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Nation Building through
Quality Research and Innovation

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**Nation Building through
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I. AGRICULTURE, VETERINARY SCIENCE AND FORESTRY



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Genetic Diversity and Population Structure Analysis of some Myanmar Mango (*Mangifera spp.*L.) Accessions using Simple Sequence Repeat Markers

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Abstract—Mango (*Mangifera indica* L.) is a favorite fruit in the world especially in the Indo-Pakistan sub-continent. It is a rich source of vitamins, β -carotene, minerals, and antioxidants. Mango is known as “the king of fruits” for its taste and flavor. It is native to Southern Asia, especially Burma and eastern India. Since Myanmar is one of the origins of mango. A wide genetic diversity may be found in Myanmar accordingly. Some phenotypic characterizations of Myanmar mangoes have been done but the information of genetic assessments is still limited. Therefore, the present study intended to make genetic assessments of some Myanmar mango accessions collected from different geographical regions using Simple Sequence Repeat markers (SSR). This study was carried out at the laboratory of the Department of Horticulture, Yezin Agricultural University (YAU). Fully grown mango leaf samples were used to extract total genomic DNA. The DNAs were extracted by modified CTAB method and checked purity and concentration with nano spectrophotometer. The sample DNAs were amplified using five pairs of SSR primers. One SSR (MSSR80) revealed as monomorphic marker among tested 94 mango accessions. The data were analysed using Structure 2.2 and Phylip software package. The phylogenetic tree was constructed by MEGA6 software program. According to population structure analysis, 94 mango accessions could be distinguished into three populations though four accessions were assessed as admixtures. Four accessions; Parr Phyu Thee (Kinda), Pann Bin Ga Lar (Kalar Gyi), Pyo Ta Ngon (Kinda) and Yin Kwae (Kinda) stood as admixtures. No correlation between the

geographical distribution and population structure of mango was found. One accession, Sein Ta Lone (Pan Swae) stood as an outstanding accession in phylogenetic tree constructed by Phylip program although it was grouped together with Shwe Myo Sae, Ma Chit Su and others in population structure analysis. It was hard to say discrete population. Almost all accessions of a population possessed some alleles from other populations. It implied that cross pollination nature plays an important role in mango gene pool. Accordingly, wider genetic diversity would be expected among mango population in Myanmar.

I. INTRODUCTION

Mango (*Mangifera indica* L.) is a favorite fruit in the world especially in the Indo-Pakistan sub-continent. It is a rich source of vitamins, β -carotene, minerals, and antioxidants. Mango is known as “the king of fruits” for its taste and flavor. It natives to Southern Asia, especially Burma and eastern India. Hundreds of cultivated accessions have been introduced to other warm regions of the world. It is a large fruit-tree, capable of growing to a height of about 100 feet and trunk of more than 12 feet. Mango is now grown throughout the sub-tropical and tropical world in 99 countries with a total fruit production of 34.3 million tons of fruit per annum [1]. The Asia produced the majority (76%) of world mango production then followed by Americas (12%), and Africa (11.8%) which are the second and third largest producers. India is the largest producer, growing over 18 million tons (MT) primarily for domestic consumption. China produced (4.5 MT), Thailand (3.1 MT), Indonesia (2.6 MT), and Mexico (1.9 MT), respectively [1]. Although, Mexico is fifth in production it is first in export to the USA, which is 43% of the global import market [2].

Mangifera germplasm needs to be evaluated and conserved because the potential presence of