2.4.2 Syamuyoba Phillip, (2002). Characterization of Zambian pigeon pea (*Cajanus cajan* (L.) Millsp.) germplasm using morphological characters. (Supervisor: Dr. C. Gwanama).

Pigeon pea (*Cajanus* cajan (L.) Millsp) is of great importance in Zambia for its diversified use, which can lead to increased farm income and subsequently food security at household level. Its seeds have a protein content of approximately 21 % and therefore are a cheap source of protein in the human diet. The National Genebank, which has a responsibility for collecting and conserving all locally available crop germplasm, has a collection of accessions of pigeon pea that have not been characterized. Lack of characterization to obtain genetic information about these accessions has caused the germplasm not to be widely utilized by end-users such as plant breeders in the breeding programs and the magnitude of genetic variation has so far not been assessed. The objective of this study was to assess genetic variation among accessions of pigeon pea conserved at the National Genebank and to determine characters that are useful in classifying pigeon pea. Twenty-eight accessions were assessed for genetic variation based on morphological characters at Mount Makulu Central Research Station, Chilanga, Zambia during the 2000/2001 growing season. The design of the experiment was a single block and each accession was planted on a single unreplicated plot. Twenty-three characters (plant height, number of branches, leaf size, days to 50% flowering, days to 80% maturity, number of racemes, seeds per pod, 100-seed weight, growth habit, stem colour, stem thickness, leaf hairiness, leaflet shape, flower colour, second flower colour, pattern of streaks, flowering pattern, pod colour, pod hairiness, pod form, seed colour pattern, seed colour and seed shape) were measured following IBPGRI/ICRISAT (1993) pigeon pea descriptor list and analysed using cluster analysis and principal component analysis. Cluster analysis grouped the accessions into four major clusters based on commonly shared characters. Three principal components were found to explain 73.9% of the total morphological variation. Days to 50% flowering, days to 80% maturity, number of branches, number of racemes, plant height, number of seeds per pod, stem colour, flower colour, pod colour, colour of the seed coat and flowering pattern were the major sources of variation among the accessions. Based on these results, it is concluded that there is genetic variation among the accessions of pigeon pea conserved at the National Genebank. It is further concluded that

characters that were the major sources of variation are useful in classifying pigeon pea germplasm. These results could be useful in pigeon pea improvement programs.