Introduction
CHAPTER 1

INTRODUCTION

Rice is a pivotal cereal crop of the developing world and the staple food of more than half of the world’s population. It is the unique grain that is nearly entirely used as human food, unlike other cereals, which are also used extensively as feed. Worldwide, more than 3.5 billion people depend on rice for more than 20% of their daily calorie intake (IRRI, AfricaRice and CIAT 2010). Globally, rice is grown on a total harvested area of approximately 158 million hectares, producing more than 700 million tons of paddy yielding 470 million tons of milled rice annually (IRRI, AfricaRice and CIAT 2010). About 90% of the rice in the world is grown and consumed in Asia (nearly 640 million tons), with China as the lead producer. Among the rice growing countries, India is the largest grower and the second largest producer of rice in the world. Rice in India occupies 44 m ha area with an annual production of 104.32 million metric tons of milled rice during 2011-12 crop year (FAO, 2012)). The demand for rice in India is likely to 120 million mt by 2020 and it will increase to 140 million metric tons by 2025. This predicted increase in water scarcity, decrease in arable land, constant battle against new emerging pathogens and pests, and possible adverse effects from climate change such as rise in atmospheric temperature, increased soil salinity and submergence, present great challenges for rice breeders and agricultural scientists (Mew et al., 2004, Peng et al., 2004). Given the fact that there is not much scope for horizontal increase in area under rice cultivation, vertical increase in production i.e. productivity has to be undertaken as a priority area of research in genetic improvement of rice for increasing food production.

Rice initially being domesticated in Asia is now cultivated in more than 113 countries. Based on the archaeological–historical references in India, the age of rice samples excavated from Hastinapur, north Delhi between 1100 and 700 B.C. in a radiocarbon dating study. Based on the studies made on the Harappan sites, where the impression of rice grains were found, it was assumed that rice was imported to western India from the east in the 17th century B.C. and into central India perhaps a century later., accordingly, it can be reasonably be said that rice has been known in India from about 2000 B.C. or much before to Harappan civilization.. Later it was generally accepted that the cultivated rice Oryza sativa Linnaeus originated in South-west Asia and Oryza glaberrima Steud originated in Niger river delta of Africa. The two main sub species of the cultivated rice, O. sativa are japonica and indica, and both are evolved geographically and culturally over several thousand years at diverse ecosystems. Over the millennia, different types
of rice evolved under cultivation in different conditions. Today, there are four general ecosystems under which rice is grown: irrigated, rain-fed lowland, upland, and flood-prone (http://www.fao.org/rice2004/en/concept.htm). There are thousands of cultivars of japonica and indica rice grown worldwide.

Rice is a mainstay for the rural population and is mainly cultivated by small farmers in holdings of less than 1 hectare of land. It is also a wage commodity for workers in the cash crop or non-agricultural sectors and is vital for the nutrition of much of the population in Asia, Latin America, Caribbean and in Africa. It's rich genetic diversity in the form of thousands of land races and progenitor species, besides its economic significance, has aroused unending interest among scientists for several decades.

Rice higher yield and better taste are two major subjects for many breeding programs but, in contrast to disease and insect resistance, grain yield and quality are both controlled by quantitative trait loci (QTLs) showing continuous phenotypic variation in rice progeny (Yano and Sasaki, 1997). It is thus difficult for breeders to improve rice grain yield and quality using conventional methods, due to a lack of discrete phenotypic segregation in the progeny. As rice grain quality is an endosperm trait, its inheritance can be more complicated because the genetic expression of an endosperm trait in cereal seeds is conditioned not only by the triploid endosperm genotype, but also by the diploid maternal genotype and any additional possible cytoplasmic differences (Zhu and Weir, 1994). To accomplish this, crop improvement programs should aim at broadening the genetic base of the breeding stock (Vanaja and Babu, 2004). Modern molecular marker based approaches provide an opportunity of looking into the phenotypic variation in specialized segregating populations, in association with segregation of DNA markers distributed over the entire genome.

