Sweet potato is a dicotyledonous species belonging to the morning glory family, Convolvulaceae. It is a perennial crop which serves as one of the major sources of food, animal feed and industrial raw materials. It has a significant contribution as energy supplement and phytochemical source of nutrition. It is widely cultivated in the tropics, subtropics and even in some temperate zones of the developing world. Contribution of sweet potato towards health is acknowledged due to high nutrient content and its anti-carcinogenic and cardiovascular disease preventing properties. Almost all genotypes of sweet potato are excellent source of vitamin C, B_2, B_6 and E, as well as dietary fiber, potassium, copper, manganese and iron, and are low in fat and cholesterol. Sweet potato is the seventh most important crop in terms of global production. In developing countries, it ranks third in value of production and fifth in caloric contribution to the human diet. Asia is first in sweet potato production followed by Africa and South America. Since it is one of the main food sources for the poorest class of population in underdeveloped and developing countries, a major target has been to improve its nutritional value by increasing protein content and amino acids.

Improvement in nutritional value for crop species has been a major long-term goal of plant breeding programs. Humans require a diverse and nutritionally well-balanced diet for the maintenance of optimal health. Therefore global scientific research is focused upon improving the nutritional qualities of food crops. This has become an increasingly critical issue in developing countries, particularly in India, where plants are the major primary nutritional support in the human diet and animal feed. Seed storage proteins, intended as a source of nitrogen for germinating seedlings, form an important source of dietary protein for human beings. Humans require a diet with a balanced amino acid composition, but often seeds are deficient in some of these essential amino acids. Earlier, a nutritionally balanced seed albumin protein, AmA1 from *Amaranthus hypochondriacus* was identified and the full-length cDNA clone encoding *AmA1* was isolated. The amino acid composition of AmA1 shows a high proportion of essential amino acids that are otherwise deficient in the major food crops. Interestingly, the AmA1 amino acid composition closely matches the values recommended by the World Health Organization, making it more important nutritionally. Thus, *AmA1* might be a promising candidate for crop improvement by genetic engineering.

The aim of this study is to increase the nutritional value of sweet potato by introducing the seed albumin gene *AmA1* through *Agrobacterium*-mediated transformation. Earlier, the improvement of nutritional quality of white potato in terms of protein content and amino acid composition was reported. It is thus hypothesized that the introduction of *AmA1* would increase the nutritional value of sweet potato in terms of protein quality and quantity. This improvement strategy may prove to be more acceptable since *AmA1* is an edible crop derived sequence.

The prime objective was to introduce *AmA1* cDNA into sweet potato plants in such a way so that expression would be effected in both constitutive and tuber-specific manner. Earlier *AmA1* cDNA was cloned under the control of *CaMV-35S* promoter in pSB8. For tuber-specific expression, *CaMV-35S* promoter in pSB8 has already been replaced by *β-amylase* promoter of sweet potato and the construct thus resulted has been named as pSB8ß. A reporter gene construct pBI121 containing *uidA* and *nptII* genes, has also been used in this study. Furthermore, to develop a reproducible regeneration and transformation system, various genotypes and different sources of explants like leaf, petiole, roots and internodes were used with different media and hormone combinations. In the next step, successful integration and expression of transgene was confirmed by PCR, qRT PCR and by immunoblot analysis at genome, transcriptome and proteome level, respectively. Further, a comparative expression analysis of both the transcript and protein level was carried out in this study. In addition, a series of biochemical and agrophysiological characterization was also performed to assess the effect of transgene integration at different levels. Besides these proximate analysis was also performed to assess the quality traits.

Metabolites are the consequence of the interaction of the system's genome with its milieu, and are not merely the end product of gene expression but also form part of the regulatory system in an integrated manner. So as to elucidate the factors pertaining to the varietal differences, and transgene mediated changes in the level of metabolites, a comprehensive analysis of phytochemicals as well as the metabolome profiling of wild type and transgenic tubers was performed. A comparative metabolite analysis was performed to check the phytophenols and carotenoid contents in this study. Additionally, metabolite profiling of sweet potato tubers was performed using GC-MS to check the effect of transgene at metabolite level.

Chapter I, the Introduction, presents the importance, characteristics and advantages of sweet potato along with the need for its improvement. This chapter also deals with different strategies pertaining to the transformation and analyses of a transgenic crop at various levels.

Chapter II, includes the Review of Literature, and presents comprehensive review on the contemporary work on the transformation of sweet potato. In addition, it also gives a panoramic view of different works carried out in sweet potato, including the use of different methodologies regarding the downstream analysis. Moreover, it also provides a broad spectrum of AmA1 as a candidate gene for nutritional improvement(s) of a protein deficient crop.

Chapter III is about the establishment of an efficient and reproducible regeneration and transformation system in sweet potato. It discusses in details the effect of different media and hormones on different explant sources and their response.

Chapter IV gives a detailed molecular analysis of putative transformants. The introduction of transgene and its expression is analyzed at different levels, and a comparative analysis is performed *vis-à-vis* to the wild type.

Chapter V is about the biochemical and agrophysisological analysis of the selected transgenic lines. To negate the possibility of natural and/or somaclonal variations amongst the transgenic lines, a closer wild type relative (WFSP-WT) of cv. SP-6 (OFSP-6) is also considered. A comprehensive analysis of primary metabolites is performed and transgene mediated changes has also been monitored.

Chapter VI gives a detailed investigation of the transgene mediated changes in secondary metabolites. This includes the analysis of phytophenols and carotenoids. Further, metabolite profiling was also performed by GC-MS and the comparative analysis of metabolome between wild type and transgenic lines was also performed.

Chapter VII is on the conclusions of the present study and also gives the future prospects of this work.

The final part of the thesis contains the references and appendices.