1. INTRODUCTION

In recent years, aneuploids are efficiently being used in deriving many valuable basic informations on genetic mechanisms useful for increasing the efficiency of synthesizing new and better cultivars according to the need of modern agriculture. In this context monosomic and nullisomics that are deficient in one or a pair of chromosomes respectively, have been extensively utilised in locating genes on specific chromosomes and in tailoring the genotypes to specific needs through alien addition and substitution of chromosomes (Sears, 1958). However, monosomics and nullisomics were not found useful in crops which are presumably diploids where deficiency of one or a pair of chromosomes is deliterious since each chromosome of the complement in such plants is critical for gametophytic and sporophytic survival. In such cases trisomic analysis are often found fruitful as has been done in barley (Tsuchiya, 1960, 1967) maize (McClintock and Hill, 1931) and tomato (Rick and Barton, 1954).

The concept of trisomics developed with the discovery of 12 primary trisomics corresponding to 12 basic chromosome number in Datura stramonium by Blakeslee (1921). Subsequently, several other types such as secondary, tertiary and compensatory trisomics (Blakeslee, 1924; Blakeslee and Belling, 1924b; Blakeslee, 1927b) were developed which
stimulated intensive research on the use of trisomics in fundamental and applied genetical studies on crop plants.

Utilising trisomics Bridges (1921a) located genes on specific chromosomes of *Drosophila*. McClintock and Hill (1931) using trisomics identified the chromosome containing R-G linkage groups in maize. The trisomic method of identifying individual chromosomes with their respective linkage groups as a result of a modification of genetic ratios by extra chromosomes was also successfully applied to a number of crops of which successful results were obtained where a complete set of trisomics corresponding to the haploid number of a species are available, and the trisomics were morphologically distinguishable from each other and where the extra chromosomes were easily identifiable either at mitosis or meiosis.

*LYcopersicon*, maize, *solanum*, barley, wheat and spinach etc. (Sears, 1953, 1958; Tsuchiya, 1960; Janick *et al.*, 1959; Kamanoi and Jenkins, 1962) are some notable examples where trisomic analyses have been successfully employed.

Besides, the trisomics were also useful in solving many other plant breeding problems. Cole (1956) used both primary and secondary trisomics in promoting the production of hybrid embryo in interspecific crosses of *Datura*. Ramage and Tuleen (1964) established two tertiary trisomics of barley which were heterozygous for the homozygous lethal
recessive albino gene. A tertiary trisomic was produced in which the modified chromosomes carried the normal allele of albino while the normal chromosomes carried the albino alleles. Pollen from these trisomics could be used for producing heterozygous disomics and the albino stock was maintained through self pollination of heterozygous trisomics. A tertiary trisomic can also be used as a fertility restorer in a programme of hybridization utilising male sterility (Khush and Rick, 1967). The balance tertiary trisomics has been utilised for the production of hybrid barley seeds (Ramage, 1965).

Though it has been clearly established that the trisomic analysis is an indispensible tool for assigning genes and linkage groups to specific chromosomes, mapping the centromeres, and determining the independence and orientation of linkage groups, this sophisticated technique has not yet been utilized in rice, despite the identification of trisomics in this, as early as early thirties (Nakamori, 1932; Ramanujam, 1938).

In indica rice, trisomics were isolated by Karibasappa (1961), Jachuck (1963), Sen (1965) and Jagdish (1969). Though all these scientist worked on the same source they could not identify a complete set of primary trisomics. However, Iwata et al. (1970) isolated a complete set of trisomics in japonica rice utilising short duration
photoinsensitive autotriploid. Watanabe and Koga (1975) also developed another set of 12 trisomics in *japonica* rice. Utilising these two sets of primary trisomics Japanese scientists have made a good beginning for assigning the genes belonging to different linkage groups with specific chromosomes. Till date more than 22 genes have already been identified and assigned to different chromosomes (Iwata and Omura, 1975, 1976).

Their investigation also yielded valuable information on the independence of linkage group. However, such studies have not yet been taken up in *indica* rices, the linkage groups of which are different from that of *japonica* rices (Misro *et al.*, 1966; Nagao and Takahashi, 1963).

In view of the above considerations and with realisation of basic and applied significance of trisomic analysis in relation to crop improvement, the present study is, therefore, undertaken with the following salient objectives.

* To identify a complete set of primary trisomics in one genetic background.

* To study quantitative and qualitative alterations accompanied by the extra chromosome present in each trisomic.
* To identify and study the morphology and pairing of extra chromosome of each trisomic at pachytene stage of meiosis.

* To study the transmission of extra chromosome of each trisomic through hybridization and selfing.

* To identify and locate some genes and their respective linkage groups of specific chromosomes utilising the trisomics.