International Journal of Agricultural Technology 2021Vol. 17(2):443-464
Available online http://www.ijat-aatsea.com
ISSN 2630-0192 (Online)

Evaluation of the impact of pathogenic fungi on the growth of *Pisum sativum* L.- A review article

Chaudhary, N.[*], Singh, C., Pathak, P., Rathi, A. and Vyas, D.

Lab of Microbial Technology and Plant Pathology, Department of Botany, Dr. Harisingh Gour Vishwavidyalaya, Sagar (470003) M.P. India.

Chaudhary, N., Singh, C., Pathak, P., Rathi, A. and Vyas, D. (2021). Evaluation of the impact of pathogenic fungi on the growth of *Pisum sativum* L.- A review article. International Journal of Agricultural Technology 17(2):443-464.

Abstract In India pea is the second greatest protein source followed by chickpea for the people of the country, over the years due to pathogen attack and climate change, the yield of pea has reduced categorically which generated great concern among scientists, policymakers, and common people thus resulting into the development of strategies to assess the impact and severity of the disease spread around the country various measures were taken into the account to find out the best method to control the disease. It has been found that pea is most susceptible to fungal pathogens. After reviewing the literature it is deduced that there are enormous species of fungi reported showing beneficial as well as harmful relationships with the pea and other crop plants worldwide. Disease in the pea plant is mainly caused by microorganisms like fungi, bacteria, and some nematodes, but much of the losses are occurred due to fungal pathogens (generally soil-borne). In the present review the most common diseases of pea caused by soil-borne fungi are *Fusarium oxysporum* f. sp. *pisi*, *Fusarium solani* f. sp. *pisi*, *Rhizoctonia solani*, *Pythium ultimum*, *Aphanomyces euteiches*, *Thielaviopsis basicola*, and *Sclerotinia sclerotiorum*. The present article deals with the evaluation of the aggressiveness, detrimental effect and taxonomic and symptomatic status of fungal pathogens.

Keywords: Agric areas, Pathogenic fungi, *Pisum sativum*, Soil micro-biota

Introduction

India is regarded as the major producer, consumer, and importer of pulses in the world. As the larger population are vegetarian, therefore, dependency on the pulses for the major source of proteins found to be more. Pulses contain 18 to 25 % of protein, provide the cheapest sources of protein for human consumption (Upadhyay *et al*., 2019). Pea is considered to be the ancient pulse domesticated around the same time when most of the cereals were domesticated. Pea belongs to the family Leguminoseae, and commonly called garden pea, field pea, dry pea, (United Kingdom, United State of America), Batani(India), Erbese(Germany), Ater(Ethopia), Pois(France),

[*]**Corresponding Author:** Neelam, C.**; Email:** neelamc177@gmail.com

Takarmanyborso(Hun.) (Pandit, 2010). Duke (1981) reported that peas are of four types i.e. Garden pea {*P. sativum* sp. *Hortense* (Asch. &Graebn.)}, Drypea {*P. sativum* sp. *Arvense*(L.) Poir.}, Edible podded peas (*P. sativum* sp. *macrocarpon*), and Early dwarf pea (*P. sativum* var. *humile*). The present study deals with the evaluation of field pea. Field pea is a self-pollinated diploid (2n=14) cool-season pulse crop, temperature ranging from 12–18 ℃, and the relatively humid climate favors the healthy growth of it (Kindie *et al.,* 2019). The economical yields of the pea vary greatly in yield per hectare of the pea in the growing regions (Table1). Pea seeds are rich in protein, vitamins, minerals, and fiber, on average dry pea accounts for 10.9 percent water, 22.9 percent protein, 1.4 percent fat, 60.7 percent carbohydrate, 1.4 percent crude fiber, and 2.7 percent ash (Duke, 1981). The protein concentration in seeds may vary from 15.5 to 39.7 percent (Davies *et al*., 1985; Bressaniand Elias, 1988). As a nutritious legume, pea occupied a positive position in the healthy food of the human diet menu. While, this crop is subjected to several diseases (fungal, bacterial, and viral origin), but fungal diseases are a major factor in reducing their production in India (Arora,1990). Fungal plant pathogens of pea have been listed to cause considerable losses in pea yield worldwide (Soylu and Dervis, 2011). World pea production has declined from 1993 to 2012 (Figure1), which is due to *Fusarium* wilt (*Fusarium oxysporum* f. sp. *pisi*), Root rot (*Rhizoctonia solani* and *Pythium ultimum*), Root rot (*Aphanomyces euteiches*), and other fungi that can be associated with pea root rots, include Black root rot (*Thielaviopsis basicola*), Footrot (*Fusarium oxysporum, Fusarium solani,* and *Fusarium culmorum)* and White mold (*Sclerotinia sclerotiorum*), while saprophytes like *Aspergillus* spp., *Penicillium* spp., *Rhizopus* spp. associated with pea seeds and producing toxins that affect seed germination rate. And some of the fungal diseases agents such as Ascochyta blight complex (*Ascochyta pisi, Mycosphaerella pinodes,* and *Phoma medicaginis* var. *pinodella*), Alternaria leaf and stem spot (*Alternaria alternata*), Powdery mildew (*Erysiphe pisi*), and Downy mildew (*Peronospora viciae*) found to cause foliar diseases in the pea plants (Kerr, 1963; Blad *et al.*, 1978; Tu, 1987; Hashmi and Thrane, 1990; Persson *et al.*, 1997; Kraft and Pfleger, 2001; Marcinkowska, 2002; Begum *et al.,* 2004; Koike *et al.,* 2007; Upadhyay *et al.,* 2019). Under the favorable and right conditions, these diseases could significantly decrease both yield and quality (Figure 1). Their effect on yield may vary between the country (Basu *et al.,* 1973; McLaren *et al.,* 2006).

Table 1. A Comparative figure of the five highest pea producers in terms of yield, Area, and production compared to the total world production of pea

	Canada			Russian Federation			China			India			France			World		
	A[a]	P[y]	Y[c]	A	P	Y	A	P	Y	A	P	Y	A	P	Y	A	P	Y
2002	0.98	1.28	1.31	0.76	1.27	1.67	0.95	1.50	1.58	0.67	0.61	0.91	0.34	0.66	4.92	6.02	9.63	1.60
2003	1.15	1.93	1.68	0.72	1.05	1.47	0.94	1.40	1.49	0.66	0.59	0.89	0.37	0.62	4.41	6.15	9.89	1.61
2004	1.24	3.10	2.49	0.72	1.24	1.72	0.88	1.06	1.21	0.71	0.73	1.02	0.36	0.68	4.71	6.34	11.74	1.85
2005	1.27	2.99	2.36	0.71	1.13	1.58	1.00	1.16	1.16	0.79	0.79	0.99	0.32	0.33	4.21	5.57	11.29	1.72
2006	1.23	2.52	2.05	0.71	1.15	1.62	0.90	1.01	1.13	0.78	0.71	0.91	0.24	0.02	4.21	6.39	9.82	1.54
2007	1.44	2.93	2.03	0.62	0.86	1.39	0.98	1.08	1.10	0.81	0.85	1.05	0.16	0.59	3.61	6.32	9.37	1.48
2008	1.58	3.57	2.26	0.64	1.26	1.98	0.93	1.10	1.19	0.68	0.75	1.10	0.10	0.45	4.50	6.11	10.07	1.65
2009	1.49	3.38	2.27	0.77	1.35	1.75	0.88	0.96	1.10	0.72	0.66	0.92	0.12	0.55	4.72	6.38	10.46	1.64
2010	1.39	3.02	2.17	0.82	1.19	1.45	0.87	0.91	1.05	0.76	0.67	0.88	0.24	0.07	4.44	6.58	10.31	1.57
2011	0.91	2.12	2.31	1.11	2.02	1.82	0.87	1.19	1.36	0.73	0.59	0.82	0.19	0.67	3.58	6.14	9.73	1.58
2012	1.31	3.34	2.14	1.16	1.66	1.43	0.93	1.11	1.20	0.74	0.63	0.85	0.14	0.57	4.05	6.33	9.86	1.56

Where a = Area (ha $\times 10^{6}$). B = Production (t $\times 10^{6}$). C = Yield (t ha^{-1})
Adopted from: Source: http://apps.fao.org (February 2015).

