

Assessment of genetic variation and population structure in Iraqi barley accessions using ISSR, CDDP, and SCoT markers

NAWROZ TAHIR¹, DJSHWAR LATEEF², KAMARAN RASUL¹, DIDAR RAHIM²,
KAMIL MUSTAFA², SHOKHAN SLEMAN², AVIN MIRZA³, REBWAR AZIZ¹

¹Horticulture Department, College of Agricultural Engineering Sciences,
University of Sulaimani, Sulaimani, Iraq

²Biotechnology and Crop Sciences Department, College of Agricultural Engineering Sciences,
University of Sulaimani, Sulaimani, Iraq

³General Directorate of Agriculture in Sulaimani, Ministry of Agricultural and Water Resources,
Sulaimani, Kurdistan Region, Iraq

Electronic Supplementary Material (ESM)

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Table S1. Code, name of 59 barley accessions included in this investigation

Accession Code	Origin	Accession Name	Accession Code	Origin	Accession Name
V1	South of Iraq	Shoaa	V31	Middle of Iraq	Scio/3
V2	South of Iraq	Boraak	V32	Middle of Iraq	Victoria
V3	South of Iraq	Radical	V33	Middle of Iraq	Black-Bhoos-B
V4	South of Iraq	Arivat	V34	Middle of Iraq	Irani
V5	South of Iraq	16 HB	V35	Middle of Iraq	A1
V6	South of Iraq	Furat 9	V36	Middle of Iraq	MORA
V7	South of Iraq	Al-warka	V37	Middle of Iraq	ABN
V8	South of Iraq	Numar	V38	Middle of Iraq	Arabi aswad
V9	South of Iraq	Al-amal	V39	Middle of Iraq	Clipper
V10	South of Iraq	Rafidain-1	V40	Middle of Iraq	Bhoos-H1
V11	South of Iraq	Al-khayr	V41	Middle of Iraq	BN2R
V12	South of Iraq	BN6	V42	Middle of Iraq	BA4
V13	South of Iraq	IBAA-99	V43	North of Iraq	Qala-1
V14	North of Iraq	Saydsadiq	V44	North of Iraq	Black-kalar
V15	Middle of Iraq	Bhoos-244	V45	North of Iraq	White-kalar
V16	Middle of Iraq	IBAA-265	V46	North of Iraq	Black-Akre
V17	North of Iraq	White-Akre	V47	North of Iraq	Black-Garmiyan
V18	North of Iraq	Black-Bhoos Akre	V48	North of Iraq	Black-Chiman
V19	North of Iraq	Black-Zaxo	V49	North of Iraq	Ukranian-Zarayan
V20	North of Iraq	White-Zaxo	V50	North of Iraq	White-Zarayan
V21	South of Iraq	Bhoos-912	V51	North of Iraq	Abrash
V22	North of Iraq	White-Halabja	V52	North of Iraq	Bujayl 1-Shaqlawa
V23	South of Iraq	Samr	V53	North of Iraq	Bujayl 2-Shaqlawa
V24	South of Iraq	GOB	V54	North of Iraq	Bujayl 3-Shaqlawa
V25	South of Iraq	Abiad	V55	South of Iraq	Rehaan
V26	South of Iraq	CANELA	V56	South of Iraq	Sameer
V27	South of Iraq	MSEL	V57	South of Iraq	Warka-B12
V28	South of Iraq	Acsad strain	V58	South of Iraq	Al-Hazzar
V29	South of Iraq	Acsad-14	V59	South of Iraq	IBAA-995
V30	South of Iraq	Gk-Omega			

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Table S2. Sequences, annealing temperature, and polymorphism information parameters of the ISSR markers used in this investigation

