

Supplementary Figure S1: Sequence search analysis (BLAST) for the partial *HKT1;4* gene cloned from bread wheat genotype (A) Kharchia-65 and (B) HD-2329.

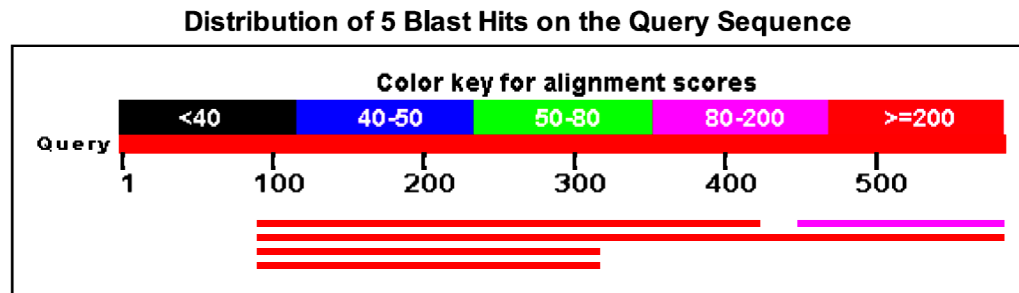
A

BLAST Results

HKT1;4-Kharchia-65

RID [UNVNHVA3016](#) (Expires on 08-11 17:06 pm)
Query ID Id|Query_82223
Description None
Molecule type nucleic acid
Query Length 583
Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.5.0+

Graphic Summary



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Triticum aestivum partial mRNA for HKT protein (HKT1,4.1 gene)	551	551	56%	7e-153	97%	HG934161.1
Hordeum vulgare subsp. spontaneum high-affinity K+ transporter 4 gene, complete sequence	472	472	84%	5e-129	84%	HQ696002.1
→ Triticum durum HKT1;4-2 mRNA, complete cds	311	311	38%	1e-80	92%	KF443079.1
Triticum durum HKT1;4-1 mRNA, complete cds	311	311	38%	1e-80	92%	KF443078.1
Triticum monococcum putative sodium transporter HKT7-A2 (HKT7-A2) mRNA, complete cds	183	183	23%	3e-42	91%	EF062819.1

Alignments

Triticum aestivum partial mRNA for HKT protein (HKT1,4,1 gene)

Sequence ID: **emb|HG934161.1|** Length: 331 Number of Matches: 1
Range 1: 1 to 331

Score	Expect	Identities	Gaps	Strand	Frame
551 bits(298)	7e-153()	320/331(97%)	0/331(0%)	Plus/Plus	

Features:

Query	92	GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGTGAAGGACCA	151
Sbjct	1	GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGTGAAGGACCA	60
Query	152	TCCCACGGAGGAGACCCCGGGGGTCAAGGTTGCTCAAGAGCACGGCTCTGTACAACCTCTC	211
Sbjct	61	TCCCACGGAGGAGACCCAGGGGAGCAGGTTGCTCAAGAGCACGGCTCTGTACAACCTCTC	120
Query	212	CTACCTCGCCATCTTCATCATCGCCATCTGCGTCACCGAAAGGGAAAACCTCGAGGAAGA	271
Sbjct	121	CTACCTCGCCATCTTCATCATCGCCATCTGCGTCACCGAGAGGGAAAACCTCGAGGAAAA	180
Query	272	CCCCCTCAACTTCAGCTTGTCTCAGCATCGTCGTCGAAGTCGTCAGGCAAGCCCTTCTAA	331
Sbjct	181	CCCCCTCAACTTCAGCTTGTCTCAGCATCGTCGTCGAAGTCGTCAGGCAAGCCCTTCTAA	240
Query	332	CGCAAATCAAAAAAGCCTGAAAACGAATAACAAATATGACTGCTACTTACTTCCGGCGTT	391
Sbjct	241	CGCAAATCAAGAAAAGCCTGAAAACGAATAACAAATATGACTGCAACTTAGTCCGGCATT	300
Query	392	GTTGGTTTCCCTTCATGGAAGCTGACATGTTT	422
Sbjct	301	ATTGGTTTCCCTTCATGGAAGCTGACATAATTT	331

