Chapter- 7

Conclusion
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CONCLUSION

Mango is the ‘King of fruits’, fifth largest and important fruit of tropical world belongs to the family Anacardiaceae. India produces 70% of the world’s Mangoes. The soil and climatic conditions of India are highly suitable for Mango cultivation. The fruit is large, fleshy, drupe containing a laterally compressed stone, housing the seed. Mango cultivars vary considerably in fruit size, colour, shape, flavour, texture and taste.

India is the home of about 1,000 varieties of Mango. Most of them are the result of open pollination arisen as chance seedlings. However, only a few varieties are commercially cultivated throughout India.

Bacteria seem to be the most primitive living organisms, diagnosis of a bacterial disease and identification of the causal bacterium is based on the symptoms of the disease, the constant presence of large numbers of bacteria in the affected area.

Bacterial black spot diseases of mango casual organism is *Xanthomonas campestris* pv. *mangiferaeindicae*, the mango leaves, stems and fruits are all susceptible to infection, on leaves it produce angular, water soaked spots, which delimited by the veins. Stem lesions appear as blackened cankers that form longitudinal cracks with bacterial exude. Fruit drop occurs especially when infection start on young fruits or when stalks become fruit infected. The disease attacks through natural openings such as stomata, wax and oil glands, leaf and fruit abrasions, leaf scars and at the apex of branches in the panicle, in young trees the diseases can cause dieback of branches.
Plants with the disease symptoms were collected randomly from major mango production districts in Karnataka are Kolar, Tumkur, Chitradurga, Belgaum, Dharwad, Koppala, Chikkamagalur, Chikkaballapura, Mysore and Bangalore Rural, fields parts such as leaves, fruits and stem, brought to the laboratory and screened for the target pathogen Xanthomonas campestris pv. mangiferaeindicae by direct plating, liquid assay methods and identified the isolates on the basis of morphological, cultural, biochemical and pathogenicity tests as per the standard microbiological procedures and results were compared with the authentic culture.

Genetic variation was identified by the Polymerase Chain Reaction-Random Amplified Polymorphic DNA (PCR-RAPD), Xanthomonas campestris pv. mangiferaeindicae isolates selected from different district and regions of Karnataka, The RAPD analysis Band statistics and cultivar similarity of RAPD markers further confirmed polymorphism among the studied 15 Xcm accessions.

Population analysis dendrogram generated based on the UPGMA analysis from the 15 bacterial genotypes data clearly grouped into two broad clusters at 80.6% dissimilarity. The group 1 contains 8 strains (KUM, DAS, PAV, GOB, PER, BET, MUT, RAYL) and remaining group contains 7 strains (MLK, TVG, BELG, YAR, KRC, BIS, LIN) formed a cluster. The PER and BET strains shared very low variability and formed cluster at 30.6% dissimilarity.

In order to control the growth of Xanthomonas campestris pv. mangiferaeindicae pathogen in vitro conditions by Antagonistic organisms, Antibiotics, commercial formulates and macro fungus and plant extracts using different solvents like pet ether, chloroform, methanol and water.
Among all the control methods, commercial formulates are very effective to control the *Xanthomonas campestris* pv. *mangiferaeindicae* followed by the other control methods.