO). After purification and identification, the isolation

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Table 1. Agronomic and soil properties of commercial bean fields studied.

Factors	Fields												
	1	2	3	4	5	6	7	8	9	10	11	12	13
Bean market class[a]	P	W	R	R	R	P	R	R	R	P	R	R	W
Field size (ha)	2	2	1.2	1	1	0.5	1	1.5	1	0.3	3	0.3	2
Herbicide[b]	T	P	T	T	0	B	T	T	R	T	T	T	P
P-Fertilizer[c]	1	1	0	0	1	1	0	0	0	1	0	0	1
Planting date (day)	26	30	30	30	30	27	35	30	30	30	10	16	20
Planting depth (cm)	5	4	4	5	15	5	10	10	7	6	10	5	8
Previous crop[d]	W	A	W	W	B	P	P	A	A	W	W	P	W
Region[e]	A	A	A	A	A	K	K	K	K	K	O	O	O
Soil EC (ds/m)	1.3	3.6	3.5	1.3	2.9	1.7	2.2	1.1	2.1	3.3	1.8	1.5	1.5
Soil pH	7.7	7.4	7.6	7.7	7.5	7.5	7.5	7.4	7.7	7.7	7.8	7.5	7.4
Clay (%)	24	38	32	44	30	36	31	44	32	38	44	32	40
Sand (%)	54	32	36	26	36	28	38	18	36	28	14	36	28
Silt (%)	22	30	32	30	34	36	31	38	32	34	42	32	32
Urea[c]	1	1	1	0	1	0	1	0	1	1	1	0	0

[a] P = Pinto, R = Red, and W = White beans.
[b] B = bentazon, P = paraquat, R = roundup, and T = trifluralin.
[c] 0 = Not applied and 1 = applied.
[d] A = Alfalfa, B = bean, P = potato and W = wheat.
[e] A = Abhar, K = Kheirabad and O = Khodabandeh.

frequencies of each major root rot pathogen was determined as the total number of isolations from 12 seeds expressed as a percentage (Naseri and Mousavi, 2015).

For soil samples, 1 ml aliquots of the 10^{-4} dilution of a soil subsample in Ringer's solution were plated on soil-extract-streptomycin-agar (James, 1958). The number of colony forming units (CFU) per gram for the four root rot pathogens was counted. Thus, 52 soil samples collected from 13 fields were examined (Naseri and Mousavi, 2015).

Statistical analysis

In an attempt to improve data homogeneity, data for the soil populations of root rot pathogens at pod maturity stage were log-transformed before statistical analysis. In order to simplify interpretations of significant associations within the large data set, principal component analysis (PCA) was used to compare root rot pathogens infecting root, seed and soil between bean growing regions (R software, Development Core Team, 2006). Thus, a total of 12 infection variables were described for the three infection courts (root, seed and soil) and four fungal pathogens. The non-metric variables, pathogen species and region, were regarded as factors in the first and second PCAs to determine the significant differences in the soil populations and frequencies of isolations from roots and seeds between the pathogens and regions. The PCA method enabled joint analysis of the regional information at which variables were of a heterogeneous nature. This also allowed us to reduce the number of variables accounting for the total variance in the dataset. A new variable, which was defined by PCAs, combined the 12 infection variables into a linear regression. The significance of differences was examined using Monte Carlo permutation tests. The third PCA compared the associations of agronomic and soil variables with root, seed and soil infestations.

Results

Pathogen effect

All the four major bean-root-rot patho-

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gens, *F. solani*, *R. solani*, *M. phaseolina* and *F. oxysporum*, were isolated from root, seed and soil samples collected from the 13 farmers' fields studied as experimental sites. In the two-dimensional plot of the first PCA (PCA1) based on frequencies of the pathogens isolated from roots and seeds, and soil populations examined at 13 experimental sites, the first principal component (PC1) accounted for 57.6% of the total data variance. The horizontal axis, PC1, was termed as plant infection indicator due to receiving high positive loadings from frequencies of the four pathogens isolated from roots (0.86) and seeds (0.89; Fig. 1). PC1 accounted for the largest proportion of the total variance and may, therefore, be considered as the major descriptor of infections caused by bean-root-rot pathogens under production field conditions.