Grain quality is an important consideration in rice production. There is tremendous variation for grain quality characters in different subspecies and varieties of rice, providing the basis for the differentiation of rice that are preferred for medicinal or for ceremonial purposes, or for use in specialty products such as flour, noodles, sake, sweets, or fast foods (Li, 2003). Preferences for rice grain performance and cooking quality vary among rice consumers living in different parts of the world or even among people living in different regions of the same country.
The primary components of rice grain quality include appearance, eating, cooking, milling and nutritional qualities. The texture of cooked rice is largely dependent upon the amount of amylose in the grain. These factors influence how the rice grain cooked. Short, medium, and long grain cultivars are evaluated for amylose content and the temperature at which the starch gelatinizes to meet the criteria that are set for each grain type by the industry. Each of these components consists of attributes that are determined by the physico-chemical properties of the rice grain and the standards depend on the socio-cultural factors such as the history and traditions of the localities where rice is grown. The second major criterion is taste. Good eating quality relates to stickiness, sweet flavor, gloss of the cooked rice and palatability (Mutters, 2000). Rice starch is the major component of grains and a common ingredients used in the food industry. Starches are mainly used in foods as an agent for thickening and gelling. Starch properties depend on the physical and chemical characteristics such as mean granule size, granule size distribution, amylose/amylopectin ratio and mineral content. Rice starch granule being very small in size provides a texture perception similar to that of fat and is non-allergic due to the hypoallergenicity of the associated proteins. Rice starch, in its gelatinized form, has a bland taste and is smooth, creamy and spreadable.

Rice yield is the other major agronomic trait in crop breeding programs and is the final product of the manifestation of several interrelated components, such as number of tillers per plant, grain number per panicle and grain weight and is therefore a very complex quantitative trait. The dissection of such a complex trait by means of QTL mapping approach will help to better understanding of molecular mechanism involve in such complex trait. Molecular understanding of complex traits and the fine map of loci responsible for it assist breeders to enhance the yield potential of rice. Demand for QTL analysis of complex traits is increasing because of its potential to facilitate the effective manipulation of traits of importance in rice breeding. The first step in this approach is to map chromosomal locations responsible for the quantitative traits by following the segregation of trait with molecular marker. A segregating population with contrasting background is necessary for the segregation analysis. The genotyping data of segregating population developed by molecular markers helps to locate the markers in linkage groups and construct a molecular linkage map. Yield improvement is always an important priority for plant breeder and most of the yield components govern by quantitative trait loci (QTL). Thousands of QTLs have been identified for yield components however few of
these were cloned. The identification of candidate gene(s) involve in the development of quantitative trait has been difficult because of their minor effect and interaction with the environment. However, rapidly developing marker technology, statistical methodology and availability of rice genome sequence leads to predict candidate genes in the QTL region. Such regions are generally large, containing hundreds if not thousands of putative genes. Fine mapping of the QTL can reduce the number of candidate genes to below hundred. But, even after fine mapping, it is difficult to pinpoint the causal gene for the development of desirable phenotype. Once the candidate QTLs/genes are identified, fine mapping can be carried out to find a tightly linked marker to the trait, eventually allowing the cloning and characterization of the specific genes for the production of transgenics or significantly assist in a conventional breeding program through marker aided selection. During the past decade, many attempts have been made to characterize the QTLs for grain yield. Identification of candidate genes at QTL interval for yield components will greatly help in genetic manipulation of yield which will ultimately lead to the development of high yielding rice varieties. Along with the identification of candidate gene for map based cloning, development of fine map of QTL region has importance to generate more reliable tightly linked molecular marker for marker assisted breeding.

The present study aimed to see the allelic diversity of the genes involved in starch biosynthetic pathway in a set of diverse germplasm lines and fine map the QTLs for yield and yield contributing traits using a F2 mapping population developed from NPT derived population.

In the view of above, the present investigation therefore, is undertaken with the following objectives.

I: Phenotyping, validation of gene based markers and allelic diversity for starch related properties in rice (amylose content and alkali spreading value).

II: Development, phenotypic and molecular characterization of F2 derived population for fine mapping of a major QTL (qSPP4-I) for yield components in NPT derived population in rice.