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## Genetic diversity analysis among pigeon pea genotypes using the SSR marker

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**P**igeon pea is an important pulse crop grown in tropical and subtropical regions of the world. Inspite of all the efforts made over past few decades for improvement of pigeon pea through conventional breeding ,its productivity has remained constant. Thus it is needed to improve the effectiveness and efficiency of conventional breeding methods .The efficiency of conventional breeding can be improved by using molecular markers. Determination of genetic diversity of any given crop species is a suitable precursor for improvement of the crop because it generates baseline data to guide selection of parental lines and design of a breeding scheme. Here an attempt is made to access the molecular diversity using SSR marker .SSR marker have the advantage of high abundance, random distribution within the genome, high polymorphism information content and co-dominant inheritance. The objectives taken are to indentify polymorphic SSR marker for pigeon pea, to characterise the promising lines using polymorphic markers to determine the extent of genetic divergence among the lines to determine the genetic relationship among pigeon pea cultivars.

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