

Working Report: Plant Health Initiative Work Package 2

Post-Flowering Stalk Rot (PFSR) of Maize: A disease of complex etiology resurging in South Asia

Sudha k. Nair, Zerka Rashid

International Maize and Wheat Improvement Center (CIMMYT), ICRISAT Campus, Hyderabad, India

Background and Objective:

Post-flowering stalk rots (PFSR) are reported from all major maize growing ecologies and are caused by at least six genera of fungal pathogens, which generally occur as a complex, along with secondary colonizers (Afolabi et al., 2008). PFSR are expected to be exacerbated by the changing climates in Latin America, Asia and Sub-Saharan Africa, especially increases in temperature. The level of impact is determined by a number of factors, including the weather during the growing season, the amount of stress on the plants, hybrid genetics and the populations of the stalk rot pathogens in the field. In Asia, PFSR is reported from many countries, including Nepal, Cambodia, China, India, Indonesia, Laos, Pakistan, Philippines, Thailand and Vietnam (Lal and Singh, 1984; Yang et al., 2010; Subedi et al., 2016). Among the different stalk rots in the complex, *Fusarium* stalk rot (FSR), Charcoal rot (CR) and Late wilt, are more prevalent and destructive in the Asian tropics (Khokhar et al., 2014). Due to the complex nature of the stalk rot complex, with multiple primary and secondary infections, we still do not have comprehensive understanding of the prevalence and spread of the stalk rot pathogens in different maize agro-ecologies in Asia. This limits the capacity to plan defensive strategies, including development and deployment of resistant varieties. As these diseases affect the crop, at a much later stage in the life cycle, the economic impact of the disease is high, and hence is one of the biggest challenges faced by small and marginal farmers. Hence, characterizing the pathogen spectrum that causes this disease is important towards planning of IPDM strategies including resistance breeding. Hence this study is being undertaken in maize growing areas in India and Nepal as part of Work Package 2 of PHI contributing to Output-6 (WP2-OP6: Knowledge on P&D shifts and virulence variation with strategies for augmenting IPDM and resistance breeding).

Materials and Methodology:

Figure 1: Mapping of PFSR samples collected from India and Nepal
(The different color place holders indicate different seasons/years)



The study in 2022-2024 involved collection of PFSR affected maize plant stalks from different maize growing agro-ecologies across India and Nepal, isolation of the pathogens and morphological and molecular characterization using pathogen specific primers. Two hundred and thirty-four (234) Infected samples were collected from seven maize growing states across India and 72 samples were collected from 20 locations in Nepal (Table 1, Fig. 1). A total of 199 and 42 pure cultures were isolated from infected samples from India and Nepal respectively. The colony and microscopic morphology were studied for initial identification of the pathogen genera. Genomic DNA was extracted from the pure cultures of *Fusarium* spp. identified and translation elongation factor (TEF-1) region of the fungi was amplified using published primer sequences (O'Donnell et al., 1998).

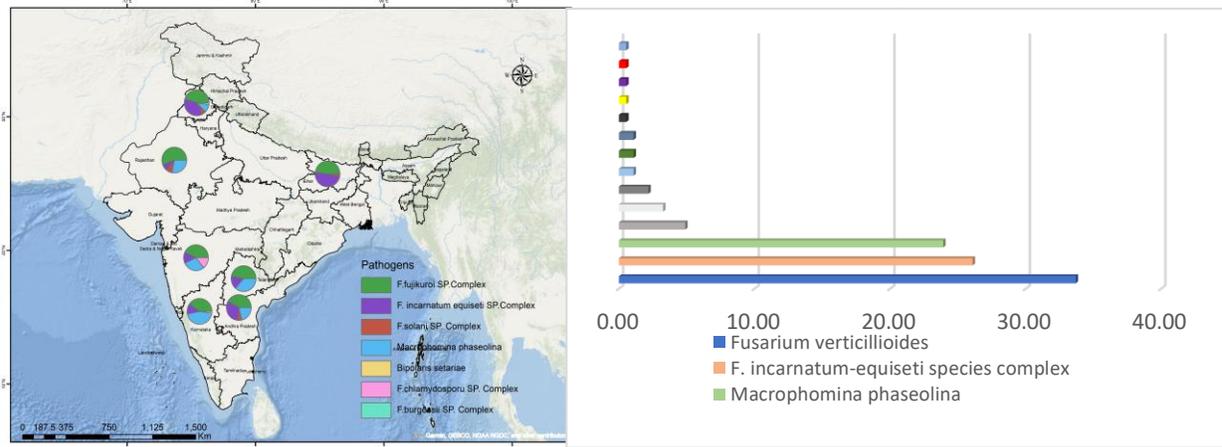
Table 1. List of the locations surveyed for collection of post flowering stalk rot samples during 2022 to 2024

