AgroScience Today

Popular Article

e-ISSN: 2583-0147

Volume 5 Issue 3
Page: 0825 - 0829

Cross-pathogenecity of formae speciales of Fusarium oxysporum in Cucurbits

Shumaila Shahid[1*], Harshawardhan Choudhary[2] and Koku K. Tara[2]

[1] Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India.

[2] Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi, India.

Corresponding author's e-mail: *shumaila24amu@gmail.com*

ABSTRACT

***Fusarium oxysporum* is a devastating pathogen which causes huge economic losses to several crops including cucurbits. *F. oxysporum* has different formae speciales (f. sp.) which have similar morphological characters, but in general they are host-specific. The f. sp. of *F. oxysporum* pathogenic to cucurbits are mostly host-specific and distinguished on the basis of host species. However, some exceptions to the concept of host specificity of the f. sp. are there, where cross-pathogenicity exists in the formae specials infecting cucurbits. Mostly, the f. sp. of *F. oxysporum* is not pathogenic to single host plant only, but is also able to infect other plants in the family cucurbitaceae. However, aggressiveness of cross-pathogenicity may vary according to the host plant it infects.**

Fusarium oxysporum which is a soil-borne phytopathogenic fungus has gained great attention in the recent years owing to its wide host-range as well as the economic losses it causes to a variety of crops (Khan *et al.*, 2017; Shahid, 2023). Cucurbits are one of the oldest and economically important vegetable crops (Wehner and Guner, 2004) and are rich in minerals, vitamins and dietary fibre. *Fusarium* wilt disease caused by *F. oxysporum* is considered as one of the most devastating disease of cucurbits causing significant losses to cucurbits all over the world (Shahid *et al.*, 2023). The most economically important crops of the cucurbitaceae family attacked by this pathogen are muskmelon, watermelon, cucumber, bottle guard, bitter gourd, pumpkin, squash etc.

Generally, *F. oxysporum* shows high functional as well as genetic diversity (Steinberg *et al*. 2016). The strains which have similar host-ranges are grouped in to intraspecific groups, known as formae speciales (f. sp.). Each wilt disease of the plant species in the family cucurbitaceae is due to different formae speciales (f. sp.) of *F. oxysporum*. Even though all the f. sp. of *F. oxysporum* are morphologically similar, but host-specificity is present in them. On the basis of virulence on a specific host/group of hosts, *F. oxysporum* is further divided into different formae speciales. For e.g. the formae speciales that attack cucumber is *F. oxysporum* f. sp. *cucumerinum,* muskmelon is *F. oxysporum* f. sp. *melonis,* bitter gourd is *F. oxysporum* f. sp. *momordicae,* bottle gourd is *F. oxysporum* f. sp. *lagenariae,* watermelon is *F. oxysporum* f. sp. *niveum*, etc.

The concept of formae speciales was first emerged to differentiate the strains of the fungus named *Puccinia graminis* revealing similar morphological features/characters but dissimilar host-ranges. Hence, this new rank was titled as the "spezialisierten formen" (Eriksson 1894). Later in 1940, Snyder and Hansen described 25 "biologic forms" within the pathogen, *F. oxysporum* according to their host-ranges. Later, Gordon (1965) designated these forms of pathogenic strains of *F. oxysporum* as the formae speciales or f. sp. The narrow host specificity of the fungus has led to formae speciales concept, each formae speciales grouping strains with the similar range of host (Edel-Hermann and Lecomte, 2019). Differentiation of *F. oxysporum* into its formae speciales (f. sp.) is based on their host-range which is usually limited to either one or a very few plant species, and at present >150 formae speciales in *F. oxysporum* have been designated (Michielse and Rep, 2009). Virulence genes or even the entire chromosomes can go through horizontal transfer which confers host-specific virulence or host-specific pathogenicity (Mehrabi *et al.*, 2011). In some cases, the pathogenic specificity is governed by the specific genes which encode for "virulence factors" which are the determinants of host, e.g. secreted proteins (called effectors) as well as enzymes that are involved during the synthesis of toxins which are host-specific (van der Does and Rep, 2007).