The vertical axis, PC2, captured 30.2% of the data variance. This PC was termed the soil infestation indicator because of having a high positive loading (0.89) for the density of root-rot-pathogen populations in field soils (Fig. 1). This significant contribution of pathogens populations in the soil to the second PC of PCA1 demonstrated the considerable role of prevalence of the bean-root-rot pathogens studied in field soil to characterize fungal infections associated with this complex soil-borne disease in bean crops.

The multivariate analysis, PCA1, demonstrated that the infection of root, seed and soil significantly differed among the four major root rot pathogens (Monte Carlo permutation test; $P = 0.0019$; Fig. 1). The horizontal axis, plant infection indicator, distinguished *F. solani* and *R. solani* from *M. phaseolina* and *F. oxysporum*, indicating more frequent isolations of *F. solani* and *R. solani* from root and seed samples in comparison with *M. phaseolina* and *F. oxysporum*. In addition, the highest and lowest plant infections were detected for *F. solani* and *F. oxysporum*, respectively. Based on the vertical axis, soil infestation indicator, *F. solani* and *F. oxysporum* were distinguished from *R. solani* and *M. phaseolina*. This indicated denser soil populations of the two Fusarium species than *R. solani* and *M. phaseolina* in the bean-root-rot pathosystems studied. *F. solani* and *R. solani* had the densest and sparest populations in the soils sampled from bean production fields.

Region effect

All the four major bean-root-rot pathogens, *F. solani*, *R. solani*, *M. phaseolina* and *F. oxysporum*, were isolated from root, seed

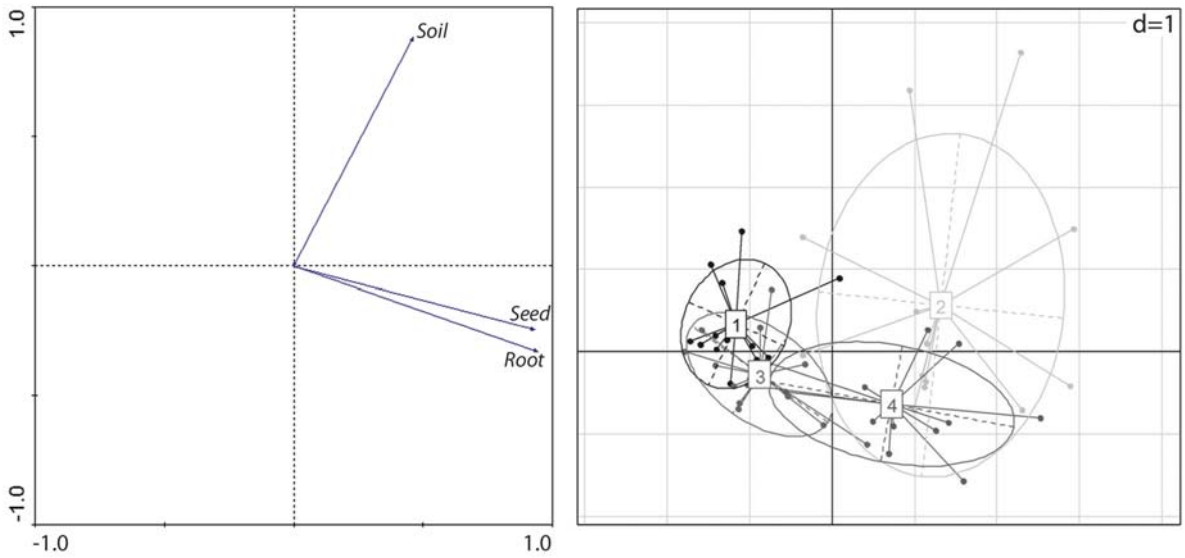


Figure 1. Principal component analysis (PCA1) of infections by *F. oxysporum* (1), *F. solani* (2), *Macrophomina phaseolina* (3) and *Rhizoctonia solani* (4) in bean root and seed, and field soil according to pathogen.