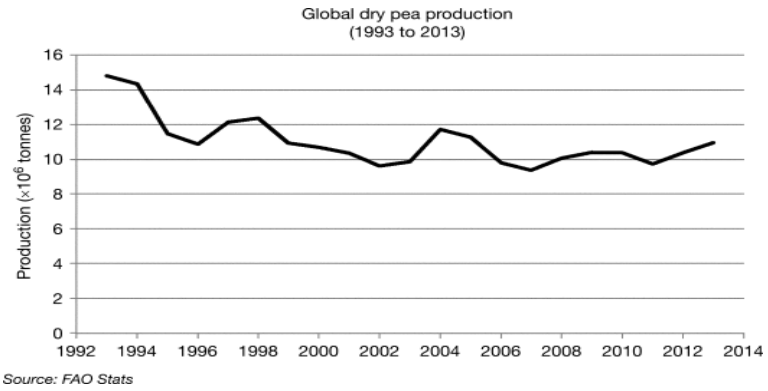

Figure 1. Showing the Global declination of dry pea production from 2003 to 2012 due to various diseases

Fusarium oxysporum f. sp. pisi

Pathogen distribution

Fusarium is a soil-borne cosmopolitan fungus reported from different parts of the world. It is not only found in the temperate and tropical areas of the world but also reported to occur in the diverse environment of the arctic and desert areas (Gerlach and Nirenberg, 1982; Harveson, 2011). Vascular wilt disease is the most destructive disease caused by *formae speciales* of *Fusarium oxysporum* (Nelson, 1964; Ansari, 2003). A wide variety of hosts of any age like tomato, tobacco, legumes, cucurbits, sweet potatoes, and banana are highly affected by the *Fusarium oxysporum* (Thurston, 1998).

Pathogen taxonomy

Fusarium belongs to class-Ascomycetes, order-Hypocreales, genus-*Fusarium* (Lindbeck, 2009). *Fusarium* was enlarged by Link in 1809 for the species with fusiform, non-septate spores borne on a stroma (Booth, 1971; Rangaswamy *et al*., 2016). In 1935 Wollenweber & Reinking (Germany) organized the genus into sixteen sections, sixty-five species, fifty-five varieties, twenty-two forms, and Gerlach and Nirenberg (1982), reported seventy-eight species. In the 1940s Snyder & Hansen (USA), compiled and reduce the sixteen sections into nine species, and those species in section *elegans* into a single species and Nelson *et al.* (1983) mentioned thirty species. In 1955 Bilai and 1959 Railoof Russia, mentioned nene sections, twenty-six species, twenty-nine varieties, and fifty-five species respectively. Gordon mentioned twenty-six species in Canada (Vasudevaand Srinivasan, 1952). Messiaen and Cassi (1968) of France, mentioned nine species. Booth (1971a; 1971b) England mentioned forty-eight species and one hundred ten forms and varieties. Mato in Japan mentioned ten species (Nyvall and Haglaund, 1972). Joffe (1974) Israel, mentioned thirteen sections, thirty-three species, fourteen varieties. Leslie and Summerell summarized information for seventy species of *Fusarium* (Leslie, and Summerell, 2006; Prasad and Kumar, 2017). Historically strains of *F. oxysporum* are divided into *formae speciales* supported virulence on a specific host or group of hosts (Correll, 1991; Singh *et al*., 2013; Deharia *et al*., 2014). At the species level, the presence or absence of macro and microconidia along with the shape of the conidia are considered for taxonomic evaluation and comparison purposes (Snyder and Toussoun, 1965).

Cultural and morphological characters

The optimum growth of *F. oxysporum* was reported to be between 25^0 to 28^0C, inhibited above 33^0C, and not favored below 17^0C. The optimum radial growth and maximum sporulation were favored at 6.5 pH, followed by pH 7.5 (Khan *et al*., 2011; Bhale, 2012). The effect of the pH on the germination of the chlamydospores of *F. oxysporum* plays an important role which has been confirmed and reported from the different experiments conducted over a wide range of pH (Chuang, 1991; Kumari, 2012; Refai *et al*., 2015). *F. oxysporum* produces scanty to numerous aerial mycelium, with different pigmentation like pink, white, salmon, and purple on the reversed side of the colony in culture plate and tube (Figure 2B) (Gerlach and Nirenberg, 1982; Nelson *et al*., 1983; Kumari, 2012). Being an asexual fungus *F. oxysporum* produces spores, three different kinds of spores produced by this fungus i.e. microconidia (Figure 2C), macroconidia, and chlamydospores (Nelson *et al*., 1983). As mentioned by Beckman (1987) that morphological characterization is done based on the shape of microconidia, macroconidia, and the formation and disposition of chlamydospores.

Symptomology and epidemiology of *Fusarium oxysporum* f. sp. *pisi*

The first symptoms are generally yellowing of the lower leaves, stems or the stem becomes slightly thickened and brittle near the soil line. In a cross-section of the stem often seems discoloration of xylem vessel, firstly lemon to orange-brown and finally black (Figure 2A). The affected crop by this fungus dies at once or slowly. The disease seems to occur in patches in the field (Sinha *et al.,* 2018). A healthy plant gets infected when the *F. oxysporum* contaminated the soil where the crop is growing, the fungus invades by the sporangial germ tube or get entry through the roots of the crops. The healthy root could be infected by *Fusarium oxysporum* directly or through the root tips or maybe through wounds in the roots or at the formation point of lateral roots. When the pathogen gets to enters the plant, the mycelium grows through the cortex intercellularly. Mycelium enters the vessel through the xylem's pits. Mycelium remains in the vessels and advances upward with the ascent of sap towards the stem and crown of the plant. Over the time, mycelium matures and produces microconidia which are distributed throughout the plant. It has been seen that when the microconidia germinated within any vessel, penetrates the wall of the xylem vessel which promotes the production of microconidia in the adjacent vessel (extento.hawaii.edu) (Aslam *et al*., 2019).

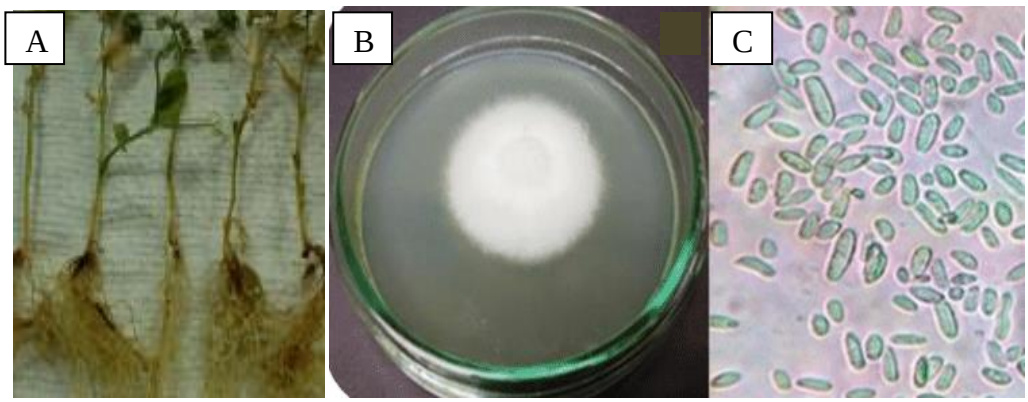

Figure 2. (A) Yellow, red, orange, or rustic discoloration of the vascular tissue (Source: Lyndon Porter); (B) Colony growth and color of *Fusarium oxysporum* f. sp. *pisi* (C) micro-conidia of *Fusarium oxysporum* f. sp. *pisi* (Aslam *et al*., 2019)

Fusarium solani f. sp. pisi

Pathogen distribution

Fusarium solani f. sp. *pisi* is another soil-borne species that has abilities to be pathogenic and saprophytic for plants. It is mostly found in the tropical, temperate region, and mainly the Pacific north-west (Kawate *et al*., 1992). Similar to *F. oxysporum* this species also occurs ubiquitously in agricultural soils worldwide.Macro and micro-climatic factors are considered as one of the most important influences in determining the development and distribution of the *Fusarium* wilt (Kraft and Pfleger, 2001).

Pathogen taxonomy

It belongs to Ascomycetes; Class-Sordariomycetes, Order-Hypocreales, Family-Nectriaceae, Genus-*Fusarium,* species-*solani.* This fungus is thought to be the primary causal organism of the pea root complex in the pea around the globe (Kraft and Pfleger, 2001).

