CHAPTER I
INTRODUCTION

Cotton (Gossypium spp.) called as “King of fibres” or “White gold” is the world’s prominent natural fibre for textile industry. It is grown for its lint production. Cotton contributes 35.0 per cent of the global fabric needs and 60.0 per cent of clothing in India (Vision 2050, CICR). Seventy per cent of cotton in the world is produced by four leading countries namely India, China, Pakistan and the USA (Liu et al., 2015). In India, more than 10.0 million farmers cultivate cotton and about 30 million people are employed in value addition. India ranks first in cultivated area and production among all cotton growing countries in the World. Cotton is cultivated in eleven states of India. Area under cotton cultivation was 124.44 lakh ha, production was 343.90 lakh bales with productivity of 505.46 kg/ha during the year 2017-18 (CAB, 2018).

Among various factors influencing the cotton production, diseases are the major factors which affect the yield and quality of produce (Mohammed et al., 2003). Cotton is affected by several diseases from seedling to maturity stages by various agents like fungi, bacteria and virus. Favourable weather conditions play a crucial role in disease incidence among different cotton growing zones of India. Among the cotton diseases, bacterial blight caused by Xanthomonas citri pv. malvacearum is a major disease prevailing along the entire cotton growing regions of India. Yield losses have been estimated to range from 10 to 30% and may exceed 50% in Asia and Africa (Thaxton and El-Zik, 2001). The lint yield loss varied from 5 to 35% (Delannoy et al., 2005). In India, bacterial blight of cotton has been recorded in all cotton-growing regions every year with 30% yield loss caused by different X. citri pv. malvacearum races (Patil et al., 2003).

X. citri pv. malvacearum is an economically important bacterial pathogen causing angular leaf spot disease/leaf blight disease in cotton (Vauterin et al., 2000; Abdo-Hasan et al., 2008). Races of X. citri pv. malvacearum were identified by inoculating them into ten cotton host differential lines and so far nineteen races have been described in different parts of the world (Hunter et al., 1968; El-Zik et al., 2001).
Characterization of bacterial pathogen was very much important for selecting the appropriate breeding procedure for incorporating resistance (Ahmed, 1997). The study of the plant pathogen population structure can provide an insight into genetic diversity, evolutionary history and host adaptation (Vinatzer et al., 2014). Genetic variability study of a bacterial pathogen aims in its detection and assessment of its taxonomy and epidemiology (Singh et al., 2016). Many genotyping methods have been widely used to study the genetic diversity of the genus Xanthomonas (Valverde et al., 2007). REP-PCR fingerprinting has been proved to be highly diagnostic and has been used to assess genetic diversity within the bacterial population (Rademaker et al., 2000) including Xanthomonas at the pathovar level (Louws et al., 1999).

Effector proteins are essential for virulence and host specificity of all bacterial species with T3 secretion system (Grant et al., 2006). X. citri pv. malvacearum isolate race 18 contained 3 to 5 more effectors than other strains (Phillips et al., 2017). Different X. citri pv. malvacearum races contain different combinations of avirulence (avr) that define the race and determine cultivar specificity (Chakrabarty et al., 1997).

Management of plant diseases without damaging the environment are desirable and biocontrol agents are the best alternatives for successful control of plant diseases (Vinodkumar et al., 2017). The use of microbial based biocontrol agents as replacement for chemicals has attracted interest in many recent reports (Zhao et al., 2012). Genus Bacillus has huge potential to explore as biopesticides in plant disease control among beneficial bacteria (Pérez-García et al., 2011). Antagonistic potential of Bacillus spp. against Xanthomonas spp. has been explored in various host plants like rice, cabbage, cauliflower, soybean, anthurium, tomato, etc., Like Bacillus, actinomycetes are ubiquitous microorganisms with high potential to produce variety of bioactive molecules against the phytopathogens (Xue et al., 2013, Zeng et al., 2013). Very few studies have been conducted for the management of cotton bacterial blight using Bacillus spp. and actinomycetes, which have enormous potential in the management of the disease. Further exploration and use of these organisms are essential for successful management of disease in the field circumstances.
Many synthetic chemicals have been used to induce resistance in plants through various chemical pathways (Gozzo, 2004; Walters et al., 2005). Acibenzolar-S-methyl (ASM) was the first chemical inducer successfully commercialised and found to show varied levels of resistance to many pathogens on several plant hosts (da Rocha and Hammerschmidt, 2005). Salicylic acid treated cotton seedlings challenge inoculated with *X. citri pv. malvacearum* recorded lowest disease incidence in pot culture conditions (Gayathri and Bhaskaran, 2005).

Chandrasekaran and Chun (2016) reported the induction of PAL genes by *B. subtilis*, which induced the disease resistance against soft rot disease. Yim *et al.* (2014) observed higher accumulation of PR proteins in tomato plants inoculated with *Methylobacterium* when challenged with *Xanthomonas campestris pv. vesicatoria* and *Pseudomonas syringae pv. tomato*. Understanding the population structure, pathogenicity nature and genetic diversity of *X. citri pv. malvacearum* among different isolates, detection of effector genes in the pathogen, defense gene analysis in cotton and identification of suitable antagonists and chemical inducers against the pathogen will be a holistic approach to combat this disease.

Keeping all these points in view, the present investigation was carried out with the following objectives

1. Mapping of *X. citri pv. malvacearum* isolates from different cotton growing regions of India

2. Assessing the virulence and identification of races of *X. citri pv. malvacearum* isolates associated with cotton

3. Diversity analysis of *X. citri pv. malvacearum* isolates through molecular tools

4. Disease management using antagonists and chemical inducers *in vitro* and *in vivo* conditions

5. Identification of *avr* gene family/effecter proteins from *X. citri pv. malvacearum* isolates

6. Molecular analysis of *X. citri pv. malvacearum* defense genes in cotton