Region	Season	Year
Bihar, India	Dry	2022, 2023
Punjab, India	Spring, Rainy	2022, 2023, 2024
Rajasthan, India	Rainy	2022
Telangana, India	Dry, Rainy	2022, 2023
Andhra Pradesh, India	Dry, Rainy	2022, 2023
Karnataka, India	Dry, Rainy	2022, 2023
Maharashtra, India	Dry, Rainy	2022, 2023, 2024
Nepal	Rainy	2023, 2024

Amplified product was used to obtain the raw sequence from SeqStudio Genetic Analyzer at National Fungal Culture Collection of India (NFCCI), Pune, India. BLASTN analysis was done with the sequences deposited at CBS-KNAW Fungal Biodiversity Centre’s Fusarium MLST website (<https://fusarium.mycobank.org/>) for Fusarium species identification.

Results and Inference:

Figure 2: Pathogens characterized from PFSR infected maize samples from India

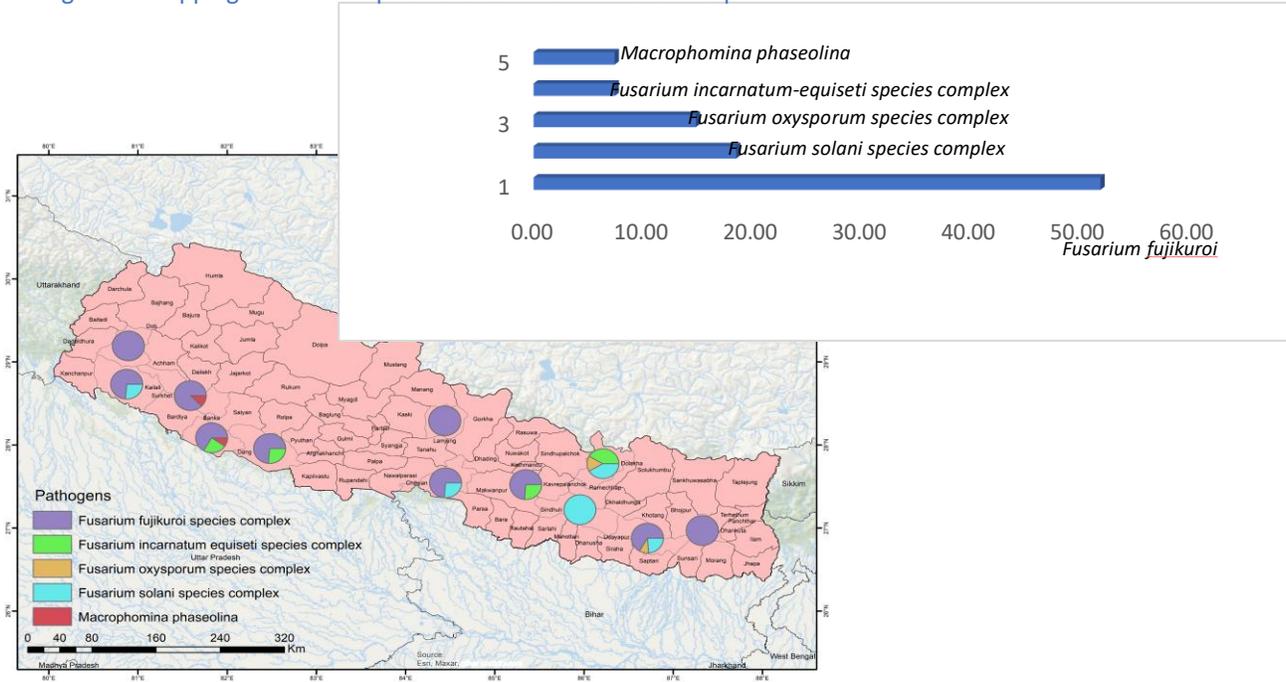


Ten pathogen species/species complex causing PFSR disease were identified from the samples collected from India and five from Nepal (Figure 2; Figure 3). Eight of the pathogen species detected belonged to the *Fusarium* genus. Apart from *Fusarium* Spp., *Macrophomina phaseolina* and *Sarocladium Zeae* were detected, of which the former represented ~24% of the diseased sample isolates from India. Eight different species/species complex of *Fusarium* were identified, where *F.verticillioides* (~34%) was the

major species identified. It has been reported as the major causal pathogen of PFSR in India (Khokhar et al., 2014), apart from *M.phaseolina*. In Nepal, the major pathogen species reported was *F.verticillioides*

