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*Chapter - 6*

*Summary*

Bacterial wilt caused by *Ralstonia solanacearum* is a major constraint for mainly solanaceous vegetables production in the hot and humid tropics and subtropics. The pathogen is soil-borne and seed borne, can survive in soil for a long period, has a wide host range, and can be transmitted via water, soil and seedlings.

Solanaceous vegetables are one of the important crops, which suffers badly from bacterial wilt disease caused by *Ralstonia solanacearum*. The disease assumes severe proportion and appears quite causing loss of the crops in Karnataka, India (Singh, 2005; Umesha *et al.*, 2008).

In Karnataka, the selected solanaceous crops were grown in about 35,429 hectares, 16,641 hectares, 1,91,519 hectares and 59,980 hectares of land for tomato, eggplant, chilli and potato respectively (Anon., 2003). However, many diseases became a limiting factors for the successful cultivation of these crops. Among the diseases, the crops in Karnataka suffers badly from bacterial wilt caused by *R. solanacearum* and disease assumes severe proportion and appears quite causing loss in yield. Not much information is available on the field survey, sample collection, detection and characterization of the wilt pathogen in Karnataka. Hence, during the present work the following aspects are investigated with reference to the selected solanaceous crops grown in Karnataka.

The present study is concentrated on the detailed study of the wilt bacterial pathogen on most of the solanaceous vegetable crops like tomato, eggplant, chilli and

potato cultivated in different agroclimatic regions of Karnataka and to clear understanding of the present status of the disease.

Further, the main approach of this present investigation was first to understand the local strain profile and then to determine the pathogenic variants, race and biovar of *R. solanacearum* from the four solanaceous host crop plants *i.e.*, tomato, eggplant, chilli and potato. In the present study, selected vegetable crop producing regions located at various districts of Karnataka was selected as the case study. Then on-farm visits were conducted to test the disease incidence (%) and to collect the samples from the infected plants.

Visual observations for the disease symptoms were made at the visited crop fields. The infected plants showed characteristic wilt symptoms. They were flaccid appearance showed drooping off of upper branches with or without discolouration of the leaves and often discolouration yellow to brown was observed. The cross and longitudinal section of the suspected plants showed water soaked and vascular discolouration. Further, roots of the plants suspected to be wilt infected were uprooted and observed for the discolouration of the vasculature. Potato tubers were also observed for the similar symptoms. The samples like root, stem, leaves, seeds and tubers from all the infected plants were harvested and brought to the laboratory for further analysis.

The collected samples were used to determine the occurrence of the target wilt causing bacterial phytopathogen both from seeds and the infected plant materials. The field survey recently found that bacterial wilt was most important and prevalent disease at various regions in the State. Bacterial wilt is considered to be a most important limiting

factor for the successful cultivation of solanaceous vegetables. The survey carried out during 2005 to 2007 revealed the occurrence and present status of the disease in Karnataka. Disease was prevalent in most of the regions in Karnataka. Both the studies by visual observation for the disease symptoms at crop fields and laboratory analysis of the collected samples revealed that disease affected the crops severely at Mandya, Mysore, Hassan, Bangalore (R), Kolar, Chikkamagalore, Dharwad, Haveri, Raichur and Chitradurga districts with varied per cent of disease incidence and severity and were recorded as wilt infected districts in Karnataka.

The pathogen infected the solanaceous crops grown in summer than kharif and rabi seasons. The detection and isolation of the *R. solanacearum* from the infected plant materials like stem, root, leaves, seeds and tubers revealed varied density of inoculum concentration and was recorded as colony forming units (*cfu*). However, the isolation of pathogen showed higher population density in stem and root revealed probable soil borne nature and that from the infected seeds also revealed the seed borne nature in the form of latent infection.

Characterization of the *R. solanacearum* isolates was done by cultural morphological characters, nutritional, enzymatic, biochemical tests and pathological tests. Further, the study to reveal host specificity and host infectivity by cross host inoculation tests revealed the pathogen exhibits a nature of a complex species with its host specificity and cross infectivity even among the solanaceous hosts.

The comparison of variations within the species revealed the prevalence of race-I and biovar-3 of the *R. solanacearum* causing wilt of the solanaceous crops in Karnataka.

However, there might be possible existence of other race and biovar of the pathogen in latent form or on other hosts in Karnataka. Hence, there is a need to further understanding the nature of complex and diversified species of this wilt pathogen by obtaining different strains from the other hosts using advanced and molecular tools.

Now-a-days, impetus of predicting climate change effects or increasing, global climate change will also affect plant disease in concert with other global change phenomena. Many reports revealed that climate change could first affect disease directly by either decreasing or increasing the encounter rate between pathogens and host by changing ranges of the two species. Hence the disease severity should be positively correlated with increase in virulence and aggressiveness of pathogens. However, disease management strategies may require adjustment under climate change (Boland *et al.*, 2004). Since climate change effects are challenging to study but of potentially great important. Further research would be required to study the climatic change effects especially on host range, disease epidemiology, severity, pathogen population density and host pathogen interaction in bacterial wilt causing *R. solanacearum*, a diversified pathogen with global importance.