



Genetic Diversity of *Vitex negundo* L. (Lagundi) in the Philippines using Inter-simple Sequence Repeat (ISRR) Marker Analysis

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ABSTRACT – *Vitex negundo* L. is now gaining popularity because of its use in cough medicines. It is listed as one of the ten medicinal plants being promoted by the Department of Health due to its anti-inflammatory properties. In order to improve breeding methods for the cultivation of lagundi, knowledge about its genetic diversity is needed since this could distinguish possible cultivars of the plant. This preliminary study was done using a molecular marker analysis on lagundi from fifteen different sites in the Philippines. Based on inter-simple sequence repeat (ISSR) markers, there is usually a common locus or pattern of bands that is present in all samples from the fifteen geographic locations that can be attributed to the fact that all samples belong to one species. Moreover, the samples also exhibited a great number of polymorphisms that suggests the genetic variation found within the species. It is then possible to say that although *V. negundo* is considered to have only one species, it can be further classified into several morphotypes based on the several clusters as revealed by the dendrogram. There was no correlation between the sample clusters and their geographic locations, since the groupings were not consistent with their locations. Nonetheless, results of this study in the establishment of genetic diversity patterns of *V. negundo* in the Philippines can provide baseline information for future research that could finally lead to the identification of lagundi cultivars that yield a high quality of active compound for medicinal purposes.

Keywords: *Vitex negundo*, ISSR markers, genetic diversity



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