(53%), followed by *F.solani* (19%). The *Fusarium* species that is found to gain prominence is *Fusarium incarnatum equiseti* species complex, which was first reported in India in 2020 from Karnataka and Telengana (Swamy et al., 2020). In the present study, it was detected in ~27% of samples studied, which included the samples from Bihar, where in the Dry season of 2022, there has been severe incidence of

Figure 3: Mapping of PFSR samples collected from India and Nepal



PFSR in farmers' fields (Arshad Anwar, BAU, Personal communication). This *Fusarium* species complex has not yet been reported as a major pathogen causing PFSR in India yet, and hence host resistance deployment efforts were also not targeted towards this pathogen. Similarly, in Nepal also, FIEC has never been reported, but the present study showed 15% samples infected with this pathogen. Initial studies on differential response of standard genotype set points to similar pattern of responses to *F.verticillioides* and FIEC, with higher levels of severity observed for the latter (Figure 4).

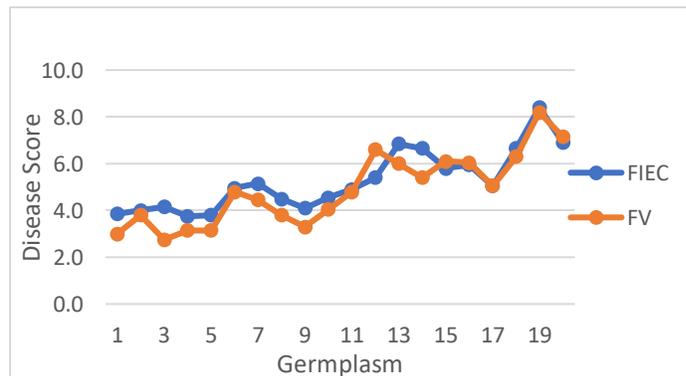


Figure 4: Differential response of standard genotype set with known *F. verticillioides* reaction

Apart from this important finding, multiple pathogens were detected suggesting possible co-infection (Table 2), and in majority of such cases, the co-infection was observed between *F. verticillioides* and *F.*

incarnatum equiseti complex or *F. verticillioides* and *M. phaseolina*. This also suggests the importance of resistance breeding for combined resistance to multiple pathogens.