Cultural and morphological characters

The optimum growth of *Fusarium solani* was found between 20 to 25 ℃ (In PDA medium), about 3 to 5 days of incubation growth of colony appears (Figure 3B). It produces a whitish color colony with both macroand microconidia (Figure 3C,D) and chlamydospores (Figure 3E). Macroconidia are generally curved but not often some of the individuals are nearly straight. Macroconidia are borne on long phialides which are produced in sporodochia, sometimes they produce so numerously on the culture that they merge to form a mat on the surface. These spores have blunted rather than sharply pointed ends,

although foot cells are usually quite evident. Very often the macroconidia contain an insoluble blue, green, or yellowish pigment, which appears to be firmly attached to the inside of the conidial wall (Smith, 2007).

Symptomology and epidemiology of *Fusarium solani* f. sp. *pisi*

The symptoms of plants infected by *Fusarium solani* f. sp. *pisi* include turning of leaves yellow starting at the base of the plant and progressing to the top of the plant. The infected plant contains a black to a brown lesion at the base of the below-ground stem (Figure 3A). The exudes release by the plants in the rhizosphere acts as the chemical receptors or communicators for the pathogen to grow towards the root of the plants moreover these excludes often help pathogen to proliferate on the root surface before these pathogens get to enter the cortical region. Alternatively, the pathogen may enter the root through the rifts in the root or by the injury to the root, this fungus needs to penetrate the root cortex and get inside the vessel to cause wilting disease (Smith, 2007).

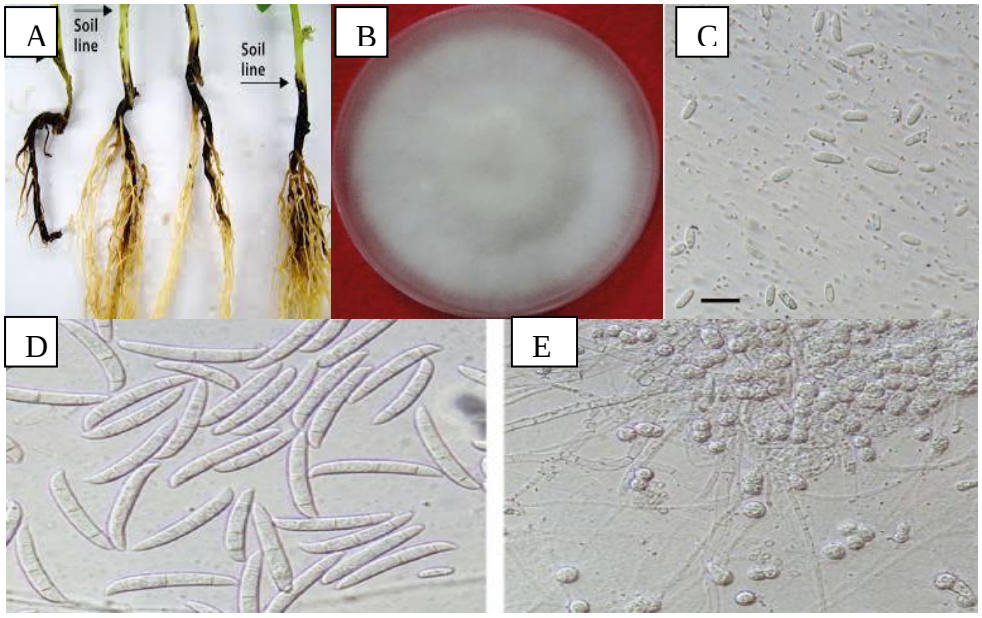

Figure 3. (A) Showing the root-lesion on the pea at the below-ground stem caused by *Fusarium solani* f. sp. *pisi*, (B) Colony on PDA, (C) microconidia, (D) macroconidia, and (E) chlamydo spores

Rhizoctonia solani

Pathogen distribution

Rhizoctonia solani is reported to be present all over the world, mostly found in temperate and subarctic environmental conditions. It is considered to

be the most destructive plant pathogen and infects a wide range of economically important plants including agronomical, ornamental, and forestry species (Anderson, 1982; Sneh *et al*., 1991). The fungus basically and commonly infects the hypocotyls, epicotyls and seed of pea (Kraftand Kaiser, 1993).

Pathogen taxonomy

Rhizoctonia belongs to Basidiomycetes, Class-Agaricomycetes, Order-Cantharellales, Genus-Rhizoctonia (Moore, 1987). De Candolle (1815) firstly established the concept of genus *Rhizoctonia*. Quite a century later the concept of this genus has been reviewed by Parameter and Whitney (1970), found consistent with De Candolle. A swiss author summarized the essential character of the genuswhich is the production of the sclerotia of uniform texture and association of the mycelium with the root of the living plants. This set of features has not been used in the past classification to the unrelated fungi like *Rhizoctonia* s. *lato* (Moore, 1987). Therefore, the taxa to the genus *Rhizoctonia* was included based on some vegetative characters which persisted for a long time. Approximately one hundred twenty epithets have been assigned to the *Rhizoctonia* species complex, but taxonomic reviews have reduced this number to thirty-seven (Andersen and Stalpers, 1994) or forty-nine (Roberts, 1999), depending upon the authors. *Rhizoctonia solani* (teleomorph = Thanatephoruscucumeris Frank (Donk)) is majorly the foremost studied species within the shape genus (Gonz á lez, 2006). The form genus *Rhizoctonia* is considered as a heterogeneous assemblage of filamentous fungal taxa which do not produce asexual spores and have common features with their anamorphic states.

Cultural and morphological characters

The *Rhizoctonia* grows on PDA medium in Petri dishes,room temperature (25-28^{0}C) is the optimum temperature for growth. The optimum pH for the growth of *R. solani* is 4.5, the colony is mostly brown and shows dense growth zonation in culture (Figure 4B). Mycelium obscure surface mycelium and touches the cover of Petri dishes. Under the microscopic study, it was found that the septate multinucleate hyphae {Figure 4C(BN) of *R. solani* appear hyaline when younger and gradually turned to brown as they grow and mature. The hyphae of this fungus have individual cells partitioned by a septum of the double-nut-shaped pore. It has been seen that the hyphae of this fungus often branched at 90^{0}angles and possess three or more than three nuclei per hyphal cell. The other characters like the formation of sclerotia in culture, presence of monilioid cells {Figure 4C(M)}, fast vegetative hyphal growth {Figure 4C(h)} or a complex dolipore septal apparatus are also reported in this species complex but not constantly, although it is present in a large number of

species. It is to be remembered while working with this fungus that the sclerotia formed within the substrate, the formation of the sclerotic number varies among isolates (Akhter *et al.,* 2014). Conidia, clamp connections, rhizomorphs, and cultural pigmentations aside from brown are never observed. The basidial structure of the sexual state is characterized by a vertically branching hymenium succeeded by layers of elongated basidia slightly wider than basal hyphae (Ajayi-Oyetunde and Bradley, 2017).

Symptomology and epidemiology of *Rhizoctonia solani*

At the early stage the roots and the hypocotyls of the young plant show small, elongated, sunken, reddish-brown lesion and at later stage symptoms includes yellowing of the lowermost leaves followed by wilting of the plants (Figure 4A). Due to the presence of the sclerotia, *R. solani* can survive many years in the soil. The sclerotia of this fungus have thick outer layers which permit its long-time survival. The fungi are attracted toward the plants by the chemical stimuli releases by the growing plants or the decomposing plant residue. The penetration process of this fungus to the host plant is accomplished in a number of ways. The entry to the host may occur directly by the penetration of the fungus into the plant cuticle/epidermis or by the natural openings. When hyphae come and attach with the plant they begin to produce an appressorium which allows the pathogen to enter the plant cell and absorb nutrients from plants, pathogen also releasesplant cell wall degrading enzymes which allow the pathogen to grow and colonize inside the dead tissue and to forms the sclerotia. After the successful establishment of the pathogen in the host tissues, the formation of sclerotia begins and the varied symptom related to the disease, such as soil rot, stem rot, damping-off, etc. (Ceresini, 2011).

