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***Short Note***

# SALIENT RESEARCH FINDINGS ON VARIABILITY IN *FUSARIUM UDUM*, THE INCITANT OF WILT IN PIGEONPEA

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*Fusarium* wilt caused by *Fusarium udum* is one of the most important soil borne disease and was first reported from Bihar state in India [1]. The disease incidence has been increasing year after year and most of the released cultivars became susceptible to the disease indicating the development of more virulent races of the pathogen in major pigeonpea growing areas of the state.

A roving survey [2] was carried out in major pigeonpea growing districts of Andhra Pradesh *viz.*,Warangal, Khammam and Ranga Reddy districts to assess the wilt incidence and to collect the isolates from the wilt affected fields. Data collected during survey revealed that, maximum (53.2%) incidence of wilt was observed in Parvathagirimandal of Warangal district and minimum (4.4%) of that in Vyra mandal of Khammam district. From wilt affected plant samples 26 Fusarium isolates were isolated, identified and purified. Pathogenicity of all the isolates was proved by adopting root dip inoculation technique on a susceptible pigeonpea cultivar, LRG 30. Results showed that all isolates were pathogenic and produced visible symptoms of loss of turgidity and wilting by the 35$^{th}$ day after transplanting.

All 26 isolates of *F. udum* were studied for existence of variability in respect of cultural and morphological characters [3]. Across the isolates micro- and macroconidial sizes varied between 7.27×2.88µm (Fu 24) to 13.25×2.68µm (Fu 10) and 23.37×3.17µm (Fu 18) to 40.05×4.71µm (Fu 8) respectively. Chlamydospores were observed in all the isolates and their diameter measured between 9.47µm (Fu19) to 15.57µm (Fu1).

According to colony characters isolates were categorized into four groups *viz*., white cottony and fluffy growth (Fu 4,Fu 5,Fu 9,Fu 12,Fu 13,Fu 17 and Fu 24), white cottony dense growth with smooth margin (Fu1,Fu 2,Fu 6,Fu 7,Fu 8,Fu 10,Fu 11,Fu 15 and Fu 25), white sparse growth in concentric rings (Fu3,Fu 14,Fu 16,Fu 21 and Fu 26) and white sparse growth (Fu18,Fu 19,Fu 20,Fu 22 andFu 23). Highest colony diameter was noted with isolate Fu 21 (89.33mm), while lowest with isolate Fu 22 (55.00mm). Considerable variation was observed in substrate pigmentation for all the isolates. Majorly, the isolates developed different colours *viz*., yellow (Fu1, Fu 5, Fu 6, Fu 8, Fu11, Fu 12, Fu 13, Fu 17, Fu19 and Fu 20), pale yellow (Fu 10, Fu 15, Fu 23 and Fu 25), reddish yellow (Fu 3, Fu 4, Fu 21 and Fu 24), brownish yellow (Fu 2, Fu 14,Fu 18), pink (Fu 7, Fu 16 and Fu 26) and light pink (Fu 2, Fu 14 and Fu 18). Maximum sporulation was observed with isolates Fu 4, Fu 6, Fu 7, Fu 9, Fu 12, Fu 13, Fu 19 and Fu 24, while minimum was recorded with isolate Fu 20 and Fu 22.

Based on similarity in morphological characters, the 26 isolates were categorized into 5 groups and from each group one representative member was selected. These isolates were evaluated for variability in pathogenicity by using a set of seven host differentials (ICP 2376, ICP 8858, ICP8859, ICP 8862, ICP8863, ICP87119, and Bahar) and three locally growing cultivars (LRG 30, LRG41 and WRG27).Isolates varied greatly for virulence, disease incidence, disease reaction, latent period and virulence index. As all five isolates induced symptoms on all the host differentials, they were considered as virulent isolates. However, among the isolates tested Fu 15 (1.89) followed by Fu 5 (1.82) were found highly virulent with highest mean virulence index and the isolate Fu 24 (0.96) was found least virulent with lowest mean virulence index.

Among the isolates tested significant variation was found in bio-chemical composition. Maximum total sugar was found with isolate Fu2 (16.40mg) while the minimum was noticed in Fu 25 (5.70mg). Similarly, total protein content among the isolates was highest with isolate Fu 21 (15.40mg) and lowest with isolate Fu5 (8.00mg). Across the isolates, totalfree amino acid was ranged between 5.50mg (Fu8) to 20.16mg (Fu15).

All the 26 isolates produced Poly Methyl Galacturonase (PMG) and Pectin Methyl Esterase (PME) enzymesand varied significantly in production of these enzymes. PMG activity varied from 25.20 percent (Fu 9) to 64.39per cent (Fu 5) while PME activity varied from 6.40 (Fu 3) to 29.00(Fu 24) across the isolates.

Effect of culture filtrates [4] at 25ppm, 50ppm, 75ppm, 100ppm and undiluted concentrations of all the 26 isolates of *F.udum* was studied against seed germination, root length and seedling wilt of pigeonpea. Highest seed germination and lowest disease incidence were recorded with culture filtrate of Fu 24 and that of least was recorded with culture filtrate of isolate Fu 1. Results also depicted that germination and root length were reduced and seedling wilt was increased as the concentration of culture filtrate increased.

Polymorphism was observed between the isolates of *F.udum* from different pigeonpea growing areas of Andhra Pradesh. RAPD analysis [5] of 26 isolates of *F.udum* was done with ten base oligonucleotide operon primers. Out of 30 primers used for amplification, 18 were able to amplify the DNA of the fungal isolates. Of all the primers used, the numbers of amplified products were higher for the primers OPL2, OPH14, and OPC6, followed by OPL1 and OPB6. Least number of products was generated by OPC9 and OPB7 followed by OPB8. Data obtained through Randomly Amplified Polymorphic DNA studies differentiated the isolates into 2 major clusters A and B.

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