ABSTRACT

Beans (*Phaseolus vulgaris* L.) are important food legume both economically and nutritionally, and consumed in diverse recipes throughout the world. Progressive improvement strategies through biotechnological approaches could improve understanding of genes expression and molecular process that could be manipulated to generate new common bean varieties that are suitable and desired by the local farmers and consumers. Construction of cDNA library containing full-length cDNAs is a robust method for gene discovery and plays an important role in characterizing gene structure through computational analysis. The research work presented in this thesis is a part of an international consortium called '*Phasecomic*' (as for *Phaseolus* Genomic). In this consortium, our responsibility was to study the transcribed genes from bean-pod-tissue. Therefore, the objective of this study was to isolate and annotate cDNA sequences from bean (genotype BAT93) pods-tissue. From University of Geneva, Switzerland bean seeds were collected and pods-tissues were harvested from field grown plants. Total RNAs were isolated from early [5 Days after anthesis (DAA)] and late (20 DAA) stages bean-pod-tissue and mRNAs were purified from isolated total RNAs. Two full-length cDNA libraries were constructed using CloneMinor Kit and generated recombinant clones were sequenced. In total, 5864 reads (5'ends) provided a good quality sequences which were useful in identifying full-length cDNA clones generated from both cDNA libraries. Results analysis suggested that a total, 1011 reads were indicative of full-length cDNAs. The full-length sequencing and analysis suggested that the average size was about 1.3 kb in length. Comparative analysis of transcripts for their G+C content and sequenced composition analysis indicated that ORF have higher (45%) G+C content than UTRs. The majority (40.5%) of transcripts were with UGA as its stop codon. We also found 6 and 4 full-length transcripts which encodes for important proteins involved in the fatty acid and isoprenoid pathway, respectively. Functional annotation of the full-length cDNAs based on InterPro signature indicated coverage of a broad range of gene ontology categories. Based on our finding, we reveal that *P. vulgaris* BAT93 genome is rich in A+T in the coding region. In conclusion, the generated 1011 full-length cDNAs and its annotation could serve as an important informative data in the bean improvement programmes. The generated data and full-length cDNA clones could also serve as foundation for the further research on bean pod transcripts and its deduced protein sequences. The full-length cDNA clones can be used in genetic engineering of beans as well as in bean breeding programs which could potentially contribute to food security, poverty alleviation, and economic development.