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Molecular identity of native coconut (*Cocos nucifera* L.) germplasm from South Kalimantan, Indonesia

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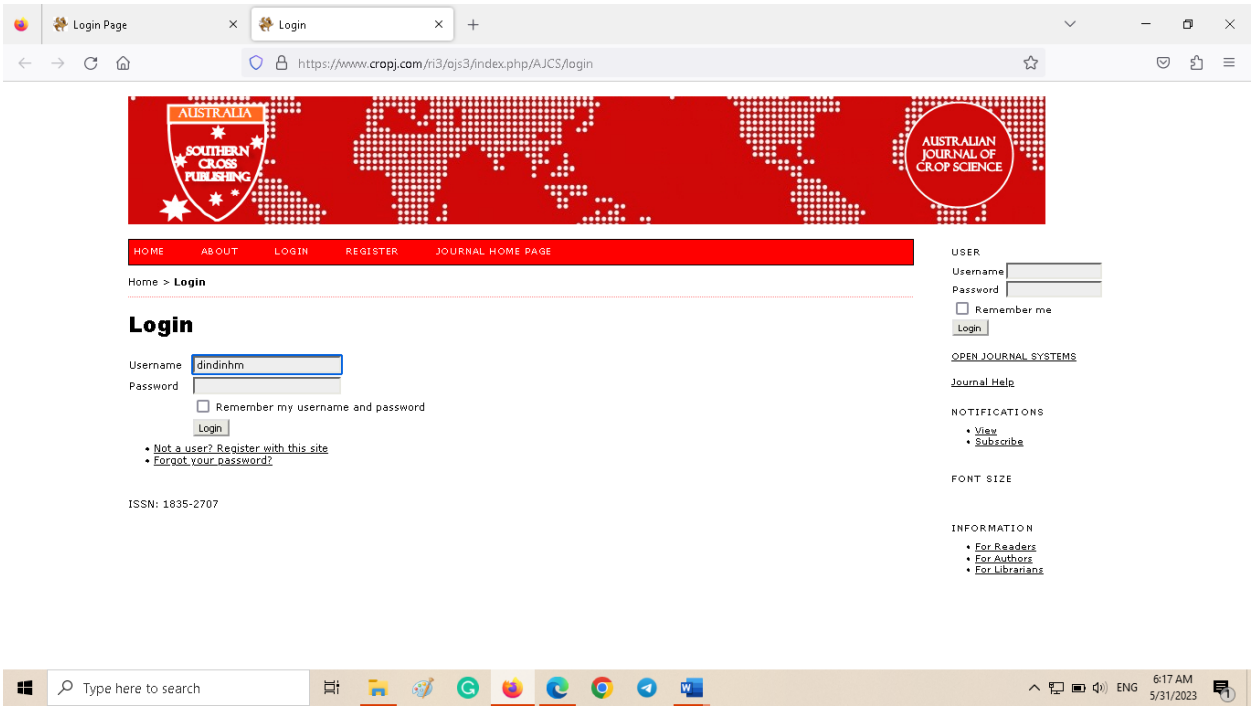
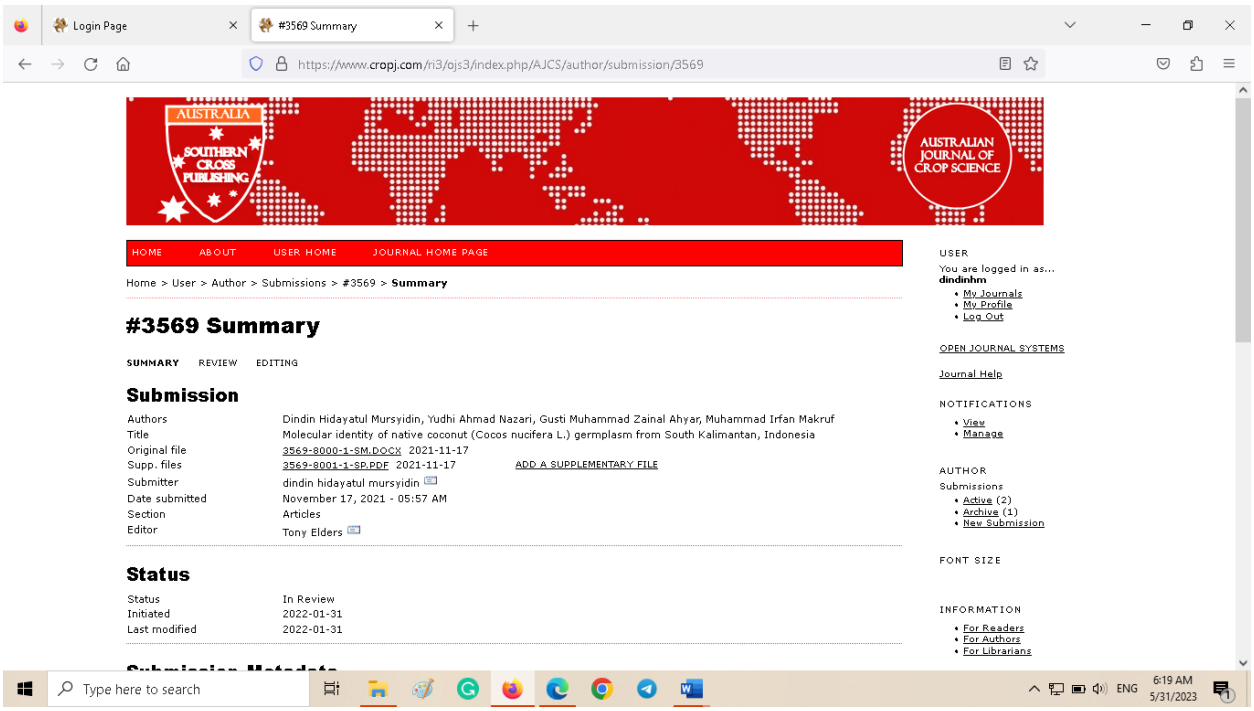
Abstract

Coconut (*Cocos nucifera* L.) is an agricultural commodity that is very prospective to be developed in Indonesia and other tropical countries, but its development is constrained by various factors. This study