Sugarcane (Saccharum spp. hybrid) is one of the important commercial crops and is the principal source of raw material for sugar, accounting for about 78% of world's sugar production. Sugarcane also produces valuable by-products and co-products. Currently sugarcane is considered as one of the best converters of solar energy into biomass and sugar (Yadav and Solomon, 2006). India is the second largest producer of sugarcane in the world with a total cane production of 355.52 million tons cultivated in about 4.90 million hectares (FAOSTAT, 2008).

Sugarcane production throughout the world is significantly constrained by several virus diseases (Smith and Rott, 2003). Among them, mosaic disease caused by potyviruses is the most wide spread and occurring in almost all sugarcane growing countries. The mosaic disease caused severe economic losses to sugar industry and is responsible for the decline of important commercial clones in several countries. Estimated yield losses from the disease vary greatly, losses of 30-40% were commonly reported and some times 60-80%. The incidence of mosaic disease in commercial sugarcane fields appears to be 100% in some varieties in almost all sugarcane growing states of India (Hema et al., 2008).

Worldwide, mosaic disease was reported to be caused by Sugarcane mosaic virus (SCMV), a definitive species of the genus Potyvirus, family Potyviridae (Fauquet et al., 2005). But, in India and several other Asian countries like Pakistan, Bangladesh, Sri Lanka, Indonesia, Thailand and Vietnam Sugarcane streak mosaic virus (SSMV), an unassigned member of probably a new genus in the family Potyviridae was also reported to be the causal agent of the disease apart from SCMV (Hema et al., 2008). Sorghum mosaic virus (SrMV) also infects sugarcane in some countries and causes mosaic disease (Smith and Rott, 2003)

Since its first report in the year 1998, the correct taxonomic position of SSMV is still ambiguous. Initially the virus was thought to belong to the genus Tritimovirus in the family Potyviridae because the first obtained SSMV partial 3'-terminal genome sequences showed maximum similarity with that of Wheat streak mosaic virus (WSMV), type species of the genus and there was no significant similarity with other members of Potyviridae (Hema et al., 1999). Later it was
reported that the virus does not belong to any of the existing six genera of *Potyviridae* (Hema *et al.*, 2002). So far, the SStMV genome was not completely sequenced. However, in previous studies only partial genome sequences of SStMV were analyzed and thus the taxonomic position of SStMV and its relationships with other members in the family *Potyviridae* remained uncertain (Hema *et al.*, 2002). Analysis of whole genome sequence data of SStMV justifies its correct taxonomic position in the family *Potyviridae*.

The two distinct viruses, SStMV and SCMV induce very similar interveinal chlorotic streak mosaic symptoms in infected sugarcane and sorghum and are indistinguishable based on the visible symptoms. Some virus infected sugarcane cultivars rarely or never show obvious signs of mosaic symptoms. Furthermore, symptom expression may also be influenced by environmental conditions such as soil fertility, water availability and temperature that misleads the symptom based diagnosis. Mixed infections of these two viruses are also common in sugarcane (Rao *et al.*, 2004; Viswanathan *et al.*, 2008). Thus the differential diagnosis of these two viruses is essential to screen sugarcane germplasm, imported / exported sugarcane, virus-free planting material generated by tissue culture technology, to study the molecular epidemiology of the two viruses and for routine laboratory testing. Further, the differential diagnosis of these two viruses is important, because they have differences in their transmission properties in nature (Hema *et al.*, 2008) which can be exploited in the management of these virus diseases in commercial fields.

So far SStMV was reported from India and a few other Asian countries only (Hema *et al.*, 2008). Countries wishing to import sugarcane varieties from SStMV prevalent regions are concerned about the accidental introduction of SStMV through infected sugarcane plant material. Quarantine procedures for sugarcane viruses involve growing plants for upto 2 years and disease screening by regular visual inspections as well as various other techniques (Saumtally *et al.*, 1996). If the plant material is found to be infected, it is destroyed, hence loss of valuable sugarcane planting material with superior agronomic traits. Moreover, sugarcane crop is being maintained year after year permanently for hybridization and breeding purposes (Balamuralikrishnan *et al.*, 2003). Therefore, the virus built up is very fast over the period and drastically reduces the crop stand and vigour during subsequent years. Consequently, there is a need for rapid and reliable method for the elimination of
In light of the above information, the following are the objectives of the present study.

**Objectives**

1. To analyse complete nucleotide sequence and genome organization of *Sugarcane streak mosaic virus* with an aim to determine its correct taxonomic position in the family *Potyviridae*.

2. To develop duplex-immunocapture-RT-PCR (D-IC-RT-PCR) for simultaneous detection and discrimination of SStMV and SCMV.

3. To generate SStMV-free sugarcane (*Saccharum* spp. hybrid) from infected plants by *in vitro* meristem tip culture technology.