Cowpea (Vigna unguiculata (L.) Walp) is one of the most important protein sources in the diet of tropical Africa, Brazil and India. All evidence points to an African origin of V. unguiculata. Development of specific markers is necessary for cultivar identification and protection, and cultivar purity determination. Studies on genetic variation of seed protein composition can be useful in identification of particular genotypes available for the improvement of the protein content and/or the amino acid composition. The major seed storage protein in Leguminosae are globulins that includes legumins, vicilins and lectins. The major component in cowpea is vicilin: a legumin-like globulin is also present. No haemo-agglutinating fractions were detected.

Vigna unguiculata accessions collected in different regions of Mozambique were analysed by using vicilin genes.

The vicilin genes were amplified from genomic DNA by polymerase chain reaction (PCR) using left and right primers (VICL and VICR) designed by using Phaseolus vulgaris vicilin sequences. The PCR products appeared as 9 bands approximately in a range from 900 to 600 bp. They were cloned using TOPO TA Cloning system. The single insert were selected by PCR colony screening using as primers M13 forward and M13 reverse. Complete sequences were obtained for vicilin genes. Sequence analysis was used to evaluate the vicilin genetic diversity among cowpea and other different Leguminosae species.

The DNA sequences were aligned using the Clustal W program and the alignment was slightly manually improved. The ambiguously aligned regions were excluded from the analyses.

The analyses allowed the identification of the genetic relationships between different samples from Mozambique ecotypes.