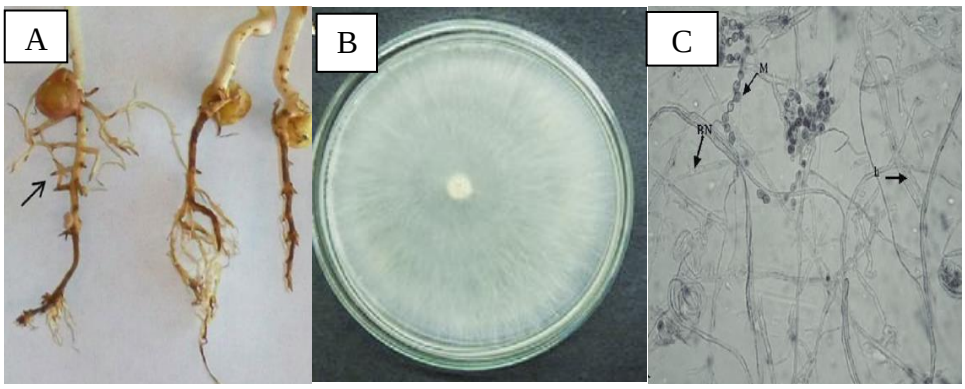

Figure 4. A: Showing lesions symptoms on hypocotyl, tap root and secondary roots, B: Colony, C: binucleate (BN), vegetative hyphae (h), and monilioid cells (M)(Ceresini, 2011)

Pythium ultimum

Pathogen distribution

Pythium spp. are cosmopolitan, widely distributed throughout the world ranging from tropical to temperate (Plaats-Niterink, 1981) and even arctic (Hoshino *et al*., 1999) and antarctic regions (Knox and Paterson, 1973; Hsieh, 1976; Hsieh and Chang, 1976; Rusuku *et al*., 1997; Hon-Hing, 2009). *Pythium* presents as saprophytes, mutualists, and parasites (Vander Plaats-Niterink, 1981; Ichitani and Goto, 1982; Berlese and Toni, 1888; Butler, 1907; Al-Sheikh and Abdelzaher, 2010a, b).

Pythium attack wide variety of plant belongings to woody and herbaceous and causes seedling damping-off, stem rot, root rot, and rotting to different fruits, tubers, and rhizomes, they do this by producing cell wall degrading enzyme-like pectin lyase that breaks the intracellular middle lamella, in turns leading to maceration, softening and subsequent death of the infected tissue (Chen *et al*., 1998).

Pathogen taxonomy

Pythium belongs to Division-Oomycota, Order-Peronosporales, Family-Pythiaceae, Genus-*Pythium.* Schröter (1897) nominated Pythiaceae in which he described *Pythium* having globose sporangia and Nematosporangium with filamentous sporangia. The identification of *Pythium* species is based only on a morphological basis (Middleton, 1943; Waterhouse, 1968; Dick, 1990). Recently, morphological characteristics of a species are increasingly supported by molecular characteristics.

Cultural and morphological characters

The optimum growth of *Pythium* was found on Potato Dextrose Agar (PDA) medium between 25 to 30 ℃ and the minimal temperature supporting mycelial growth of these spp. was around 5 ℃. Zoospores were formed at 15 to 35 ℃. *Pythium* on a rich PDA grows excellently with the appearance of cottony mycelium. Main hyphae were up to 10 µm wide, zoosporangia consisted of terminal complexes of swollen hyphal branches of varying lengths and up to 22 µm wide. Antheridia were mostly intercalary, may be terminal, broadly sac-shaped, 11 to 15 µm long, and 9 to 15 µm wide (Matsumoto *et al*., 1999; Levesque and Cock, 2004; Kageyama *et al*., 2005; Tsukiboshi *et al*., 2007).

Symptomology and epidemiology of *Pythium ultimum*

Infected plants by *Pythium* are often stunted and light green because of the lack of root development. Infection by *Pythium* show yellow to light brown

discoloration, appear stunted with some lateral and fine feeder roots. As the infection progresses the soft outer root layers rot away, exposing the central core, and appear as *Rhizoctonia* like 'spear points'.Due to *Pythium* root rot, the cortex of the root sloughs off, leaving behind a strand of vascular tissue in the plant. The presence of the thick-walled and round oospores and/or zoosporangium in the cells of the plant root is the key sign of the invasion by the pathogens to the host. *Pythium* grows and colonizes a plant by producing hyphae, threadlike, filamentous cells that extract nutrients from the host plant. When the hyphae of the opposite mating type interact with each other they produce oospores which serve as the overwintering structures and oospores germinate to produce hyphae or zoosporangium, and zoosporangium produces zoospores that swim to infect the healthy plants. (Martin *et al*., 1999).

Aphanomyces euteiches

Pathogen distribution

Aphanomyces euteiches Drechsler is a soil-borne fungus found worldwide. *Aphanomyces* root rot (ARR) affects the plant species of the leguminaceae family. This fungus spends half of it's life-cycle on the host and a half of it's life-cycle in soil. It is the most devastating pea disease in several countries, causing up to 80% losses each year (Gaulin *et al*., 2007).

Pathogen taxonomy

The classification of *Aphanimyces* for host specificity is based on the ability of the pathogen to progress into hypocotyls or epicotyls and initiate symptom development. However, *Aphanomyces euteiches* classified asoomycetes in the kingdom chromista, in the order saprolegniales and it is the only genus that has species that are pathogenic to the plants. *A. euteiches* havecoenocytic hyphae, cellulose in its cell wall (true fungi have chitin), and produce motile spores (zoospores). Nuclei are diploid (2N) in vegetative hyphae and all spore stages (Teresa J and Grau, 2007). *Aphanomyces euteiches* is first described in the United States in 1925 (Papavizas and Ayers 1974; Hagedorn, 1984).

Cultural and morphological characters

The optimal temperatures for the growth of *Aphanomyces euteiches* are about 16 ℃, and 20 to 28 ℃ for disease progression (Burke *et al*., 1968;1969). *A. euteiches* are diploid, homothallic pathogen (Lin and Heitman, 2007), produces both oospores (sexual reproduction) and zoospores (asexual reproduction). Hyphal diameters range of *Aphanomyces euteiches* is about 4 to 12 micrometers. Antheridia are generally diclinous, with monoclinous very rarely present. Antheridia's number per oogonium varies from one to four, with most of the

oogonia having two or three antheridia attached. Asexual reproduction of the fungi occurs by zoosporangia and zoospores. Primary zoospores (Figure 5B) (before leaving zoosporangium) are cylindrical, 30 x 3 to 3.5 mm in size. After being, they become rounded, turning into immobile spores, 8 to 12 mm in diameter. Spores assembled at the operculum of the zoosporangium, forming big heads of fifty and more spores. A dormant period (1 to 2 hours) later, the encysted spores produce secondary zoospores, being reniform or pear-shaped, having two flagella, 12-15 x 6-8 mm in size. After active movement, the zoospores encyst, then sprout with germinating tubes. The organs of sexual reproduction are oogonium, antheridium, and oospores. After conjugation of oogonium and antheridium, a spherical or ellipsoid oospore (Figure 5C) with thick colored walls is formed. The oospores are 21 to 24 mm in size on average. The fungus remains in the soil or on vegetation residues as oospores for 10 years (Kotova, 1969; Kask, 1984; Kirpicheva, 1990; Chatterson *et al*., 2015).

Symptomology and epidemiology of *Aphanomyces euteiches*

Symptoms of root rot (Figure 5A) caused by the *A. euteiches* are numerous and the most common symptoms include brown discoloration and cortical decay of lateral roots (Chatterson *et al*., 2015). Moreover, symptoms of *Aphanomyces* root rot (ARR) are relatively common among both annual and perennial hosts, but timing and pattern of disease occurrence often differ, because it is a root-infecting pathogen and primary symptoms appeared on roots and subterranean stem tissues. The root tissue appears grey initially after infection by the pathogens and water-soaked, which resulted in honey-brown or blackish-brown in appearance and therefore roots are reduced in volume and functions. It is the most common symptom which advances from root to the stems that are often symbolized by chlorosis of cotyledons and necrosis of epicotyls or hypocotyls. These primary symptoms of root and stem are eventually lead to secondary symptoms of chlorosis, necrosis, and wilting of the foliage. The damping-off disease is not commonly associated with the ARR, instead, the infected seedlings are stunted and become less competitive to weeds. It is often seen that plants infected by ARR have less nodulation.In field conditions, the disease is most common in the clay soil having extensive irrigations and where drainage is poor (Teasdale *et al*., 1978; Heyman *et al*., 2007; Teresa and Grau, 2007). The entire life-cycle of this pathogen completes in the plant rhizosphere with the exception that it's mycelium after infection to the host resides in the hypocotyl or epicotyl.Oospores are considered to be the survival structure of the pathogen under the non-host environment and act as the source of the primary inoculum. When the oospores get it's host they germinate to complete it's life-cycle (Levenfors, 2003).