Hordeum vulgare subsp. spontaneum high-affinity K⁺ transporter 4 gene, complete sequence

Sequence ID: **gb|HQ696002.1|** Length: 2473 Number of Matches: 1
Range 1: 487 to 973

Score	Expect	Identities	Gaps	Strand	Frame
472 bits(255)	5e-129()	418/496(84%)	14/496(2%)	Plus/Plus	

Features:

Query	92	GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGTGAAGGACCA	151
Sbjct	487	GTACCTGCCTCCATACACGACATGGTTTCCATTCCAAGAGAGCTCCATCGTGGCAGACCA	546
Query	152	TCCCACGGAGGAGACCCCGGGGGTCAAGGTTGCTCAAGAGCACGGCTCTGTACAACCTCTC	211
Sbjct	547	CCCCACGAAGGAGACCCAGGGGCTCAGGCTGCTCAAGAGCGCGCTTCTGTACAACCTCTC	606
Query	212	CTACCTCGCCATCTTCATCATCGCCATCTGCGTCACCGAAAGGGAAAACCTCGAGGAAGA	271
Sbjct	607	CTACCTCGCCATCTTCGTCGTCGCCATCTGCGTCACCGAGAGGGAAAACCTAGAGGAAGA	666
Query	272	CCCCCTCAACTTCAGCTTGTCTCAGCATCGTCGTCGAAGTCGTCAGGCAAGCCCC-TTCTA	330
Sbjct	667	CCCGCTCAACTTCAGCTTGTCTCAGCGTCGTCGTCGAAGTCGTCAGGCAAGCCCCACTCCA	726
Query	331	ACGCAAATCAAAAAAGCCTGAAAACGAATAACAAATATGACTGCTACTTACTTCCGGCGT	390
Sbjct	727	AAGCAAATC-GAGAA-CCTGAAAACGAATAA---AGACGAATACAGCTTCATTCTCTGC--	779

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Query 391 TGTGGTTTCCCTTCAT----GGAAGCTGACATGTTTTATCCTTACATTCGCGAGTGCGG 446
Sbjct 780 -GTTGATTTCCCTTCATGGAAGGAAGCTGACATGTTTGTCTTTCACATTCGCGAGCGCTT 838
Query 447 ATGGAAATGGGGGCTTCTCCATGGGCTACAGTTGCAATAGACAGATCAGCCCGGACGCGC 506
Sbjct 839 ACGGAAATGTGGGCTTCTCCATGGGCTACAGCTGCAGTAGACGGATCAACCTGGACCGGG 898
Query 507 TGTGCACCGACGGGTGGACCGGCTTCGTGGGAGGTGGAGTGATCTGGCAAGCTCATCC 566
Sbjct 899 TGTGCCTCGACAGGTGGACCGGCTTCGCCGGAAGGTGGAGCGATCTGGCAAGCTCATCC 958
Query 567 TCATTCGTTGTGATGC 582
Sbjct 959 TCATTC-TTGTAAATGC 973

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Triticum durum HKT1;4-2 mRNA, complete cds

Sequence ID: **gb|KF443079.1|** Length: 1686 Number of Matches: 1

Range 1: 1263 to 1487

Score	Expect	Identities	Gaps	Strand	Frame
311 bits(168)	1e-80()	206/225(92%)	0/225(0%)	Plus/Plus	
Features:					
Query 92	GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGTGAAGGACCA	151			
Sbjct 1263	GTACCTCCCTCCATACACGACATGGTTTCCATTTGGAGAGAGCTCCAGCGTGAAGGACCA	1322			
Query 152	TCCCACGGAGGAGACCCCGGGGGTCAAGTTGCTCAAGAGCACGGCTCTGTCACTCAACTCTC	211			
Sbjct 1323	TCCCACGGAGGAGACCCAGGGGGTCAAGTTGCTCAAGAGCACGGCTCTGTCACTCAACTCTC	1382			
Query 212	CTACCTCGCCATCTTTCATCATCGCCATCTGCGTCAACCGAAAGGGAAAACCTCGAGGAAGA	271			
Sbjct 1383	CTACCTTGCCATCTTTGTTCATCGCCATCTGCGTCACTGAGAGGGAAAAGCTCAAGGAGGA	1442			
Query 272	CCCCCTCAACTTCAGCTTGCTCAGCATCGTTCGTCGAAGTCGTCAG	316			
Sbjct 1443	CCCCCTCAACTTCAACTTGCTCAGCATCGTTCGTCGAAGTCGTCAG	1487			