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and soil samples collected from the three study regions (Abhar, Kheirabad, Khodabandeh). According to the second PCA (PCA2), the infection of root, seed and soil significantly differed among the three main bean growing Zanjan's regions studied (Monte Carlo permutation test; $P = 0.079$; Fig. 2). The horizontal axis (plant infection indicator) of PCA2 distinguished Abhar and Khodabandeh regions from Kheirabad, indicating more frequent isolations of the pathogens from root and seed samples collected from Abhar and Khodabandeh when compared to Kheirabad region. In addition, the highest and lowest plant infections were detected for Khodabandeh and Kheirabad regions, respectively. Based on the vertical axis (soil infestation indicator), Abhar region was distinguished from Khodabandeh and Kheirabad regions. This indicated denser soil populations of the root rot pathogens in the soil of Abhar's bean fields compared to Khodabandeh and Kheirabad. Among the regions studied, the densest and sparest populations of the pathogens in the soils were sampled from bean fields located in Abhar and Kheirabad, respectively.

Association of infection with agro-ecosystem

According to the third PCA, the five principal components accounted for 75.1% of total data variance (Table 2). The first PC of PCA3 determined the associations of bean class and herbicide application with frequencies of *F. oxysporum* isolated from root and *F. solani*, *M. phaseolina* and *R. solani* isolated from seed samples. PC2 indicated linkages of bean class, P-fertilizer application and soil EC to frequencies of *F. oxysporum* and *F. solani* isolated from bean seed, and soil populations of *F. oxysporum* and *R. solani*. Based on loading values obtained for PC3, planting depth corresponded with isolation frequencies of *F. solani*, *M. phaseolina* and *R. solani* from bean root and soil population of *R. solani*. PC4 described relationships between planting depth, soil pH, urea application, frequency of *F. oxysporum* isolated from seed, and soil populations of *F. oxysporum* and *M. phaseolina*. Herbicide application, planting date and previous crop were associated with soil populations of *F. solani* and *R. solani* according to PC5 loadings.

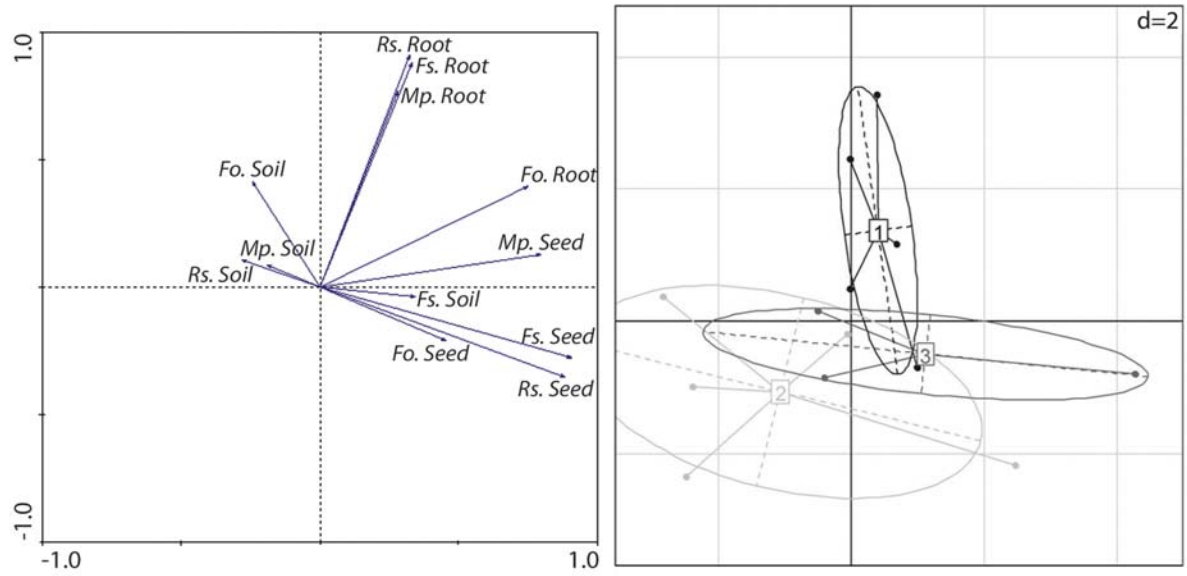


Figure 2. Principal component analysis (PCA2) of infections by *F. oxysporum* (Fo), *F. solani* (Fs), *Macrophomina phaseolina* (Mp) and *Rhizoctonia solani* (Rs) in bean root and seed, and field soil collected from Abhar (1), Kheirabad (2) and Khodabande (3) according to region.