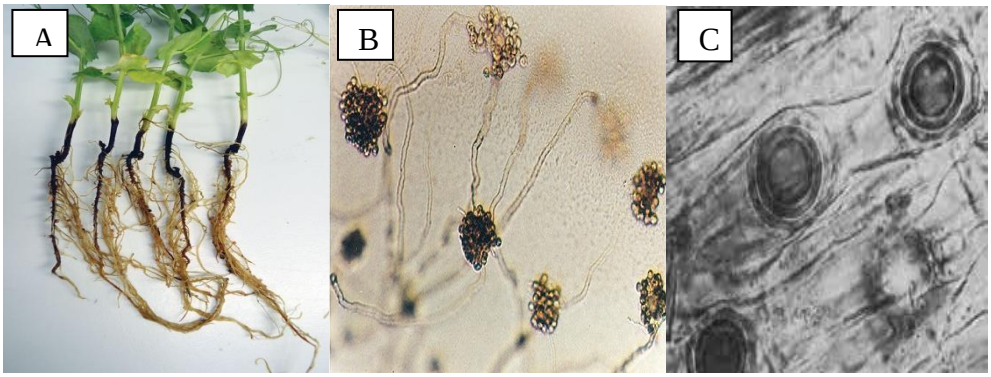

Figure 5. (A) Infected root, (B) Encyst primary zoospores, (C) Oospores

Thielaviopsis basicola

Pathogen distribution

Thielaviopsis basicola has been reported from most regions of the world, most commonly in areas with cool and moist climates. The fungus is found in all major production areas for very susceptible crops e.g. pea (Yarwood, 1981). It is a hemi-biotrophic plant pathogen, with an initial biotrophic phase as it invades and colonizes living cells followed by a necrotrophic phase with the death of the plant cells.Chlamydospores of *T. basicola* can survive in the soil for several years and serve as the primary source of inoculums (Hoodand Shew, 1997).

Pathogen taxonomy

Thielaviopsis basicola aresoil-bornefungi in the Phylum-Ascomycota, Class-Sordariomycetes, Order-Microascales, Family-Ceratocystidaceae. Reproduction in *T. basicola* takes place asexually by producing two types of conidia, endoconidia, and aleuriospores. These sporesare produced in abundance in all and are used as the basis for taxonomic identification (Nag Raj and Kendrick, 1975; Jardine *et al*., 1850).

Cultural and morphological characters

T. basicola grows well on Czapekdox agar medium at pH 8-9.5 and temperature 22–26 ℃, under fluorescent lamps (intensity of 80 µmol $^{m-2\ s-1}$) with 12 h light: 12 h dark. The colony surface pigmentation are either dark brown to black, gray to olive green or light brown, produced some aerial mycelium (branch, smooth, septate, hyaline; Figure 6B), and the chlamydospores were borne either in clusters or singly and were generally longer than those seen in the light brown group. The chlamydospores were formed singly from the hyphae and were composed of 5 to 9 cells (Figure 6C) (Punja and Sun, 1999).

Symptomology and epidemiology of *Thielaviopsis basicola*

The most common symptoms that appear are dark-black lesions on the roots and below-ground stems (Figure 6A) these lesions could show similarities with the *Fusarium* root rot on a pea. Under microscopic observation presence of dark-colored chlamydospores is noted. The acutely infected plants stunted and leaf tissue began to turn yellow, starting at the base of the plant and moving up the plant (Harman and Dillard, 2001; Abawi and Hanson, 2005). The pathogen colonizes the root tissue and after two to eight weeks of crops grown, the cortical cell die and resulted ina brown and blackened appearance in the roots, and in turn, cells of the root reduces the initiation of the new tissue in both roots and shoots (Mondal, 2005). Chlamydospores survive in the soil for many years" (Pscheidt and Ocamb, 2014). Temperature ranging from 12.7^0C to 16.11^0Cis the most favorable condition for the pathogen severity. Alkaline soil favors the disease, which can be prevented by lowering the pH of 4.8 or 5.5 (Mondal, 2005). The fungus is disseminated and spread via different vectors including fungus gnats and shore fly, from an infected plant to a healthy plant or when spores are splashed from plot to plot when watered.

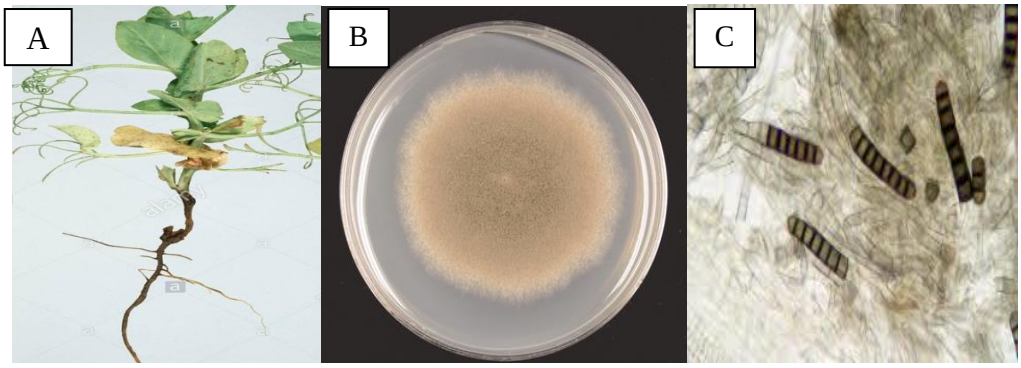

Figure 6. (A) Infected root (B) Colony (C) Chlamydospores (Etebu, 2015)

Sclerotinia sclerotiorum

Pathogen distribution

S. sclerotiorum has a broad range of cosmopolitan distribution throughout, though it is most common in temperate regions. It was originally believed to occur only in cool, moist areas, but is now known to occur in hot, dry areas as well. *S. sclerotiorum* is capable of infecting more than 400 host plants and causes millions of dollars of crop yield losses each year (Bolton *et al.*, 2006). The pathogen is a homothallic fungal species. The fungus is responsible for white mold disease and is also known by other names such as cottony rot, watery soft rot, white rot, and crown rot (Bolton *et al.*, 2006).

The pea plant can be infected through any plant organ and the pathogen can spread through soil or air. Generally, the infection can be initiated at any stage during the growing season if moisture and temperature requirements are met and causes mid-stem, leaf, and pod rot. In the soil, germinated sclerotia can initiate mycelial infection of pea roots and stems and cause stem rot, *S. sclerotiorum* reported causing epidemics during later stages of the pea growing season when plants are flowering.

Pathogen taxonomy

Sclerotinia sclerotiorum is a plant-pathogenic fungus and is classified as a member of Amastigomycota, class-Discomycetes, order-Helotiales, and family-Sclerotiniaceae (Purdy, 1979). It is found in different literature that the scientific name of *Sclerotinia sclerotiorum* (Lib.) de Bary, has been renamed several times and genera in the family Sclerotiniaceaemoved through redistribution (Korf and Durmont, 1972; Bolton *et al.*, 2006).

Cultural and morphological characters

The optimum growth of pathogen found on PDA medium is at 20 $\pm 2^0$C in darkness for 15 days, the pH of the medium should be 5.0 (before autoclaving), for better growth. The pathogen produces aerial mycelium, which was hyaline, branched well developed, and appeared cottony, consisting of closely septate hyphae which were both inter and intracellular. The hyphae were measured to be 2.0 to 11.5 µm in width having dense granular protoplasm. In culture, sclerotia found to be round to irregular in shape and measured 1.5 to 7 mm in width and 2 to 15 mm in length. Cup-shaped apothecia were developed on the germination of sclerotia. Apothecia were brown and were round to globate type. The length of apothecia measured from 5 to 21 mm, whereas diameter ranged from 0 to 7 mm with a number ranged from 1 to 9 per sclerotium (Husain and Choudhary, 2018; Prova *et al*., 2018).

Symptomology and epidemiology of *Sclerotinia sclerotiorum*

The water-soaked spots on stems, leaves, fruits having an irregular shape are the most common symptoms of *Sclerotinia sclerotiorum*. When these spots were covered, cottony mycelial growth appeared and the cottony mycelium usually produces numerous sclerotia, black seed-like reproductive structures, and the plant becomes a soft, slimy, water-soaked mass. Sclerotia form in and outside the stem, pods, and are dropped to the soil during harvest. Sclerotia of *Sclerotinia sclerotiorum* survive in the soil in adverse climate. When climates get cool and the mist environmental conditions facilitate sclerotia germinations to produce apothecia and these apothecia produce sexual spores called ascospores, which are forcibly discharged from the apothecium

into the air, ascospores colonize senescing flowers and infection can spread into the stem (Adams and Ayers 1979; Grau and Hartman 1999; Wu and Subbarao 2008).