aimed to determine the genetic identity, as well as diversity and relationships of native coconut germplasm from South Kalimantan, Indonesia, using a cpDNA (*matK*) marker. The results show that this germplasm has a low-level genetic diversity, π% = 0.0258. However, the phylogenetic analysis revealed that native coconut germplasms from this region have separated into different clades, two for Maximum Likelihood and three for Neighbor-Joining, where *Genjah Kuning 3* has closely related to an outgroup. Thus, this information is important as a fundamental reference in developing new high-yielding coconut in the future.

Keywords: Coconut; genetic diversity; breeding program; cpDNA.
Abbreviations: *matK* _ *Maturase* K; ML _ Maximum Likelihood; NJ _ Neighbor-Joining.

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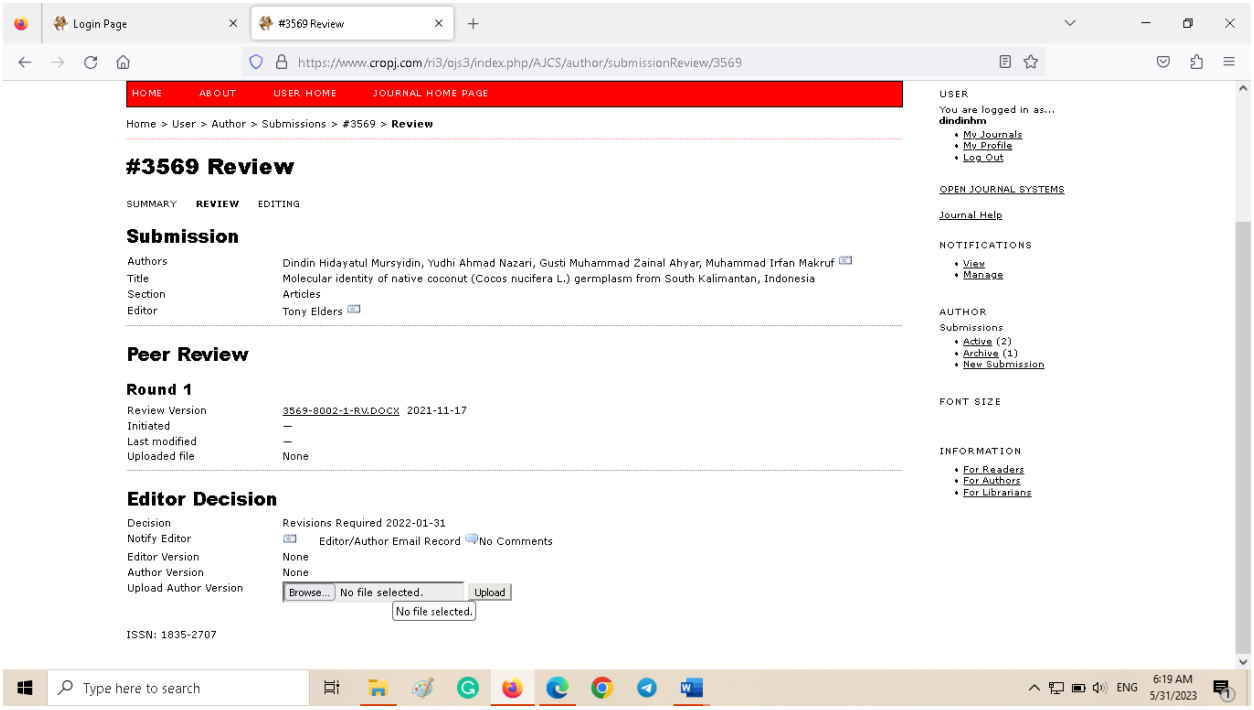
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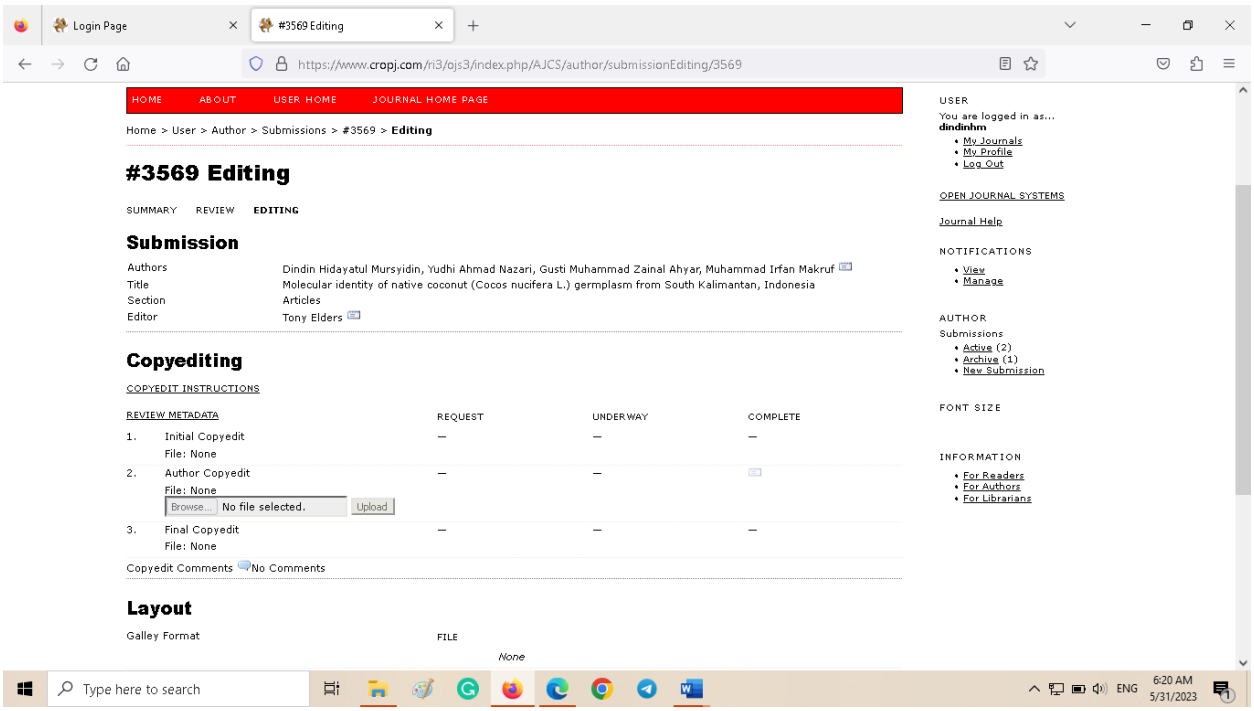
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