



Fingerprinting Some Varieties of Grape Vines (*Vitis Vinifera* L.) Using SSR Marker in Duhok Governorate

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Abstract

This study was carried out to investigate the cultivar identification of some grape cultivated in Duhok region using SSR (simple sequence repeat) DNA markers. Identification the cultivars is often difficult especially in the early stage of plant age and closely related cultivars, thus the DNA fingerprinting resolve the cultivars distinguish which are not influenced by the environment and easy detecting methods. However, using SSR markers to discriminate grapes cultivars are not enough. In this study nine primer pairs were selected for fingerprinting 38 grape cultivars. The Phylogenetic analysis reveal the genetic relationship of the grape cultivars to two g distinguished groups, each group divided in subgroups. Darwin software used to construct a dendrogram UPGMA cluster from the 9 SSR loci.

Key words: High blood pressure, Prevalence, Quinshul Community

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Introduction

In the recent years the Simple sequence repeat (SSR) markers have been increasingly used in DNA fingerprinting, characterization of stock and rootstock varieties, evaluation of genetic variability, pedigree studies and genetic mapping in grape plants (Riaz et al., 2004; Ortiz et al., 2004; Dzhambazova et al., 2007; Riaz et al., 2008; Schuck et al., 2009; Vargas et al., 2009)

Considering that the knowledge about the genetic diversity of specie movides subsidies to a breeding program, this study aimed to confirm the identity and estimate the genetic diversity among ten grapevine cultivars using eight microsatellite markers.

The present study was conducted to assessment of genetic variability some grape cultivars using SSRs markers cultivated in Duhok governorates.

Materials and Methods

The present study was conducted to assessment of genetic variability some grape cultivars using SSRs markers cultivated in Duhok governorates.

the molecular analyses were conducted in Scientific Research Center\ College of Science, University of Duhok. The total DNA was extracted from 3 gm fresh of young leaves, according to (Weigand *et al* 1993).

Nine pairs of microsatellite primers were analyzed, and sequences are described in (Cipriani *et al.* 1999), the names and the sequences of these primers are shown in Table (1). The amplification reactions were conducted in a thermocycler in a 25 mL volume containing 10 mmol L⁻¹ Tris-HCl pH 9.0, 50 mmol L⁻¹ KCl, 1.5 mmol L⁻¹ MgCl₂ 0.2 mmol L⁻¹ of each dNTP, 0.2 mmol L⁻¹ of each primer, 0.1U Taq polymerase (Pharmacia) and 50 ng genomic DNA.

