GENETIC VARIATION AND MEDICINAL ACTIVITY IN *OCIMUM GRATISSIMUM* L. OF KENYA

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ABSTRACT

Hydro-distilled volatile oils from the leaves of *Ocimum gratissimum* L. (Lamiaceae) from 13 populations of different silvicultural zones were evaluated for antimicrobial activity against Gram positive (*Staphylococcus aureus, Bacillus spp*.) and Gram negative (*Escherichia coli, Pseudomonas aeruginosa, Samonella typhi, Klebsiella pneumoniae, Proteus mirabilis*) bacteria and a pathogenic fungus *Candida albicans*. All the essential oils were active to the tested microbials with different strength. The highest antimicrobial activity against Gram positive bacteria (*Staphylococcus aureus*) and Gram negative bacteria (*Pseudomonas aeruginosae* and *Proteus mirabilis*) was observed from the eastern Kenya (Meru) oil. Meru oil was overall the best and its effectiveness was consistent on nearly all the microbes tested. The oil from the plant growing in the coastal region of Kenya (Mombasa) showed the best effect only on Gram negative bacteria (*Escherichia coli* and *Proteus mirabilis*). Both oils (Meru and Mombasa) were dominated by monoterpenes accounting for 92.48 % and 81.37 % respectively. The monoterpene fraction was characterized by a high percentage of eugenol (68.8 %) for Meru oil and 74.10 % for Mombasa oil. The other major monoterpene was methyl eugenol (13.21 %). Camphor (0.95 %) was observed only in the Meru oil. (*Cis*)-Ocimene, (*trans*)-ocimene and β-pinene were present in both Meru and Mombasa oils. The sesquiterpenes present in fairly good amounts in both oils were germacrene D and (*trans*)-caryophyllene. The minor sesquiterpenes were α-farnesene (0.85 %) and β-bisabolene (0.74 %) which were present in the Meru oil only.

After establishing the best storage conditions and genomic DNA extraction protocol for O. gratissimum L. which was the detergent SDS and the reducing agent dithiothreitol; genetic

diversity studies involving twelve populations were perfomed using the amplified fragment length polymorphic (AFLP) markers. Six thousand, two hundred and thirty seven different AFLP bands were generated by the seven primers used. The total number of bands scored per primer ranged from 595 (ACT-CTG) to 1335 (ACT-CAA), with an average of 891 bands per primer. The size of the amplified fragments ranged from 50 to 472 base pairs (bp).

Estimates of Nei's unbiased genetic diversity showed some populations with similar gene diversity (Mill house II and Njoro with H = 0.13; Savona isle, Riat, Chesigei and Mariakani with H = 0.15; Kibarani and Roret with H = 0.10). Kibarani and Roret were the least diverse (H = 0.10) and Kiganjo as the most diverse (H = 0.19). The results showed some great variation in the levels of genetic diversity as also shown by Shannon's information index (I). There was some percentage polymorphic loci correspondence with the diversity estimates. In most cases, populations with high diversity estimate also showed high percentage polymorphic loci. The genetic variation was within populations as opposed to among populations. There was small genetic differentiation in the populations. The F_{ST} was zero.