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Phytochemical analysis and antimicrobial activity of cassia species

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The trend of using natural products has increased and the active plant extracts are frequently screened for new drug discoveries. The present study deals with the screening of Cassia leaves for their antimicrobial activity against various strains of bacteria. Plant Cassia belongs to family *Caesalpiniaceous*, is a diffuse offensively odorous under shrub. Cassia was shade dried, powdered and was extracted using different solvent sand the antimicrobial activity test performed by the agar well diffusion method. Preliminary phytochemical analysis of the plant extracts fractions showed the presence of carbohydrates, amino acids, phytosterols, fixed oils and phenolic compounds. The C. occidentalis showed high activity across *Pseudomonas aeruginosa* and *Staphylococcus aureus* bacteria. The present study indicates the potential usefulness of Cassia leaves in the treatment of various diseases caused by microorganisms.

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Genetic interactions of multifoliate-pinna (mfp), afila (af), tendril-less (tl), unifoliata (uni) and leaflet development (lld) mutants and their mapping studies in pea *Pisum sativum*

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Pisum sativum commonly called as grain pea, garden pea, green pea, field pea etc., is one of the agriculturally important plants of Fabaceae family. The grains produced by this crop are a source of carbohydrates and proteins. The species has been extensively used in physiological studies and as an important model for studying the compound leaf development. There have been a number of studies conducted in pea, aimed at understanding the genetic basis of its leafblade morphology because of several reasons. These include its being a pulse crop and variation in leafblade pattern and growth properties from other model systems. In pea, a suite of mutants in which morphologies of stipule or leafblade are different from normal (wild type) are available. The analyses of mutants have added knowledge about genetic control of compound leaf morphogenesis. The interactions of MFP, AF and TL in leafblade development have been studied earlier. The effects of interactions of LLD, MFP, AF and TL with UNI in leafblade development remain to be explored. One of the objectives of present work was to increase the knowledge about the roles of five of the above mentioned genes namely UNI, TL, AF, MFP and LLD in leafblade development and their co-regulation in biomass partitioning among root, stem, stipule, leaf blade and seeds. With this regard, the leafblade morphologies of all the 16 genotypes were compared qualitatively and quantitatively. Thus, it became possible to make deductions about the interactive roles of mentioned genes in compound leafblade patterning. It was also observed that LLD act as a master regulator of pinna development in compound leaf.Another objective of the present study was to locate the position of mfp and lld mutations on the established linkage groups of pea.

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