Triticum durum HKT1;4-1 mRNA, complete cds

Sequence ID: **gb|KF443078.1|** Length: 1692 Number of Matches: 1

Range 1: 1269 to 1493

Score	Expect	Identities	Gaps	Strand	Frame
311 bits(168)	1e-80()	206/225(92%)	0/225(0%)	Plus/Plus	
Features:					
Query 92	GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGTGAAGGACCA	151			
Sbjct 1269	GTACCTGCCTCCATACACGACGTGGTTTCCATTTGAAGAGAGCTCCGGCGTCAAGGACCA	1328			
Query 152	TCCCACGGAGGAGACCCCGGGGGTCAAGTTGCTCAAGAGCACGGCTCTGTCACTCAACTCTC	211			
Sbjct 1329	ACCCAGGGAGGAGACCCAGGGGGTCAAGCTGCTCAAGAGCACGGCTCTGTCACTCAACTCTC	1388			
Query 212	CTACCTCGCCATCTTTCATCATCGCCATCTGCGTCAACCGAAAGGGAAAACCTCGAGGAAGA	271			
Sbjct 1389	CTACCTCGCCATCTTTGTTCATCGCCATCTGCATCAACCGAGAGGGAAAAGCTCAAGGAGGA	1448			
Query 272	CCCCCTCAACTTCAGCTTGCTCAGCATCGTTCGTCGAAGTCGTCAG	316			
Sbjct 1449	CCCCCTCAACTTCAACTTGCTCAGCATCGTTCGTCGAAGTCGTCAG	1493			

B

BLAST Results

HKT1;4-HD-2329

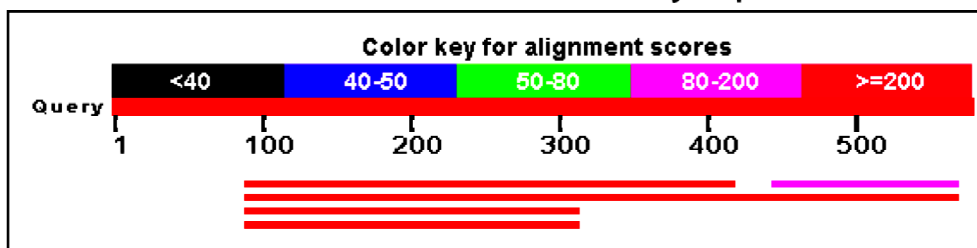
RID [UNUYUR6X01R](#) (Expires on 08-11 16:54 pm)

Query ID [Icl|Query_91553](#)
Description None
Molecule type nucleic acid
Query Length 581

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.5.0+

Graphic Summary

Distribution of 5 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Triticum aestivum partial mRNA for HKT protein (HKT1,4.1 gene)	529	529	56%	3e-146	95%	HG934161.1
Hordeum vulgare subsp. spontaneum high-affinity K+ transporter 4 gene, complete sequence	453	453	82%	2e-123	84%	HQ696002.1
→ Triticum durum HKT1;4-2 mRNA, complete cds	300	300	38%	3e-77	91%	KF443079.1
Triticum durum HKT1;4-1 mRNA, complete cds	300	300	38%	3e-77	91%	KF443078.1
Triticum monococcum putative sodium transporter HKT7-A2 (HKT7-A2) mRNA, complete cds	172	172	21%	6e-39	91%	EF062819.1