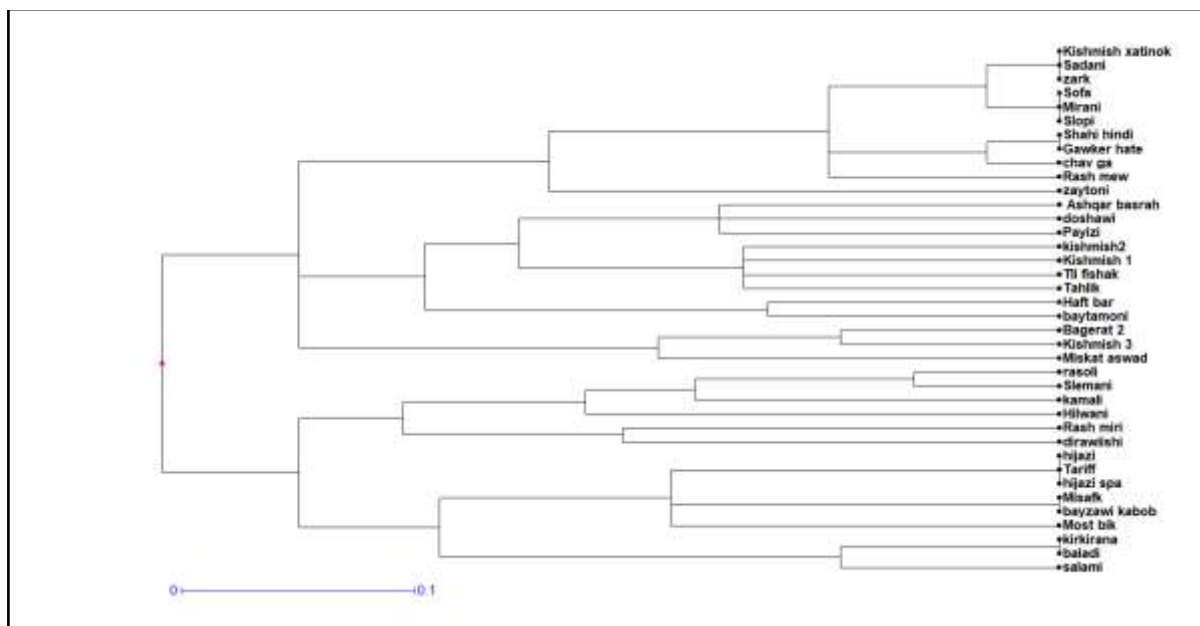
Primers names	Sequences
VrZAG21	(F) 5'-TCA TTC ACT CAC TGC ATT CAT CGG C -3' (R) 5'- GGG GCT ACT CCA AAG TCA GTT CTT G -3'
VrZAG47	(F) 5'- GGT CTG AAT ACA TCC GTA AGT ATA T -3' (R) 5'- ACG GTG TGC TCT CAT TGT CAT TGA C -3'
VrZAG62	(F) 5'- GGT GAA ATG GGC ACC GAA CAC ACG C -3' (R) 5'- CCA TGT CTC TCC TCA GCT TCT CAG C -3'
VrZAG79	(F) 5'- AGA TTG TGG AGG AGG GAA CAA ACC G -3' (R) 5'- TGC CCC CAT TTT CAA ACT CCC TTC C -3'
VVMD8-cjvh	(F) 5'- CCA GTG TGG GTC ACT TGT GT -3' (R) 5'- GGA TCA CCT ACA GAC AGT CCA A -3'
VVIN74-cjvh2	(F) 5'- TGG CAT AAC TTT GAT GGG TAA A -3' (R) 5'- GTC ACC CTT GTT TCA CTC CAG TA -3'
RUN1 MG	(F) 5'- ATA AAG CTC TTC GTA TAA AT -3' (R) 5'- CGA TAT GTG CTG ACC CAC A -3'
MrRUN1	(F) 5'- CCT GAA GCG GAA ATT CTC AG -3' (R) 5'- TGC ATG GAA ATC ACA AGC ATC T -3'
VrZAG25	(F) 5'- CTC CAC TTC ACA TCA CAT GGC ATG C -3' (R) 5'- CGG CCA ACA TTT ACT CAT CTC TCC C -3'

The program used in the PCR reactions consisted of one cycle at 95°C for 5 min, 35 cycles at 94°C for 45 s; variant depend on the primer annealing temperature for 45 s and 72°C for 45 s, followed by a final cycle at 72°C for 8 min.

The products of SSR amplification visualized in the gel were recorded and the molecular weight were measured. To visualize the way cultivars were grouped, the dendrogram was prepared using the Unweighted Pair Group Mean Average method (UPGMA), using Darwin program software

Results and Discussion

Nine primer pairs were selected for fingerprinting All the 39 samples were successfully amplified using theSSR primers.The Phylogenetic analysis reveal the genetic relationship of the grape cultivars to two g distinguished groups, each group divided in subgroups as shown in Figure (1). Darwin software used to construct a dendrogram UPGMA cluster from the 9 SSR loci.



The results of clustering indicated that the grape cultivars could be distinguished clearly using SSR markers. The SSR marker consider an efficient technology to fingerprinting and molecular characterization of organism, especially in plant species. The present study analyzed of nine SSR primers in genomes of grape cultivated. sing SSR markers as a tool for genetic mapping, cultivars identification, genetic diversity investigations, parentage analysis, as well as molecular fingerprint construction are highly accepted throughout the world. The SSR analysis data reported here might provide worthy information for further grape protection, exploitation and utility, grape selection and breeding research in the whole world. Moreover, the established SSR data could enable researchers to preserve the valuable genetic cultivars for variety improvement, offer reference for the future studies on grape cultivars. (Dong *et al.*, 2018).

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