Conclusion

Pea is one of the staple food crops for humans throughout the globe. Besides being a proteinaceous crop it also contributes to the economy of the country. Therefore, it is time to reinvestigate the source and causes of diseases in pea. Any crop primarily grows in the soil, a reservoir for organisms ranging from a single cell to multicellular, diversely interacting with each other, either beneficially or harmfully, balancing the ecosystem and function of the soil dynamics. Here, an attempt has been made to elucidate what has been done in past and what is needed to be done at present, so that in the future impact of the disease may be minimized which is caused by the pathogenic fungus in the pea crop. The fungal pathogens have various parameters under which their severity of pathogenicity is mapped for instance pH, soil moisture, macro, and micronutrient, and variety of cultivar are the major factors that determine the pathogenesis in pea. It has been reviewed here regarding morphological characters, symptomology macro and microscopic details, the taxonomy of the pathogenic fungi, and variability in pathotype. However, it is concluded that the *Fusarium oxysporum* f. sp. *pisi* wilt of pea is an aggressive pathogen compared to other fungal pathogens known to causes diseases in the pea. Through this article an attempt has been made to revive the interest of researchers, to discover a better solution to protect the pea and soil health under the conditions prevailing worldwide. The modern tools and techniques help and strengthen us to develop our strategies to get a greater yield of a pea, healthy soil, and sound economy.

Acknowledgments

The authors NC, CS, PP, and AR are thankful for providing financial support from UGC, and express their gratitude towards the Head Department of Botany, Dr. Harisingh Gour Vishwavidyalaya, Sagar (MP) India for support and encouragement.

References

Abawi, G. S. and Hanson, L. E. (2005). Black root rot. In: Compendium of Bean Diseases, 2nd Edition. Editors Schwartz, H. W., Steadman, J. R., Hall, R. and Forster, R. L. APS Press, St. Paul, MN, pp.12-13.

Adams, P. B. and Ayers, W. A. (1979). Ecology of *Sclerotinia species*. Phytopathology, 69:896-899.

Ajayi-Oyetunde, O. O. and Bradley C. A. (2017). *Rhizoctonia solani*: taxonomy, population biology, and management of *Rhizoctonia* seedling disease of soybean. Plant Pathology, 67:3-8.

Akhter, W., Khurshed, M., Bhuiyan, A., Sultana, F. and Hossain, M. (2014). Integrated effect of a microbial antagonist, organic amendment, and fungicide in controlling seedling mortality (*Rhizoctonia solani*) and improving yield in pea (*Pisum sativum* L.). Plant biology and pathology/Biologie et pathologieve ́ge ́tales, pp.21-28.

Al-Sheikh, H. and Abdelzaher, H. M. A. (2010a). Isolation of *Aspergillus sulphureus*, *Penicillium islandicum* and *Paecilomyces variotii* from agricultural soil and their biological activity against *Pythium spinosum*, the damping-off organism of soybean. Journal of Biological Sciences, 10:178-189.

Al-Sheikh, H. and Abdelzaher, H. M. A. (2010b). Differentiation between two isolates of *Pythium ultimum* var. *ultimum* isolated from diseased plants in two different continents. Journal of Biological Sciences, 10:306-315.

Andersen, T. F. and Stalpers, J. A. (1994). A checklist of *Rhizoctonia* epithets. Mycotaxon, 51:437-457.

Anderson, N. A. (1982). The genetics and pathology of *Rhizoctonia solani*. Annual Review of Phytopathology, 20:329-347.

Ansari, S. (2003). Ecofriendly Management of Vascular wilt of lentil Lens culinaris Medik**. (**Ph**.** D**.** Thesis). G**.** B**.** Pant University of Agriculture and Technology, Pantnagar**.**

Arora, P. C. (1990). Studies on root rot and wilt diseases of Pea *(pisum sativum* L.). college of agriculture Haryana Agricultural University HISAR.

Aslam, A., Muhamamd, U., Ghazanfar, Munir, N. and Hamid, M. I. (2019). Managing Fusarium Wilt Of Pea By Utilizing Different Application Methods Of Fungicides. Pakistan Journal of Phytopathology, 31:81-88.

Basu, P. K., Cr ̂te, R., Donalson, A. G., Gourley, C. O., Haas, J. H., Harper, F. R., Lawrence, C. H., Seaman, W. L., Toms, H. N. W., Wong, S. I. and Zimmer, R. C. (1973). Prevalence and severity of diseases of processing peas in Canada, 1970-71. Canadian Plant Disease Survey, 53:49-57.

Beckman, C. H. (1987). The nature of wilt disease of plants. American Phytopathological Society, Saint-Paul, MN, USA.

Begum, N. (2004). Evaluation of Mycoflora Associated with Pea Seeds and Some Control measures. Plant pathology Journal, 3:48-51.

Berlese, A. N. and Toni, J. B. D. (1888). Phycomyceteae. In: Saccardo's Sylloge Fungorum, Saccardo, P.A. (Ed.). R. Friedlander and Sohn, Berlin, Germany, pp.181-322.

Bhale, U. N. (2012). Physiological studies of fungicides resistant and sensitive *Fusarium oxysporum* f. sp. spinaciae. International Journal of Ayurvedic and Herbal Medicine, 2:171-175.

Bilai, V. I. (1955). The fusaria (biology and systematic). Akademia Naukwe Ukrainskii, SSR, Kiev.

Blad, B. L., Steadman, J. R. and Weiss, A. (1978). Canopy structure and irrigation influence of white mold disease and microclimate of dry edible beans. Phytopathology, 69:1431- 37.

Bolton, M. D., Thomma, B. P. H. J. and Nelson, B. D. (2006). *Sclerotinia sclerotiorum* (Lib.) de Bary: biology and molecular traits of a cosmopolitan pathogen. Molecular Plant Pathology, 7:1-16.

Booth, C. (1971a). The genus *Fusarium.*Commonwealth Mycological Institute, Kew, Surry, England, pp.114.

Booth, C. (1971b). The genus *Fusarium.* Kew surrey: Common Wealth Mycological Institute, England, pp.137.

Bressani, R. and Elias, L. G. (1988). Seed quality and nutritional goals in pea, lentil, faba bean and chickpea breeding. In: Summerfield RJ (ed.) World Crops: Cool Season Food Legumes. Kluwer Academic Publishers, Dordrecht, The Netherlands, pp.381-404.

Burke, Dw., Mitchell, J. E. and Hagedorn, D. J. (1968). Temperature and Moisture effects on infection of Pea seedlings by *Aphanomyces euteiches* in soil. Phytopathology, 58:1045.

Burke, Dw., Mitchell, J. E. and Hagedorn, D. J. (1969). Selective conditions for infection of pea seedlings by *Aphanomyces euteiches* in soil. Phytopathology, 59:1670-4.

Butler, E. G. (1907). An account of the genus *Pythium* and some Chytridiaceae. Mem. Dep. Agri. Indian Bot. Vol. 1, Agricultural Research Institute, Pusa, pp.160.

Ceresini, P. (2011). *Rhizoctonia solani*. NC State University, pp.728.

Chatterson, S., Bowness, R. and Harding, M. W. (2015). First report of root rot of field Pea caused by *Aphanomyces euteiches* in Alberta, Canada. Plant Disease, 99:288.

Chen, W. C., Hsieh, H. J. and Tseng, T. C. (1998). Purification and characterization of a pectin lyase from *Pythium* splendens infected cucumber fruits. Bot Bull Acadmia Sinica, 39:181-186.

Chuang, T. Y. (1991). Soil suppressive of banana *Fusarium* wilt in Taiwan. Plant Protection Bulletin Taiwan, Roc33:133-141.

Correll, J. C. (1991). The relationship between Formae speciales, Races and vegetative compatibility group in *Fusarium oxysporum.*The American Phytopathological Society, 81:1061-1064.

Davies, D. R., Berry, G. J., Heath, M. C. and Dawkins, T. C. K. (1985). Pea (*Pisum sativum* L.). In: Summerfield, R. J. and Roberts, E. H. (eds) Williams Collins Sons and Co. Ltd, London, UK, pp.147-198.

De Candolle, A. P. (1815). Mémoiresur les rhizoctones, noveau genre de champignons qui attaque les racines, des plantes et en particuliercelle de la luzernecultivée. MemMusd'Hist Nat, 2:209-216.