Alignments

Triticum aestivum partial mRNA for HKT protein (HKT1,4.1 gene)

Sequence ID: **emb|HG934161.1** Length: 331 Number of Matches: 1

Range 1: 1 to 331

Score	Expect	Identities	Gaps	Strand	Frame
529 bits(286)	3e-146()	316/331(95%)	0/331(0%)	Plus/Plus	

Features:

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Query 91  GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGAGAAGGACCA 150
Sbjct 1   GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGTGAAGGACCA 60
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Query 151 TCCCACGGAGGAGACCCCGGGGGTCAGGTTGCTCAAGAGCACGGCTCTGTCACTCAACTCTC 210
Sbjct 61 TCCCACGGAGGAGACCCAGGGGAGCAGGTTGCTCAAGAGCACGGCTCTGTCACTCAACTCTC 120
Query 211 CTACCTCGCCATCTTCATCATCGCCATCTGCGTCACCGAAAAGGGAAAACCTCGAGGAAAA 270
Sbjct 121 CTACCTCGCCATCTTCATCATCGCCATCTGCGTCACCGAGAGGGAAAACCTCGAGGAAAA 180
Query 271 CCCCCCAACTTCAGCTTGCTCAGCATCGTCGTGCGAAGTCGTCAGGCAAGCCCCCTCTAA 330
Sbjct 181 CCCCCCAACTTCAGCTTGCTCAGCATCGTCGTGCGAAGTCGTCAGGCAAGCCCCCTCTAA 240
Query 331 CGCaaatcaaaaaagccagaaaacgaataaaaaTATGACTGCTTCTTACTTCCGGCGTT 390
Sbjct 241 CGCAAAATCAAGAAAGCCTGAAAACGAATAACAAATATGACTGCAACTTAGTTCCGGCATT 300
Query 391 GTTGGTTTCCCTTCATGGAAGATGACATGTTT 421
Sbjct 301 ATTGGTTTCCCTTCATGGAAGCTGACATAATTT 331

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Hordeum vulgare subsp. spontaneum high-affinity K+ transporter 4 gene, complete sequence
Sequence ID: **gb|HQ696002.1** Length: 2473 Number of Matches: 1
Range 1: 487 to 964

Score	Expect	Identities	Gaps	Strand	Frame
453 bits(245)	2e-123()	409/487(84%)	15/487(3%)	Plus/Plus	

Features:

```

Query 91 GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGAGAAGGACCA 150
Sbjct 487 GTACCTGCCTCCATACACGACATGGTTTCCATTTCCAAGAGAGCTCCATCGTGGCAGACCA 546
Query 151 TCCCACGGAGGAGACCCCGGGGGTCAGGTTGCTCAAGAGCACGGCTCTGTCACTCAACTCTC 210
Sbjct 547 CCCCACGAAGGAGACCCAGGGGCTCAGGCTGCTCAAGAGCGGCTTCTGTCACTCAACTCTC 606
Query 211 CTACCTCGCCATCTTCATCATCGCCATCTGCGTCACCGAAAAGGGAAAACCTCGAGGAAAA 270
Sbjct 607 CTACCTCGCCATCTTCGTCGTCGCCATCTGCGTCACCGAGAGGGAAAACCTAGAGGAAGA 666
Query 271 CCCCCCAACTTCAGCTTGCTCAGCATCGTCGTGCGAAGTCGTCAGGCAAGCCCC-TTCTA 329
Sbjct 667 CCCGCTCAACTTCAGCTTGCTCAGCGTCGTCGTCCAAGTCGTCAGGCACGCCCACTCCA 726
Query 330 ACGCaaatcaaaaaagccagaaaacgaataaa-aaaTATGACTGCTTCTTACTTCCGGCG 388
Sbjct 727 AAGCAAAATC-GAGAA-CCTGAAAACGAATAAAGACGAAT-ACAGCTTC--A-TTCCTGC- 779
Query 389 TTGTTGGTTTCCCTTCATGGAAG--A--TGACATGTTTTATCCTTCACATTCGGGAGTGCG 444
Sbjct 780 --GTTGATTTCCCTTCATGGAAGGAAGCTGACATGTTTTGTCTTTCACATTCGCGAGCGCT 837
Query 445 GATGGAAATGGGGGCTTCTCCATGGGCTACGGTTGCAATTGACAGATCAGCCCGGACTGG 504
Sbjct 838 TACGGAAATGTGGGCTTCTCCATGGGCTACAGCTGCAGTAGACGGATCAACTGGACCGG 897
Query 505 CTGTGCACCGACGGGTGGACCGGCTTCGTCGGGAGGTGGAGCGATTCTGGCAAGCTCATC 564
Sbjct 898 GTGTGCGCCGACAGGTGGACCGGCTTCGCCGGAAGGTGGAGCGATTCTGGCAAGCTCATC 957
Query 565 CTCATTC 571
Sbjct 958 CTCATTC 964

