Nat Prod Chem Res 2015, 3:6
http://dx.doi.org/10.4172/2329-6836.C1.008

OMICS International
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3rd International Conference and Exhibition on
Pharmacognosy, Phytochemistry & Natural Products
October 26-28, 2015 Hyderabad, India

Chemical constituents and biological studies of medicinal plants

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Green plants synthesize and store a variety of biochemical compounds some of which extractable as raw material and can be used for various scientific investigations. The aim of this study is to extract and identify biologically active volatile chemical compounds from *Tagetes minuta*. This aromatic plant was considered for extraction of essential oils using hydrodistillation method as prescribed by British pharmacopeia. Cis-β-ocimene (38.08%), caryophyllene oxide (18.04%), cis-ocimene (38.14%) and trans-β-ocimene (37.03%) are the major components of essential oil identified from fresh stem, dry stem, fresh flower and dry flower, respectively. The above compounds were identified by Gas Chromatography-Mass Spectrometry (GC-MS). This is an on-going investigation and therefore biological studies of essential oils extracted from *Tagetes minuta* are still to be considered for its application.

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HerbBOL: Herbal barcode of Life

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Numerous adverse reactions such as aristolochic acid nephropathy and herb-induced poisoning have prompted increased global concern over the safety of herbal medicines. DNA barcoding provides a powerful new tool for addressing this problem. A preliminary system for DNA barcoding herbal materials has been established based on a two locus combination of ITS2+psbA–trnH barcodes. There are 78,847 sequences belonging to 23,262 species in the system, which include more than 95% of crude herbal drugs in pharmacopeia such as those of China, Japan, Korea, India, USA, and Europe. The system has been widely used in traditional herbal medicine enterprises. For example, a detection of 100 *Rhodiolae crenulatae* Radix et Rhizoma decoction piece samples purchased from drug stores and hospitals showed that that only 40% of the samples were authentic *R. crenulata*, which is recorded in Chinese Pharmacopeia, whereas the other samples were all adulterants and may indicate a potential safety issue. A Circular Consensus Sequencing (CCS) strategy involving Single Molecule, Real-Time (SMRT) DNA sequencing technology was applied to de novo assembly and single nucleotide polymorphism (SNP) detection of chloroplast genomes. Comparisons of the three assembled *Fritillaria* genomes to 34.1 kb of validation Sanger sequences revealed 100% concordance and the detected intra-species SNPs at a minimum variant frequency of 15% were all confirmed. We recommend this approach for its powerful applicability for evolutionary genetics and genomics studies in plants based on the sequences of chloroplast genomes.

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