Deharia, K., Shukla, A., Ganaie, M. A. and Vyas, D. (2014). Indivisual and interactive role of Trichoderma and Mycorrhizae, Archives of Phytopathology and Plant Protection, Doi:10.1080/03235408.2014.882119.

Dick, M. W. (1990). Keys to *Pythium*. College of Estate Management, Reading, Pages: 64.

Duke, J. A. (1981). Handbook of legumes of world economic importance. Plenum Press, New York, pp.199-265.

Etebu, E. (2015). Agricultural soil health and pea footrot disease suppressiveness. In: Meghvansi, M. and Varma, A. (eds) Organic amendments and soil suppressiveness in plant disease management. Soil Biology, vol 46. Springer, Cham.

Gaulin, E., Jacquet, C., Bottin, A. and Dumas, B. (2007). Root rot disease of legumes caused by *Aphanomyces euteiches*. Molecular Plant Pathology, 8:539-48.

Gerlach, W. and Nirenberg, H. (1982). The genus *Fusarium*-A Pictorial Atlas, Paul Parey. Berlin, Germany, pp.406.

Gonzâlez, V., Portal, Onco, M. A. and Rubio, V. (2006). Review. Biology and Systematics of the form genus *Rhizoctonia*. Spanish Journal of Agricultural Research, 4:55-79.

Grau, C. R. and Hartman, G. L. (1999). *Sclerotinia stem rot*. In: Hartman, G. L., Sinclair, J. B. and Rupe, J. C. (eds.), Compendium of soybean diseases, 4th ed. APS Press, St. Paul, MN, pp.46-48.

Hagedorn, D. J.(ed.) (1984). Compendium of pea diseases. American Phytopathological Society, St. Paul, MN, pp.57.

Harman, G. E. and Dillard, H. R. (2001). Thielaviopsis root rot. In: Compedium of Pea Diseases and Pests, 2nd Edition. Editors J.M. Kraft and F.L. Pfleger. APS Press, St. Paul, MN, pp.17-18.

Harveson, R. M. (2011). Soil borne diseases of chickpea in Nebraska.Retrieved from http://extension.unl.edu/ publication.

Hashmi, M. H. and Thrane, U. (1990). Mycotoxins and other secondary metabolites in species of *Fusarium* isolated from seeds of Capsicum, Coriander and Fumigreek. Pakistan Journal of Botany, 22:106-116.

Heyman, F., Lindahl, B., Persson, L., Wikstrom, M. and Stenlid, J. (2007). Calcium concentrations of soil affect suppressiveness against Aphanomyces root rot of pea. Soil Biology and Biochemistry, 39:2222-2229.

Hon-Hing, H. O. (2009). The genus Pythium in Taiwan, China (1) – a synoptic review. Frontiers of Biology in China, 4:15-28.

Hood, M. E. and Shew, H. D. (1997). Initial cellular interactions between *Thielaviopsis basicola* and tobacco root hairs. Phytopathology, 87:228-235.

Hoshino, T., Tojo, M., Okada, G., Kanda, H., Ohgiya, S. and Ishizaki, K. (1999). A filamentous fungus, *Pythium ultimum*Trow var. ultimum, isolated from moribund moss colonies from Svalbard, Northern Islands of Norway. Polar Bioscience, 12:68- 75.

Hsieh, H. J. (1976). Studies on genera *Pythium* and *Pythiogeton* in Taiwan. (Master Thesis). Taipei: Taiwan University (in Chinese).

Hsieh, H. J. and Chang, H. S. (1976). Five species of Pythium, two species of Pythiogeton new for Taiwan and Pythium a fertile. Bot Bull Academia Sinica, 17:141-150.

Husain, M. A. and Choudhary, C. S. (2018). Morphological, Cultural and Physiological studies on Slerotinia sclerotiorum causing Stem rot of Oilseed brassica. International Journal of Current Microbiology and Applied Sciences, Special Issue-7:1044-1052.

Ichitani, T. and Goto, H. (1982). Distribution of *Pythium zingiberum* causing rhizome rot in ginger growing and its surrounding uncultivated soils. Ann Phytopathol Soc Japan, 48:647-676.

Jardine, W., Selby, P. J., Johnston, G., Babington, C. C., Balfour, J. H. and Taylor, R. (1850). The Annals and Magazine of Natural History: Zoology, Botany, and Geology V: pp.461.

Joffe, A. Z. (1974). A modern system of *Fusarium* taxonomy. Mycopathologia et mycologia applicata, 53:201-228.

Kageyama, K., Nakashima, A., Kajihara, Y., Suga, H. and Nelson, E. B. (2005). Phylogenetic and morphological analyses of *Pythium graminicola* and related species. Journal of General Plant Pathology, 71:174-182.

Kask, K. (1984). Root rot of peas caused *Aphanomyces euteiches*Drechsl. in Estonia. Zashchitarastenii, 53:14-24 (in Russian).

Kawate, M. K., Kawate, S. C., Ogg, A. G. and Kraft, J. M. (1992). Response of *Fusarium solani* f. sp. *pisi* and *Pythium ultimum* to Glyphosate. Weed Science, 40:497-502.

Kerr, A. (1963). The root rot *Fusarium* wilt complex of peas. Australian Journal of Biological Sciences, 16:55-59.

Khan, I. H. S., Saifulla, M., Mahesh, S. B. and Pallavi, M. S. (2011). Effect of different media and environmental conditions on the growth of *Fusarium oxysporum* causing *Fusarium* wilt of chickpea. International Journal of Science and Nature, 2:402-404.

Kindie, Y. (2019). Field Pea (*Pisum sativum* L.) Variety Development for Moisture Deficit Areas of Eastern Amhara, Ethiopia. Hindawi Advances in Agriculture, Article ID 1398612, 6 pages.

Kirpicheva, T. S. (1990). Root rot of peas in Ukraine. Zashchitarastenii, 3:23-24 (in Russian).

Knox, J. S. and Patterson, R. A. (1973). The occurrence and distribution of some aquatic Phycomycetes on Ross Island and the Dry Valleys of Victoria Land, Antartica. Mycologia, 65:373-387.

Koike, S. T., Gladders, P. and Paulus, A. O. (2007). Vegetable diseases : A Colour Handbook.

Korf, R.P. and Durmont,K.P. (1972). Whetzelinia, a new generic name for *Sclerotinia sclerotiorum* and S. tuberosa. Mycologia, 64:248-251.
Kotova, V. V. (1969). Root rot of peas, caused by *Aphanomyces euteiches* Drechsl. in the USSR. Mikologiyaifitopatologiya, 3:438-42 (in Russian).
Kraft, J. M. and Kaiser, W. J. (1993). Screening for disease resistance in pea, in: K.B. Singh, M.C. Saxena (Eds.), Breeding for Stress Tolerance in Cool-Season Food Legumes, John Wiley and Sons, New York.
Kraft, J. M. and Pfleger, F. L. (2001). Compendium of Pea Diseases and Pests. 2edn. St.Paul, MN: The American Phytopathological Society Press.
Kumari, N. (2012). Influence of Environment and Culture Media on Spore Morphology of *Fusarium oxysporum.* M.Phill. Thesis, Bundelkhand University, Jhansi.
Leslie, J. F. and Summerell, B. A. (2006). The Fusarium Laboratory Manual. Blackwell Publishi Rangaswamyng.1st ed, pp.1.
Levenfors, J. (2003). Soil-borne Pathogens in Intensive Legume Cropping - *Aphanomyces* spp. and root rots. Doctor's dissertation. ISSN 1401-6249, ISBN 91-576-6446-3.
Levesque, C. A. and Cock, W. A. de. (2004). Molecular phylogeny and taxonomy of the genus *Pythium*. Mycological Research, 108:1363-1383.
Lin, X. and Heitman, J. (2007). Mechanisms of homothallism in fungi-transitions between heterothallism and homothallism, in Sex in Fungi: molecular determination and evolutionary implications, eds Heitman J., Kronstad J. W., Taylor J. W., Casselton L. A. Washington DC: ASM Press, 35-58.
Lindbeck, K. (2009). Plant Health Australia, Threat Specific Contingency Plan: *Fusarium* wilt of chickpea, lentil & lupin *Fusarium oxysporum* f. sp. *ciceris*, *F. oxysporum* f. sp. *lentis*, *F. oxysporum* f. sp. *Lupini*. Plant Health Australia, pp.5.
Marcinkowska, J. Z. (2002). Foliar diseases of *Pisum sativum* L. in Poland. Plant Breeding and Seed Science, 46:49-54.
Martin, F. N. and Loper, J. E. (1999). Soilborne Plant Diseases Caused by *Pythium* spp.: Ecology, Epidemiology, and Prospects for Biological Control. Critical Reviews in Plant Sciences, 18:111-181.
Matsumoto, C., Kageyama, K., Suga, H. and Hyakumachi, M. (1999). Phylogenetic relationships of *Pythium* species based on ITS and 5.8S sequences of the ribosomal DNA. Mycoscience, 40:321-331.
McLaren, D. L., Conner, R. L., Hausermann, D. L. and Penner, W. C. (2006). Diseases of field pea in Manitoba in 2005. Canadian Plant Disease Survey, 86:112-13.
Messiaen, C. M. and Cassini, R. (1968). Recherchessur les fusarioses. IV. La systematique des *Fusarium*. Ann. Epiphyt. (Paris), 19:387-1055.
Middleton, J. T. (1943). The taxonomy, host range and geographic distribution of the genus *Pythium*. Memoirs of the Torrey Botanical Club, 20:1-171.
Mondal, A. H., Nehl, D. B. and Allen, S. J. (2005). Acibenzolar-S-methyl induces systemic resistance in cotton against black root rot caused by *Thielaviopsis basicola*. Australasian Plant Pathology, 34:499-507.
Moore R. T. (1987). The genera of Rhizoctonia-like fungi: Ascorhizoctonia, Ceratorhiza gen. nov., Epulorhiza gen. nov., Moliniopsis, and Rhizoctonia. Mycotaxon, 29:91-99.
Nag Raj, T. R. and Kendrick, B. (1975). A monograph of Chalara and allied genera. Wilfred Laurier University Press, Waterloo, Ont.
Nelson, P. E. (1964). Carnation as a Symptomless Carrier of *Fusarium oxysporum* f. dianthi. Phytopathology, 54:323-329.
Nelson, P. E., Toussoun, T. A. and Marasas, W. F. O. (1983). *Fusarium* species: An Illustrated manual for Identification. Pennsylvania State University Press, University Park, pp.193.