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Table 2. Principal component analysis of infections by *F. oxysporum* (Fo), *F. solani* (Fs), *Macrophomina phaseolina* (Mp) and *Rhizoctonia solani* (Rs) in bean root and seed, and field soil in association with agronomic and soil properties.

Variables	Principal components				
	1	2	3	4	5
Bean market class	**0.28**[a]	**-0.28**	-0.23	-0.11	0.13
Crop grown before bean	0.08	0.05	-0.20	0.03	**0.30**
Date of planting	-0.07	-0.12	0.04	0.00	**-0.58**
Depth of planting	-0.17	-0.00	**0.27**	**-0.39**	0.00
EC of field soil	-0.04	**-0.36**	0.04	0.20	-0.20
Herbicide application	**0.31**	0.11	-0.19	0.05	**-0.28**
P-fertilizer application	0.13	**-0.39**	-0.15	-0.15	0.05
PH of field soil	-0.09	0.07	0.10	**0.34**	0.14
Sand content	0.14	-0.13	0.18	0.24	-0.21
Urea application	-0.07	-0.24	0.23	**0.29**	-0.12
Fo in root	**0.34**	0.01	0.24	0.23	0.14
Fo in seed	0.19	**0.26**	-0.04	**-0.27**	-0.05
Fo in field soil	0.17	**-0.26**	-0.19	**-0.31**	-0.10
Fs in root	0.21	-0.23	**0.38**	-0.05	0.02
Fs in seed	**0.35**	**0.27**	-0.03	0.21	0.02
Fs in field soil	0.20	-0.21	-0.15	-0.07	**-0.29**
Mp in root	0.14	-0.05	**0.42**	-0.07	0.17
Mp in seed	**0.39**	0.17	0.09	-0.14	-0.04
Mp in field soil	-0.02	-0.19	-0.20	**0.41**	0.12
Rs in root	0.23	-0.19	**0.35**	-0.12	0.16
Rs in seed	**0.34**	0.21	-0.08	0.18	-0.13
Rs in field soil	0.08	**-0.30**	**-0.26**	0.01	**0.39**
Eigenvalues	4.4	4.0	3.5	2.6	2.1
Percentage variation	19.8%	18.2%	15.8%	11.8%	9.5%

[a] Loading values were regarded significant (bold), if > 0.25.

Discussion

Comprehensive understanding of parameters that influence the patterns of pathogens spread within cropping systems provide the essential epidemiological information to develop more efficient disease management strategies and subsequently improve productivity. In field surveys like that performed by Sahile *et al.* (2008) in northern Ethiopia, influences of crop management practices on faba bean chocolate spot (*Botrytis fabae*) and soil population fluxes were determined. Bruton and Reuveni (1985) and Höper *et al.* (1995) looked at soil populations of *M. phaseolina* and *F. oxysporum,* respectively. Mengistu *et al.* (2009) also examined the combined effects of tillage, cover crop and herbicide use on root, stem and soil infestations by *M. phaseolina* at plot scale. However, no previous study has compared the relative infectivity of different bean root rot pathogens to plant and soil. In fact, all the previous studies looked at individual root rot pathogen, and thus, the joint interactions of four major root rot

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pathogens with the bean cropping system are little understood.

Comparative studies such as the present macro-scale research improve our understanding of pathogens prevalence in the crop and soil depending on pathogen and soil. Although Naseri and Mousavi (2015) reported interrelationships among root rot pathogens infecting root, seed and soil, the effects of pathogen and region on such associations remained little understood. The findings of the present study evidenced that specifications regarding pathogen prevalence for each inoculum source and cultivation area are required to be considered in organizing the integrated management of bean root rots as a complex disease. Such information may lead us to draw up specific root-rot-control programs corresponding to the pathogen and region, e.g. with avoiding unnecessary fungicide applications.

Although all four major bean-root-rot pathogens were isolated from root, seed and soil samples collected from the 13 experimental sites studied, their isolation frequencies from the root, seed and soil differed by pathogen based on our PCA results. The first principal component explained 58% of variance in the data on pathogens prevalence in bean roots and seeds, and field soils. The PC1 as plant infection factor also recognized root and seeds infections as more important descriptors of the bean-root-rot pathosystem compared to soil population. A large number of previous studies focused on evaluating patterns of *F. solani, F. oxysporum, M. phaseolina* and *R. solani* populations in the soil. For instance, Lodha *et al.* (1990) and Amir and Alabouvette (1993) looked at soil populations of *M. phaseolina* and *F. oxysporum*, respectively. According to the present findings, the assessment of root and seed infected by the pathogens under agro-ecological conditions should provide more accurate representations of these rhizospheric events for yield-estimate, disease-control, and resistance-screening purposes. Thus, estimating root and seed infections according to bean root rot intensity not only simplifies pathologists' tasks to quantify seed-borne inocula, but also improves our epidemiological insight for management purposes. Although the first part of this statement was achieved by Naseri and Mousavi (2015), the second aim was approached with the help of the present findings.