Table 2. Locations where multiple pathogen co-infected PFSR diseased stalks were collected

Stalk rot pathogen Complex	Locations
<i>Fusarium verticillioides</i> - <i>Macrophomina phaseolina</i>	Dharwad, Gadag, Behrampur, Simbly, Malavalli, Patancheru, Daulatabad, Karimnagar, Rahuri, Peddapuram, Ahmed nagar
<i>Fusarium verticillioides</i> - <i>Fusarium incarnatum-equiseti</i> species complex	Kuresaila, Shirga, Baldaour, Khageria, Banmauki, Rannuehach, Bihpur, Belgavi, Bhagalpur, Behrampur, Sidhwanbet, Sidhwanbet, Kang-Patrapurt, Mehatpur, Kapurthala, Langroya, Sadullapur, Patencheru, Kurnool, Yesgoan, Pimpri, Malegoan, Kaldhabasti
<i>Fusarium nygamai</i> - <i>Fusarium solani</i>	Baldaour- Bihar
<i>Fusarium verticillioides</i> - <i>Fusarium nygamai</i>	Purnea, Shirga-Bihar
<i>Fusarium verticillioides</i> - <i>Fusarium incarnatum-equiseti</i> species complex- <i>F.solani</i>	Garhshanker-Punjab
<i>Fusarium verticillioides</i> - <i>Fusarium proliferatum</i>	Tamatya, Udaipur, Rajasthan
<i>Fusarium incarnatum-equiseti</i> species complex- <i>Macrophomina phaseolina</i>	Gotiya-Rajasthan, Rannabanaur, Sherigheri-Karnataka

Partners:

ICAR-Indian Institute of Maize Research (ICAR-IIMR), Ludhiana, India
National Maize Research Program-Nepal (NMRP), Rampur, Nepal
Acharya N. G. Ranga Agricultural University (ANGRAU), Peddapuram, India
Bihar Agricultural University (BAU), Sabour, India
Maharana Pratap University of Agriculture and Technology (MPUAT), Udaipur, India
Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, India
Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India
Punjab Agricultural University (PAU), Ludhiana, India
Rallis India Limited, Maharashtra, India

References:

Afolabi CG, Ojiambo, PS, Ekpo EJA, Menkir A, Bandopadhyay R (2008). Novel sources of resistance to *Fusarium* stalk rot of maize in tropical Africa. *Plant Dis.* 92, 772 – 780.

Khokhar MK, Hooda KS, Sharma SS, Singh V (2014) Post Flowering Stalk Rot Complex of Maize - Present Status and Future Prospects. *Maydica* 59: 226-242.

Lal S and Singh IS (1984) Breeding for resistance to downy mildews and stalk rots in maize. *Theor. Appl. Genet.* 69: 111-19.

O'Donnell K, Kistler HC, Cigelnik E, Ploetz RC (1998) Multiple evolutionary origins of the fungus causing Panama disease of banana: concordant evidence from nuclear and mitochondrial gene genealogies. *Proc Natl. Acad. Sci USA.* 3; 95: 2044-9. <http://doi: 10.1073/pnas.95.5.2044>.

Subedi S, Subedi H, Neupane S (2016) Status of maize stalk rot complex in western belts of Nepal and its integrated management. *Journal of Maize Research and Development*, 2: 30-42.

<http://dx.doi.org/10.3126/jmrd.v2i1.16213>

Swamy DS, Mahadevakumar S, Hemareddy HB, Amruthesh KN, Mamatha S, Kunjeti SG, Swapnil R, Vasantha KT, Lakshmidhevi N (2020) First report of *Fusarium equiseti*–the incitant of post flowering stalkrot of maize (*Zea mays* L.) in India. *Crop Prot.* 129. <https://doi.org/10.1016/j.cropro.2019.105035>.

Yang Q, Yin G, Guo Y, Zhang D, Chen S, Xu M (2010) A major QTL for resistance to *Gibberella* stalk rot in maize. *Theor Appl Genet.* 121(4):673-87. [https://doi: 10.1007/s00122-010-1339-0](https://doi:10.1007/s00122-010-1339-0)