Nyvall, R. F. and Haglaund, W. A. (1972). Site of infection of *F. oxysporum* f.sp. *pisi*race 5 on peas. Phytopathology, 62:1419-1424.

Pandit K. D. (2010). Studies On Pea Wilt Disease Caused By*Fusarium oxysporum*f. sp. *pisi*.(Agriculture) In Plant Pathology.

Papavizas, G. C. and Ayers, W. A. (1974). Aphanomyces species and their root diseases in pea and sugar beet. U.S. Dep. Agric. Tech. Bull. 1484. 158 pp.

Parameter, J. R. and Whitney, H. S. (1970). Taxonomy and nomenclature of the imperfect state. In: *Rhizoctonia solani*, Biology and Pathology. Parameter Jr J. R. (ed), University of California Press, Berkeley, pp.7-20.

Persson, L., Bødker, L. and Larsson-Wikström, M. (1997). Prevalence and pathogenicity of foot and root rot pathogens of pea in southern Scandinavia. Plant Disease, 81:71-74.

Plaats-Niterink, A. J. van der. (1981). Monograph of the genus *Pythium*. Studies in mycology, 21:1-242.

Prasad, P. and Kumar, J. (2017). Management of Fusarium wilt of chickpea using brassicas as biofumigants. Legume Research, 40:178-182.

Prova, A., Akanda, M. A., Islam, S. and Hossain, Md. M. (2018). Characterization of *Sclerotinia sclerotiorum*, an Emerging Fungal Pathogen Causing Blight in Hyacinth Bean (Lablab purpureus). The Plant Pathology Journal, 34:367-380.

Pscheidt, J. W. and Ocamb, C. M. (2014). Pacific Northwest Plant Disease Management Handbook. Corvallis, OR: Oregon State University; 607-255-4471.

Punja, Z. and Sun, Li-J. (1999). Morphological and molecular characterization of *Chalaraelegans* (*Thielaviopsis basicola*), cause of black root rot on diverse plant species. Canadian Journal of Botany, 77:1801-1812.

Purdy, L. H. (1979). *Sclerotinia sclerotiorum*: history, diseases and symptomatology, host range, geographic distribution, and impact. Phytopathology, 69:875-880.

Railo, J. (1959). Bronchusresektion bei tuberkuloser Stenose im linken hauptbronchus. The Thoracic and Cardiovascular Surgeon, 7:35-40.

Rangaswamy, E., Gopika, K., Pushpavathi, B., sokkareddy, S. and Krishna, M. S. R. (2016). An Overview of Variability in *Fusarium udum*, The Incitant of Wilt in Pigeon pea. International Journal of Applied Biology and Pharmaceutical Technology, 7:404-415.

Refai, M., Hassan, A. and Hamed, M. (2015). Monograph on the Genus *Fusarium*.Retrieved from DOI: 10.13140/RG.2.1.3104.2728.

Roberts, P. (1999). Rhizoctonia-forming fungi: a taxonomic guide. Royal Botanical Gardens, Kew. 239 pp.

Rusuku, G., Buruchara, R.A., Gatabazi, M. and Pastor-Corrales, M. A. (1997). Effect of crop rotation on *Pythium ultimum* and other *Pythium* species in the soil. Phytopathology, 52:27.

Schröter, J. (1897). Saprolegnineae III Pythiaceae. Engler&Prantl. Nat. Pflfam, 1:104-105.

Singh, P. K., Singh, M., Agnihotri, V. K. and Vyas, D. (2013). Arbuscular Mycorrhizal Fungi: Biocontrol against *Fusarium* wilt of Chickpea. International Journal of Scientific and Research Publications, 3:1-5.

Sinha, P. (2018). Management of Wilt Disease of Pulses: A Review. International journal of pure and applied bioscience, 6:696-708.

Smith, S. N. (2007). An overview of ecological and habitat aspects in the genus *Fusarium* with special emphasis on the Soil-Borne Pathogenic Forms. Plant Pathology Bulletin, 16:97-120.

Sneh, B., Burpee, L. and Ogoshi, A. (1991). Identification of *Rhizoctonia* species. APS Press. St. Paul.Minnesota USA,pp.133.

Snyder, W. C. and Toussoun, T. A. (1965). Current status on Taxonomy on *Fusarium* species and their perfect stage. Phytopathology, 55:833-837.
Soylu, S. and Dervis, S. (2011). Determination of prevalence and incidence of fungal disease agents of pea (*Pisum sativum* L.) Plants growing in Amik plain of Turkey. Research on Crops, 12:588-592.
Teasdale, J. R., Harvey, R. G. and Hagedorn, D. J. (1978). Suppression of pea (*Pisum sativum*) root rot caused by *Aphanomyces euteiches* by dinitroaniline herbicides. Weed Science, 26:609-613.
Teresa J, H. and Grau, C. R. (2007). Aphanomyces root rot or common root rot of legumes. The Plant Health Instructor. PHI-I-2007-0418-01.
Thurston, D. (1998). Tropical plant diseases. Second Edition. APS Press. The American Phytopathological Society. St. Paul, Minnesota, USA.
Tsukiboshi, T., Chikuo, Y., Ito, Y., Matsushita, Y. and Kageyama, K. (2007). Root and stem rot of chrysanthemum caused by five *Pythium* species in Japan. Journal of General Plant Pathology, 73:293-296.
Tu, J. C. (1987). Integrated control of the pea root rot disease complex in Ontario. Plant Disease, 71:9-13.
Upadhyay, V. (2019). Rust Disease of Pea: A Review. International Journal of Current Microbiology and Applied Sciences, 8:416-434.
Van der Plaats-Niterink, A. J. (1981). Monograph of the genus *Pythium*. Studies in Mycology, 21:1-244.
Vasudeva, R. S. and Srinivasan, K. V. (1952). Studies on the wilt disease of lentil Lens *esculenta* Moench. Indian Phytopathol, 5:23-32.
Waterhouse, G. M. (1968). The genus *Pythium* pringsheim. Mycological Papers No. 110, pp.1-50.
Wu, B. M. and Subbarao, K. V. (2008). Effects of soil temperature, moisture, and burial depths on carpogenic germination of *Sclerotinia sclerotiorum* and S. Minor. Phytopathology, 98:1144-1152.
Yarwood, C. E. (1981). The occurrence of *Chalara elegans*. Mycologia, 73:524-530.

(Received: 24 November 2020, accepted: 28 February 2021)