```



Triticum durum HKT1;4-2 mRNA, complete cds

Sequence ID: **gb|KF443079.1|** Length: 1686 Number of Matches: 1

Range 1: 1263 to 1487

Score	Expect	Identities	Gaps	Strand	Frame
300 bits(162)	3e-77()	204/225(91%)	0/225(0%)	Plus/Plus	

Features:

Query	91	GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGAGAAGGACCA	150
Sbjct	1263	GTACCTCCCTCCATACACGACATGGTTTCCATTTGGAGAGAGCTCCAGCGTGAAGGACCA	1322
Query	151	TCCCACGGAGGAGACCCCGGGGGTCAAGTTGCTCAAGAGCACGGCTCTGTACAACCTCTC	210
Sbjct	1323	TCCCACGGAGGAGACCCAGGGGGTGAAGTTGCTCAAGAGCACGCTTCTGTACAACCTCTC	1382
Query	211	CTACCTCGCCATCTTTCATCATCGCCATCTGCGTCACCGAAAGGGAAAACCTCGAGGAAAA	270
Sbjct	1383	CTACCTTGCCATCTTTGTTCATCGCCATCTGCGTCACTGAGAGGGAAAAGCTCAAGGAGGA	1442
Query	271	CCCCCTCAACTTCAGCTTGCTCAGCATCGTCGTCGAAGTCGTCAG	315
Sbjct	1443	CCCCCTCAACTTCAACTTGCTCAGCATCGTCGTCGAAGTCGTCAG	1487

Triticum durum HKT1;4-1 mRNA, complete cds

Sequence ID: **gb|KF443078.1|** Length: 1692 Number of Matches: 1

Range 1: 1269 to 1493

Score	Expect	Identities	Gaps	Strand	Frame
300 bits(162)	3e-77()	204/225(91%)	0/225(0%)	Plus/Plus	

Features:

Query	91	GTACCTGCCTCCATACACCACATGGTTTCCATTTGAGGAGAGCTCGGGCGAGAAGGACCA	150
Sbjct	1269	GTACCTGCCTCCATACACGACGTGGTTTCCATTTGAAGAGAGCTCCGGCGTCAAGGACCA	1328
Query	151	TCCCACGGAGGAGACCCCGGGGGTCAAGTTGCTCAAGAGCACGGCTCTGTACAACCTCTC	210
Sbjct	1329	ACCCAGGGAGGAGACCCAGGGGGTCAAGCTGCTCAAGAGCACGCTTCTGTACAACCTCTC	1388
Query	211	CTACCTCGCCATCTTTCATCATCGCCATCTGCGTCACCGAAAGGGAAAACCTCGAGGAAAA	270
Sbjct	1389	CTACCTCGCCATCTTTGTTCATCGCCATCTGCATCACCGAGAGGGAAAAGCTCAAGGAGGA	1448
Query	271	CCCCCTCAACTTCAGCTTGCTCAGCATCGTCGTCGAAGTCGTCAG	315
Sbjct	1449	CCCCCTCAACTTCAACTTGCTCAGCATCGTCGTCGAAGTCGTCAG	1493