ISSR markers	Sequences (5–3)	Annealing temperature (°C)	Allele No.	No. of polymorphism	Major allele frequency	Gene diversity	PIC
UBC-808	AGAGAG AGAGAGAGAGC	50.00	11.00	5.00	0.24	0.86	0.84
UBC-811	GAGAGAGAGAGAGAGAC	50.00	6.00	3.00	0.42	0.66	0.60
UBC-812	GAGAGAGAGAGAGAGAA	50.40	33.00	8.00	0.12	0.95	0.95
UBC-818	CACACACACACACACAG	52.80	22.00	9.00	0.36	0.84	0.83
UBC-823	TCTCTCTCTCTCTCTCC	50.00	40.00	9.00	0.10	0.96	0.96
UBC-825	ACACAC ACACACACACT	50.00	15.00	6.00	0.34	0.84	0.82
UBC-826	ACACACACACACACACC	50.00	22.00	9.00	0.15	0.92	0.91
UBC-841	GAGAGAGAGAGAGAGACTC	50.00	12.00	4.00	0.66	0.55	0.53
UBC-888	CGTCGTCGTCACACACACACA	52.00	29.00	6.00	0.12	0.95	0.94
UBC-891	ACTACTACTTGTGTGTGTGTG	52.00	38.00	8.00	0.20	0.94	0.93
UBC-847	CACACACACACACACAGC	50.00	27.00	7.00	0.10	0.95	0.94
UBC-813	CTCTCTCTCTCTCTCTT	50.00	2.00	1.00	0.63	0.47	0.36
UBC-810	GAGAGAGAGAGAGAGAT	50.00	21.00	6.00	0.24	0.89	0.88
UBC-814	CTCTCTCTCTCTCTCTA	50.00	10.00	5.00	0.36	0.79	0.76
UBC-815	CTCTCTCTCTCTCTCTG	50.00	21.00	8.00	0.17	0.92	0.91
UBC-822	TCTCTCTCTCTCTCTCA	50.00	28.00	6.00	0.12	0.94	0.94
UBC-834	AGAGAGAGAGAGAGAGGT	50.00	9.00	5.00	0.34	0.80	0.76
UBC-845	CTCTCTCTCTCTCTCTTG	50.00	23.00	9.00	0.24	0.89	0.88
ISSR-1	AGACACACACACACACAT	50.00	7.00	3.00	0.32	0.76	0.73
ISSR-6	GCCTCCTCCTCCTCCTCC	50.00	13.00	5.00	0.22	0.85	0.84
ISSR-7	AGATCCTCCTCCTCCTCC	50.00	12.00	6.00	0.54	0.68	0.67
ISSR-8	ATCACACACACACACACA	50.00	32.00	9.00	0.08	0.96	0.96
ISSR-9	CACACACACACACACATG	50.00	27.00	11.00	0.14	0.93	0.93
ISSR-10	GAGAGAGAGAGAGAGAGG	50.00	26.00	10.00	0.20	0.93	0.92
ISSR-12	AGAGAGAGAGAGAGAGCT	50.00	8.00	6.00	0.56	0.63	0.58
ISSR-14	GAGAGAGAGAGAGAGAGC	50.00	9.00	5.00	0.46	0.75	0.73
ISSR-16	ACACACACACACACACGA	50.00	7.00	3.00	0.46	0.69	0.65
ISSR-18	TGTGTGTGTGTGTGTGG	50.00	18.00	8.00	0.24	0.86	0.84
UBC-846	CACACACACACACACAAT	50.00	34.00	10.00	0.20	0.93	0.93
UBC-849	GTGTGTGTGTGTGTGTGA	50.00	20.00	8.00	0.34	0.84	0.83
UBC-852	GATAGATAGACAGACA	48.00	4.00	2.00	0.53	0.59	0.51
UBC-856	ACACACACACACACACYA	42.00	3.00	2.00	0.49	0.53	0.42
UBC-881	GGGTGGGGTGGGGTG	54.00	31.00	8.00	0.15	0.94	0.94
HB-10	GAGAGAGAGAGACC	50.00	21.00	7.00	0.25	0.88	0.87
HB-11	GTGTGTGTGTGTCTC	50.00	12.00	6.00	0.49	0.73	0.71
HB-15	GTGGTGGTGGC	50.00	8.00	4.00	0.53	0.66	0.62
ISSR-AGC6G	AGCAGCAGCAGCAGCAGCG	55.00	3.00	2.00	0.58	0.51	0.41
PCP-3	GTGCGTGCGTGCGTGC	60.00	16.00	5.00	0.36	0.82	0.81
ISCS20	DHBCGACGACGACGACGA	60.00	5.00	3.00	0.81	0.32	0.29
ISCS21	BDBACAACAACAACAACA	55.00	8.00	4.00	0.73	0.45	0.43
ISSR-CCA	DBCCACCACCACCACCA	55.00	6.00	4.00	0.71	0.47	0.45
HB-12	CACCACCACGC	48.50	5.00	3.00	0.68	0.50	0.47
B-13	CAACAACAACAACA	44.70	5.00	3.00	0.64	0.54	0.50
ISSR-CA	BDBCACACACACACA	50.00	9.00	4.00	0.31	0.80	0.77
Mean			16.32	5.80	0.36	0.77	0.74
Total				255.00			