The similar PC1 loadings for the frequencies of pathogens isolated from roots and seeds evidenced a close importance of these two plant parts in being infected by the four pathogens. One may conclude that the level of bean root rots caused by *F. solani*, *F. oxysporum*, *M. phaseolina* and *R. solani* corresponds strongly to their seed infections. Provided that future small-scale experimentation confirms our observation, the infection of seeds could be estimated by detecting the frequency of pathogens isolated from bean roots at pod maturity. Considering the close linkage of bean root rot epidemics to root and seed infections (Naseri and Mousavi, 2015), it is possible to estimate infections of the root and seed according to an easier field-assessment of the disease. For instance, fungicidal treatment of seeds produced under severe bean-root-rot epidemics should be performed for a safe cultivation or consumption in sustainable agriculture.

Furthermore, PC2 recognized the soil population as the third important criterion of bean-root-rot pathogens prevalent in bean crops. The remainder of our multivariate analysis demonstrated significant differences in infections of root, seed and soil among the four major root rot pathogens. The plant infection axis evidenced greater colonization of bean roots and seeds by *F. solani* and *R. solani* compared to *M. phaseolina* and *F. oxysporum*. Under agronomic and environmental conditions encountered in this research, *F. solani* was identified as the most pathogenic causal agent of bean root and seed rots followed by *R. solani*, *M. phaseolina* and *F. oxysporum*. Considering the significant effect of Fusarium root rot caused by *F. solani* on bean production (Naseri and Mousavi, 2015), the priority of developing an integrated root-rot-control program should be set on those strategies that

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restrict *F. solani* colonization in beans. Furthermore, the soil infestation axis indicated denser soil populations of *F. solani* and *F. oxysporum* than *R. solani* and *M. phaseolina* in the bean-root-rot pathosystems studied. This time, the priority of soil management methods should be given to lowering the two Fusarium species prevalence in field soil. To the best of our knowledge, this is the first record of a joint comparison of *F. solani*, *F. oxysporum*, *M. phaseolina* and *R. solani* infecting root, seed and soil at a large scale of bean crops. This study added new information on comparisons of root and seed infections, and soil populations according to the pathogen and region factors supplementing existing knowledge reported by Naseri and Mousavi (2015).

Isolations of *F. solani*, *R. solani*, *M. phaseolina* and *F. oxysporum* from root, seed and soil samples were recorded for the three regions, Abhar, Kheirabad and Khodabandeh studied here. It was of interest to detect more prevalent infection court in each main bean growing area for setting research and disease-control priorities in accordance with regional infection levels. According to our PCA analysis, the intensity of plant and soil infestations varied depending on the region. The plant infection axis evidenced more frequent isolations of the root rot pathogens from roots and seeds collected from Abhar and Khodabandeh than from Kheirabad. The soil infestation axis indicated denser soil populations of the root rot pathogens in the soil of Abhar compared to Khodabandeh and Kheirabad. Thus, root-rot-control and soil-management strategies should be organized to limit the prevalence of *F. solani* and *F. oxysporum* more effectively than *R. solani* and *M. phaseolina* in bean plants of Khodabandeh and field soils of Abhar. Among the regions studied, the lowest plant infections and sparest soil populations of the pathogens were detected in Kheirabad.

The identification of agronomic and soil characteristics causing such regional differences in the prevalence of pathogens within the plant and soil could provide valuable information for developing disease control programs. The present results linked the pathogen populations in the soil to bean market class (Pinto, Red and White), herbicide and urea applications, P-fertilizer, planting date and depth, previous crop, soil EC and pH. Seed infections were associated with bean class, herbicide and urea applications, P-fertilizer, planting depth, soil EC and pH. Root infections also corresponded to bean class, herbicide application, and planting depth. Therefore, soil, seed and root infections by root rot pathogens were related to nine, seven and three agro-ecological variables tested in this study, respectively. To the best of our knowledge, this is the first report of comparing infections of root, seed and soil by bean root rot pathogens in association with a number of agronomic and soil variables under commercial field conditions across different geographical areas of Iran.

