India may require about 38 million tonnes of pulses by 2017–18 to meet the WHO recommendation of 80 g protein/person/day to avoid protein malnutrition. India contributes to 90% of the total global production of pigeonpea (Cajanus cajan L.) one of the major pulses that contributes to protein dietary requirement. Pigeonpea is cultivated approximately in 3.5 mha with a production and productivity of 2.57 mt and 600-800 kg/ha respectively. The major constraints for productivity of pigeonpea are inadequate availability of improved varieties, prevalence of biotic and abiotic stress and poor crop management. The National Bureau of Plant Genetic Resources (NBPGR), New Delhi, the custodian of the genetic wealth of crops houses about 16,000 accessions of Pigeonpea. To exploit the full potential of the genetic diversity of conserved pigeonpea germplasm, a targeted screening of all the germplasm for identification of useful/superior accession is required. The identified accession may be utilised directly for increasing the crop productivity and may also be suitably modified by conventional breeding. Decoding of pigeonpea genome and development of molecular markers provides useful resources for improvement of pigeonpea. 21434 transcripts were collected from online databases. After filtering poor quality sequences with maximum stringency, we could get 1699 high quality mRNAs; identified 95 lincRNAs and 385 lncRNAs. Non-coding and weak-coding sequences were analysed for miRNAs based on their secondary structure and predicted conserved as well as novel miRNAs. The targets for the miRNAs were predicted. De-novo annotation of targets identified genes and pathways. 624 miRNAs were identified of which 73.61 per cent may act by cleavage of their targets and 26.38 per cent by translation inhibition.