ISSR – inter simple sequence repeat; PIC – polymorphism information content

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Table S3. Primer information and diversity parameters for the CDDP markers used in this investigation

CDDP markers	Sequence of primer (5–3)	Annealing temperature (°C)	No. of polymorphism	Major allele frequency	Gene diversity	PIC
ABP1-1	ACSCCSATCCACCGC	50.00	3.00	0.44	0.67	0.61
WRKYF-1	TGGCGSAAGTACGGCCAG	50.00	4.00	0.34	0.82	0.80
MYB1	GGCAAGGGCTGCCGC	50.00	2.00	0.54	0.60	0.54
MYB2	GGCAAGGGCTGCCGG	50.00	4.00	0.44	0.74	0.71
ERF1	CACTACCCCGSCTSCG	50.00	2.00	0.75	0.42	0.39
ERF2	GCSGAGATCCGSGACCC	50.00	6.00	0.39	0.77	0.74
KNOX1	AAGGGSAACTSCSAAG	50.00	2.00	0.39	0.68	0.62
MADS-1	ATGGGCCGSGGCAAGGTGC	50.00	6.00	0.63	0.55	0.51
WRKY-R3	GCASGTGTGCTCGCC	50.00	6.00	0.42	0.76	0.74
Mean			3.89	0.48	0.67	0.63
Total			35.00			

CDDP – conserved DNA-derived polymorphism; PIC – polymorphism information content

Table S4. List of Scot primers used and the information obtained in the barley tested

SCoT markers	Sequences (5–3)	Annealing temperature (°C)	No. of polymorphism	Major allele frequency	Gene diversity	PIC
SCoT2	CAACAATGGCTACCACCC	50.70	4.00	0.53	0.68	0.66
SCoT3	CAACAATGGCTACCACCG	51.30	7.00	0.71	0.48	0.46
SCoT6	CAACAATGGCTACCACGC	52.10	8.00	0.24	0.89	0.89
SCoT7	CAACAATGGCTACCACGG	51.30	9.00	0.22	0.88	0.87
SCoT12	ACGACATGGCGACCAACG	55.90	3.00	0.46	0.66	0.59
SCoT13	ACGACATGGCGACCATCG	55.40	8.00	0.31	0.86	0.85
SCoT16	ACCATGGCTACCACCGAC	54.10	13.00	0.10	0.97	0.97
SCoT22	AACCATGGCTACCACCAC	51.90	6.00	0.19	0.89	0.88
SCoT23	CACCATGGCTACCACCAG	52.40	8.00	0.17	0.90	0.89
SCoT29	CCATGGCTACCACCGGCC	57.90	14.00	0.27	0.90	0.90
SCoT32	CCATGGCTACCACCGCAC	55.90	15.00	0.05	0.97	0.97
SCoT36	GCAACAATGGCTACCACC	51.50	6.00	0.44	0.69	0.65
Mean			8.42	0.31	0.81	0.80
Total			101.00			

SCoT – start codon targeted; PIC – polymorphism information content

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Table S5. Analysis of molecular variance (AMOVA) showing genetic diversity in the Iraqi barley accessions

Method	Source	df	SS	MS	Est. Var.	%	P-value
ISSR data	among pops	2	320.99	160.49	6.59	15**	0.001
	within pops	56	2012.1	35.93	35.93	85**	
	total	58	2333.09		42.52	100	
CDDP data	among pops	2	36.76	18.38	0.74	14**	0.001
	within pops	56	247.55	4.42	4.42	86**	
	total	58	284.31		5.16	100	
SCoT data	among pops	2	73.72	36.86	1.29	9**	0.001
	within pops	56	703.13	12.56	12.56	91**	
	total	58	776.85		13.84	100	
ISSR, CDDP, SCoT data	among pops	2	431.51	215.76	8.61	14**	0.001
	within pops	56	2962.78	52.91	52.91	86**	
	total	58	3394.29		61.52	100	

ISSR – inter simple sequence repeat; CDDP – conserved DNA-derived polymorphism; SCoT – start codon targeted; df – degree of freedom; SS – sum of squares; MS – mean of squares; Est. Var. – estimated variance

Table S6. Mantel coefficient values for correlation between clusters obtained by three different molecular markers

Markers	ISSR	CDDP	SCoT	Pooled markers data
ISSR	–	0.49**	0.37**	
CDDP		–	0.36**	0.25**
SCoT			–	

ISSR – inter simple sequence repeat; CDDP – conserved DNA-derived polymorphism; SCoT – start codon targeted