Genetic fingerprint of some *Alhagi graecorum* populations based on DNA polymorphism

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2020

Supervision Sheet

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M.Sc. Thesis

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Date: / / 2020

Dedication

TO THE SOUL OF MY FATHER

Dedication

To my MOTHER❤️
She is the reason why I am here. For everything you've done for me and all that you still do, THANK YOU❤️

To my brothers "Mustafa, Hussien and Nour", you are my backbone.

To my fiancé "Ahmed", Thank You for your continuous support and encouragement.

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ABSTRACT

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The present investigation was conducted to study the genetic diversity among twenty-five Egyptian *Alhagi graecorum* genotypes collected from five locations (El-Dakhla Oasis, Ain shams university, Wadi El-Rayan, Qarun lake and Siwa Oasis) using individual- and bulked samples-based approaches. Eight ISSR primers revealed a high percentage of polymorphism (84.16%) across all the studied genotypes and (78.35%) among the five populations, while SCoT primers produced 73.57% (ten primers) and 65.38% (nine primers), respectively. Also, average polymorphism information content (PIC) for amplified DNA of individual samples was 0.860 for SCoT and 0.875 for ISSR. The genetic diversity analysis for *Alhagi graecorum* revealed similar dendrograms with some slight variations. The results of UPGMA cluster analysis and PCoA grouped the twenty-five *Alhagi* genotypes according to their geographical location. The study also included sequencing for selected unique fragments from SCoT and ISSR profiles (bulked-DNA samples). The obtained results demonstrate that ISSR was better than SCoT to detect genetic diversity among *Alhagi graecorum* genotypes.

Key words: Medicinal plant, Genetic variation, *Alhagi graecorum*, Molecular markers, SCoT, ISSR, Sequencing.

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