In the beginning, the host range was limited to only a single plant species, but later on it was reported to be of wide range for several of the formae speciales. Each strain of the pathogen exhibits selective pathogenicity or virulence to a more/less narrow host-range. Those strains which have the similar limited host-range, usually single plant species, are clustered into a "formae speciales" such as formae speciales *lycopersici* which is particularly restricted to strains causing *Fusarium* wilt of tomato, similarly, those strains of *F. oxysporum* which is responsible for banana wilt belong to the formae speciales *cubense*. In cucurbits also, the formae speciales (f. sp.) of *F. oxysporum* are distinguished by their capability to cause wilt disease in a restricted taxonomic range of the host plants.

Although the formae speciales (f. sp.) of *F. oxysporum* are host specific, but exceptions to this concept of formae speciales have been found in the formae speciales of *F. oxysporum* pathogenic to cucurbits. This is called as cross-pathogenicity or cross-infectivity. It means that a single f. sp. can infect more than one plant species of the same family. To our present knowledge, half of the f. sp. discovered so far, each is pathogenic to single host plant only, whereas the other half f. sp. comprises of those strains whose specificity of interaction is much widespread which leads to the cross-pathogenicity. Cross-pathogenicity phenomena may also be explained through horizontal gene transfer. Horizontal gene transfers among both pathogenic strains and non-pathogenic strains of *F. oxysporum* has already been demonstrated and confirmed under the controlled conditions, and revealed that competition among the populations of *F. oxysporum* near the root surface in the rhizosphere of host plant provides suitable conditions for these horizontal gene transfers.

Cross-pathogenicity of the specific isolates of *F. oxysporum* to host species besides their major hosts has been described for the formae speciales pathogenic to cucurbits. Some cross pathogenicity studies were conducted by Mc Millan (1986) through which it was demonstrated that *F. oxysporum* isolates that were isolated from the wilted plants of cucumber in the Bahamas were also pathogenic to watermelons and muskmelons. Kim *et al*. (1993) found that *F. oxysporum* f. sp. *cucumerinum*, the causal pathogen of cucumber wilt was also pathogenic to melon mainly at the seedling stage. Cafri *et al*. (2005) reported cross-pathogenicity of *F. oxysporum* f. sp. *cucumerinum* on melon. Martyn and McLaughlin (1983) have noted that few isolates of *F. oxysporum* f. sp. *niveum* also infected some summer squash cultivars. Gerlagh and Blok (1988) found that *F. oxysporum* f. sp. *melonis* was also pathogenic to the cucumber plants. The f. sp. *momordicae* of *F. oxysporum*, which causes balsam pear wilt was also revealed to cause wilt disease in pumpkins, malabar gourds and bottle gourds (Namiki *et al*., 1992). Najafina and Sharma (2009) reported that *F. oxysporum* strains isolated from wilted plants of melon or cucumber were highly pathogenic on their original host species and less aggressive on other hosts, while the symptoms of cross pathogenicity revealed that melon plants showed less harmful symptoms due to attack by *F. oxysporum* f. sp. *cucumerinum* but high cross-pathogenicity of *F. oxysporum* f. sp. *melonis* was observed on cucumber plants which showed destructive disease symptoms.

Molecular identification of formae speciales (f. sp.) of *F. oxysporum* would preferably target the pathogenicity-related genes. Even though knowledge on these aspects i.e. genetic determinants was limited, but it has substantially upgraded during the last few years. Whole genome sequencing of fourty five strains of *F. oxysporum* was performed by van Dam *et al*. (2016) to distinguish the formae speciales *melonis*, *niveum*, *cucumerinum*, *radicis-cucumerinum*, and *lycopersici* based on their effector pattern. Genomic comparison studies of whole formae speciales genomes was conducted in 2018 by van Dam *et al*. by extracting candidate effectors from eighty-two genome assemblies on the basis of which he differentiated seven formae speciales which infect the family cucurbitaceae and concluded that the effector repertoire of each of the f. sp. likely determines host specificity.

CONCLUSION

F. oxysporum is regarded as fifth important plant pathogenic fungi over the world causing huge losses to the cucurbit crops. Within the *F. oxysporum* species complex, a large number of formae speciales are present that infect several different hosts leading to vascular wilt disease. The status of formae speciales was designated on the basis of its specificity to be exclusively pathogenic on a particular host and not at all infecting the closely related hosts. However, in cucurbits, most of the formae speciales have a unique ability to infect other hosts of the same family which is called as cross-pathogenecity. It is important to have the information of cross-pathogenic isolates of *F. oxysporum* for better disease management. Molecular studies and whole genome sequencing of the pathogen *F. oxysporum* offer promising visions into the evolution and diversity of *F. oxysporum* pathogenicity for several large-scale projects in future which will definitely improve its host range identification and help in management of *Fusarium* wilt disease.