In conclusion, the agro-ecosystem was less influential on pathogens infecting the root when compared with pathogens occurring in the soil and the bean seed. Moreover, the significant contributions of bean class and planting depth into root, seed and soil infestations indicated the promising potential of these two environmental-friendly agronomic practices to control bean root rots. Lowering pathogens populations appears as important as root rot control in bean crops. For instance, the biocontrol of bean root rot pathogens in field soil may reduce crop damage as effective as disease control in terms of genotypic resistance or fungicide application. The linkages of soil suppressiveness to herbicides for *F. solani,* soil EC for *F. oxysporum* f. sp. *lactucae*, texture for *R. solani*, pH for *F. oxysporum* f. sp. *lini*, and rotation for *F. solani* f. sp. *phaseoli* and *R. solani* have been reported previously (Burke and Kraft, 1974; Höper *et al.,* 1995; Toubia-Rahme *et al*., 1995; Otten and Gilligan, 1998; Chitarra *et al*., 2013). However, this study advanced the current knowledge via evidencing the joint associations of agro-ecological characteristics with root rot pathogens infecting bean root and seed, and field soil. Further research could include more agro-

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ecological descriptors and their mechanisms to be examined in the bean-root-rot pathosystem.

The authors would like to thank all bean growers who were involved in the present regional research.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This research was financially supported by the Iranian Agricultural Research, Education and Extension Organization (project no. 4-47-16-86143).

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Received: 7 April 2019; Accepted: 6 April 2020

Σήψεις ριζών σε καλλιέργεια φασολιού σε σχέση με την περιοχή, το είδος του παθογόνου και το αγρο-οικοσύστημα

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Η κατανόηση της επίδρασης του αγροοικοσυστήματος σε παθογόνα των φυτών είναι ιδιαίτερα σημαντική όταν εφαρμόζονται μέθοδοι καταπολέμησης με στόχο την παρεμπόδιση της επικράτησης των παθογόνων πριν αυτά να μολύνουν τα φυτά. Για το λόγο αυτό μελετήθηκαν η συχνότητα εμφάνισης σοβαρών παθογόνων που απομονώθηκαν από ρίζες και σπόρους φασολιού και προκαλούν σήψεις ριζών, καθώς και οι πληθυσμοί αυτών στο έδαφος καλλιεργούμενων χωραφιών με φασόλια. Πολυμεταβλητή στατιστική ανάλυση έδειξε μεγαλύτερη συχνότητα απομονώσεων των παθογόνων μυκήτων *Fusarium solani* και *Rhizoctonia solani* από τις ρίζες και τους σπόρους σε σύγκριση με τους μύκητες *Macrophomina phaseolina* και *Fusarium oxysporum.* Δύο είδη του γένους *Fusarium* είχαν υψηλότερους πληθυσμούς στο έδαφος σε σύγκριση με αυτούς των μυκήτων *R. solani* και *M. phaseolina*. Τα παθογόνα απομονώθηκαν σε μεγαλύτερη συχνότητα από ρίζες και σπόρους που συλλέχθηκαν από τις περιοχές Abhar και Khodabandeh, Ιράν, σε σύγκριση με την περιοχή Kheirabad. Οι αγρονομικές και εδαφικές μεταβλητές συσχετίζονταν λιγότερο με τη μόλυνση των ρίζων σε σύγκριση με τη μόλυνση του εδάφους και των σπόρων. Η εμπορική ποιότητα των φασολιών, η εφαρμογή ζιζανιοκτόνων και το βάθος φύτευσης συσχετίζονταν με τις προσβολές στις ρίζες, τους σπόρους και το έδαφος. Οι παράμετροι αυτές αποτελούν αξιόπιστη βάση για την επιλογή της κατάλληλης στρατηγικής αντιμετώπισης αυτών των παθογόνων σε μια περιοχή, στο πλαίσιο της βιώσιμης γεωργίας.

Hellenic Plant Protection Journal **14:** 14-23, 2021

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