Chapter I

Introduction
INTRODUCTION
Sugar is the world’s largest primary product (FAO, 2008) and is an important component of the daily diet of the human beings. Over 127 countries are producing 166.74 million tonnes of raw sugar in the world annually, out of which 130.02 million tonnes is contributed from sugarcane alone (Anonymous, 2008a). The countries viz. Brazil, India, Australia, Mexico, Thailand, Indonesia grows the sugarcane for the production of the sugar and its byproducts.

Indian sugar industry, second largest after the textile industry is a unique agro-based industry plays a vital role in the socio-economic transformation of the country. Sugarcane (Saccharum officinarum Linn.) is one of the major economically important cash crops in India and second largest sugar producer in the world (29.09 million tones) after Brazil (33.20 million tonnes) (Anonymous, 2008b). Sugarcane is cultivated in about 51.51 lakh ha. Maharashtra, Uttar Pradesh, Karnataka, Tamil Nadu and Gujarat are the leading sugarcane producing states in the country. The sugarcane area in India is broadly classified into sub-tropical and tropical regions; the later harvest the better cane yield and sugar recovery. Maharashtra is known as sugar bowl of the country and having highest area of 10.49 lakh ha contributing 32% of the India’s total sugar production (28.33 million tones) (Anonymous, 2008c). Average cane yield of Maharashtra State is 74.9 t ha\(^{-1}\) with a sugar recovery of 11.39% as compared to India’s average 69.0 t ha\(^{-1}\) with 10.16% sugar recovery. The area under sugarcane showed an increase from 3.93 million hectares in 2003-04 to around 5.04 million hectares in 2007-08. Production increased from 233.86 million tonnes in 2003-04 to 348.2 million tonnes in 2007-08. Accordingly, yield increased from 59.4 tonnes per hectare to 69.1 tonnes per hectare in 2007-08 (Economic Survey, 2008-09; website: http://indiabudget.nic.in).

Diseases caused by a number of sugarcane pathogens that directly costs to sugar industry have seriously affected sugar production. Over 100 fungi, 10 bacteria, 3 phytoplasmas, 10 viruses and about 50 species of nematodes are identified as pests of sugarcane in different parts of the world (Singh and Waraitch, 1981). Therefore detection, quarantine and control of these pathogens, understanding their biology and epidemiology are very
important. Grassy Shoot Disease (GSD) of sugarcane is one of the important diseases caused by phytoplasma in India and other Asian countries (Viswanathan, 2000). The disease causes severe loss in number of millable canes and severity is multifold in ratoon crops. Studies show that phytoplasma infection causes 35% reduction in stalk length, 15% reduction in stalk girth and 50-60% reduction in length of internodes.

SCGS caused by Mycoplasma-like Organisms (MLOs) are cell wall-less prokaryotes, which are believed to cause many 'yellows-type' diseases of economically important crops (McCoy, 1979). Phytoplasmas are found to be associated with hundreds of plant diseases, which affect over 300 plant species. They are transmitted by phloem feeding insects such as leafhoppers or plant hoppers. Phytoplasmas are limited to the phloem of the host plant or the insect vector and cannot be cultured in vitro. Based on morphological resemblance and 16S rRNA gene sequence analysis, phytoplasmas are designated as members of the class Mollicutes. A small AT rich genome, lacks cell wall with fastidious growth requirements, characterizes members of this class. Phytoplasmas cause visual symptoms like little leaf, phyllody, stunting, yellowing, virescence, witches' broom and dieback, with little information on molecular mechanisms for the symptoms evoked in the host plants due to infection.

Phytoplasmas are an economically important group of plant-pathogenic bacteria with small genomes (w 0.5-1.3 Mbp). Knowledge of their biology is limited because they are uncultivable and experimentally inaccessible in their hosts. Phytoplasmas contain a minimal genome and lack genes coding for ATP synthases, and uptake and metabolism of sugar, making them host dependent. However, efficient techniques have been developed to sequence uncultivable organisms. Partial phytoplasma genomes sequences of Ca. P. pruni (Liefting and Krickpatrick, 2003) and Ca. P. solani (Cimerman et al., 2006) and complete genome sequence of Ca. P. australiense (Tran-Nguyen et al., 2008), Onion Yellows (Oshima et al., 2004) and Aster yellows witches’ broom (Bai et al., 2006) are now available. Phytoplasmas have low G+C content (approx 23%) which is thought to be threshold for an viable genome (Dickinson, 2003). Phytoplasmas with large genomes seem to have large repeat regions (Bai et al., 2006). Phytoplasma genomes
contain large numbers of transposon genes, insertion sequences and genes for specialized sigma factors. They also contain a unique family of repetitive extragenic palindromes (REPs) called PhREPS. Although PhREPS role is unknown, the stem loop structure of these regions plays a role in transcription termination or genome stability (Jomantiene and Davis, 2006). The Potential Mobile Units (PMUs) appear to be unique to phytoplasmas and are found to be mainly responsible for genomic variability. The dynamic genome enables the phytoplasmas to adjust to the diverse environments of plants and insects, as well as leading to the marked heterogeneity in genome size among closely related phytoplasmas. They have extensive chromosomal rearrangements among strains within subgroup and contain multiple uncharacterized repetitive sequences (Bai et al., 2006; Jomantiene and Davis, 2006; Tran-Nguyen et al., 2008).

Sequencing and annotation of several phytoplasma genomes revealed several significant differences among plant and animal mycoplasmas. Despite of their very small genomes, many predicted genes are present in multiple copies. Phytoplasmas lack many genes for standard metabolic functions such as the F-type ATPase (Oshima et al., 2004) have no functional homologous recombination pathways but do have a sec-dependent transport pathway (Bai et al., 2006) Many phytoplasmas contain 2 rRNA operons. Unlike the rest of the Mollicutes, UGA is used as a stop codon in phytoplasmas, which normally codes for tryptophan (Razin et al., 1998). Though the sequence information made available from diverse class of Mollicutes very less sequence homology (except 16S rRNA gene) is available with casual agents reported from Asian origin. Hence, SCGS genome analysis is need of today, a severe pathogen of sugarcane (Wongkaew et al., 1997; Viswanathan, 2000; Singh et al., 2002). SCGS causes severe loss in number of millable canes in ratoon crops with significant reduction in yield. This lack of information on functional genomics of phytoplasmas and genome heterogeneity necessitates the characterization the SCGS genome inhabitant in Indian sub-continent and elucidate the host response to develop the control strategies.