ACKNOWLEDGEMENTS

The authors are thankful to the Division of Plant Pathology & Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi.

CONFLICT OF INTEREST

There is no conflict of interest between the authors.

REFERENCES

C. B., Michielse and M. Rep (2009) Pathogen profile update: *Fusarium oxysporum*., *Molecular Plant Pathology*. 10 311-324.

D. Cafri, J. Katan, and T. Katan (2005) Cross-pathogenicity between formae speciales of *Fusarium oxysporum*, the pathogen of cucumber and melon., Phytopathology. 153 615-622.

D.H. Kim, R.D. Martyn and C.W. Magill (1993) Mitochondrial DNA(mtDNA)- relatedness among formae specialis of *Fusarium oxysporum* in the Cucurbitaceae., *Phytopathology.* 8 91-97.

F. Namiki, S. Izumi, T. Kayamura and T. Shiomi (1992) Specialization of pathogenic strains of *Fusarium oxysporum* in the Cucurbitaceae., Ann. Phytopathol. Soc. Jpn. 58 540-541.

H.C. van der Does and M. Rep (2007) Virulence genes and the evolution of host specificity in plant-pathogenic fungi., *Molecular Plant-Microbe Interaction.,* 20 1175-1182.

J. Eriksson (1894) Ueber dia specialisirung des parasitismus bei den Getreiderostpilzen., *Ber. Deutsch. Bot. Ges.* 12 292-331.

M. Gerlagh and W.J. Blok (1988) *Fusarium oxysporum* f. sp. *cucurbitacearum* n. f. embracingall formae specialis of *F. oxysporum* attacking cucurbitaceous crops., *Neth. J. Plant Pathol.* 94 17-31.

M. Najafinia and P. Sharma (2009) Cross pathogenicity among isolates of *Fusarium oxysporum* causing wilt in cucumber and muskmelon., Indian Phytopath. 62(1) 9-13.

M.R. Khan, S. Shahid, F.A. Mohidin and U. Mustafa (2017) Interaction of *Fusarium oxysporum* f. sp. *gladioli* and *Meloidogyne incognita* on gladiolus cultivars and its management through corm treatment with biopesticides and pesticides., Biological Control. 115 95-104.

P. van Dam, L. Fokkens, S.M. Schmidt, J.H.J. Linmans, H.C Kistler, Li-Jun Ma, Martijn (2016) Effector profiles distinguish formae speciales of *Fusarium oxysporum., Rep. Environmental Microbiology* 18(11) 4087-4102.

P. van Dam, M. de Sain, A. ter Horst, M. van der Gragt, M. Rep (2018) Use of Comparative Genomics-Based Markers for Discrimination of Host Specificity in *Fusarium oxysporum*., *Appl Environ Microbiol* 84 e01868-17.

R. D. Martyn and R. J. McLaughlin (1983) Susceptibility of summer squash to the watermelon wilt pathogen (*Fusarium oxysporum* f. sp. *niveum*)., *Plant Dis.* 67 263-266.

R. Mehrabi, A.H. Bahkali, K.A. Abd-Elsalam, M. Moslem, S. Ben M'Barek, A.M. Gohari, *et al* (2011) Horizontal gene and chromosome transfer in plant pathogenic fungi affecting host range., *FEMS Microbiology Reviews*. 35 542-554.

S. Shahid (2023) Plant diseases-A major limiting factor in production of pulses (Mung bean and Chickpea). In: Recent Research in Agriculture and Plant Sciences., *MKSES Publication, Lucknow, India*. 1-18.

S. Shahid, H. Choudhary and G.S. Jat (2023) Fusarium wilt- A major problem in cucurbits., *Agroscience Today*. 4(3) 0570-0572.

V. Edel-Hermann and C. Lecomte (2019) Current Status of *Fusarium oxysporum* Formae Speciales and Races., *Phytopathology.* 109 512-530.

W. L. Gordon (1965) Pathogenic strains of *Fusarium oxysporum*. *Can. J. Bot.* 43:1309-1318.

W.C. Snyder and H.N. Hansen (1940) The species concept in *Fusarium*., *Am. J. Bot.* 27 64-67.