

ISSR and SCoT for evaluation of hereditary differences of 29 wild plants in Al Jubail

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This survey is concerned with the hereditary differences of 29 wild plants collected from 15 stands in Al Jubail, Saudi Arabia using two molecular marker systems, viz. inter simple sequence repeat (ISSR) and start codon targeted (SCoT) molecular markers. Ten ISSR and ten SCoT primers amplified a total of 142 and 163 bands with 87% and 84% polymorphism, respectively. The average number of polymorphic bands for each pair of ISSR and SCoT primer combinations was 12.4 and 13.7, respectively. The highest genetic similarity for ISSR (0.97) and SCoT (0.90) were recognized between *Zygophyllum qatarense*-22 and *Juncus rigidus*-23, and between *Z. qatarense*-28 and *Z. qatarense*-29, whereas the lowest was (0.59) differentiated between *Z. qatarense*-6 and *Salsola imbricata*-18 for ISSR and between *Cyperus conglomeratus*-7 and *Halopeplis perfoliata*-14 for SCoT. This study confirms the value of molecular techniques such as ISSR and SCoT in assessing the hereditary differences among the selected 29 weeds for hereditary preservation and plant enhancement.