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.

Α

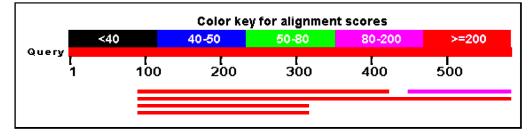
BLAST Results

HKT1;4-Kharchia-65

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

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 protein (HKT1,4.1	partial mRNA for HKT gene)	551	551	56%	7e-153	97%	<u>HG934161.1</u>
U U	subsp. spontaneum high- rter 4 gene, complete	472	472	84%	5e - 129	84%	<u>HQ696002.1</u>
Triticum durum Hł	(T1;4-2 mRNA, complete	311	311	38%	1e-80	92%	<u>KF443079.1</u>
Triticum durum Hk cds	(T1;4-1 mRNA, complete	311	311	38%	1e - 80	92%	<u>KF443078.1</u>
	cum putative sodium A2 (HKT7-A2) mRNA,	183	183	23%	3e-42	91%	<u>EF062819.1</u>

Alignments

Triticum aestivum partial mRNA for HKT protein (HKT1,4.1 gene) Sequence [D: emb[HG934161.1] Length: 331 Number of Matches: 1 Range 1: 1 to 331

Score		Expect	dentities	Gaps	Strand	Frame
551 bits	(298)	7e-153()	320/331(97%)	0/331(0%)	Plus/Plus	
Feature	s:					
Query	92	ͼϯϙϲϲϯͼϲϲϯϲϲϙϯ	ϙϲϙϲϲϙϲϙϯϙϙϯϯϯϲϲ	ATTTGAGGAGAGCTC	GGGCGTGAAGGACCA	151
Sbjct	1	ĠŦĂĊĊŦĠĊĊŦĊĊĂŦ.	ACACCACATGGTTTCC	Atttgaggagagg	ġġġċġtġyyġġyċç	60
Query	152	ТСССАСССАССАСА	ссссееееетсеетт	GCTCAAGAGCACGGC	ΤϚΤϚΤϚΑϚΑΑϚΤϚΤ	211
Sbjct	61	tcccacgeageage	cccagggggggggggggg	ϛϲϯϲϥϥͼϥͼϲϥϲϲ	tététékékkétété	120
Query	212	CTACCTCGCCATCT	TCATCATCGCCATCTG	СӨТСАССӨАААӨӨӨА ТТТТТТТТ	AAACCTCGAGGAAGA	271
Sbjct	121	¢+4¢¢+¢&¢¢4+¢+	tčAtčAtčĠččAtčtĠ	ĊĠŦĊĂĊĊĠĂĠĂĠĠĠĂ	AAACCTCGAGGAAAA	180
Query	272		GCTTGCTCAGCATCGT	СӨТСӨААӨТСӨТСАӨ	GCAAGCCCCTTCTA/	331
Sbjct	181	66666464664464464	<u>dettgetergeter</u>	ĊĠŦĊĠĂĂĠŦĊĠŦĊĂĠ	ĠĊĂĂĠĊĊĊĊŦŦĊŦĂ	240
Query	332		GCCTGAAAACGAATAA	САААТАТБАСТБСТА 		391
Sbjct	241	ĊĠĊĂĂĂŦĊĂĂĠĂĂĂ	ĠĊĊŦĠĂĂĂĂĊĠĂĂŦĂĂ	ĊĂĂĂŦĂŦĠĂĊŦĠĊĂĂ	Ċ††ÅG††ĊĊĠĠĊA††	300
Query	392	GTTGGTTTCCTTCA	TGGAAGCTGACATGTT	T 422		
Sbjct	301	attggtttccttca	tggaagctgacatatt	† 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	s(255)	5e-129()	418/496(84%)	14/496(2%)	Plus/Plus	
Feature	s:					
Query	92	ͼ ϯ ϙ ϲϲϯͼϲϲϯϲϲϙϯ	<mark>₳с₳сс₳с</mark> ₳төөтттс	ҁѧҭҭҭҩѧҩҁѧҁѧҁҁҭҁ	свосоторование	151
Sbjct	487	\$4755495545544	AGAGAGAGATAGATTC	cattccaagagagctd	catcotogcadacca	546
Query	152		ϲϲϲϲͼͼͼͼͼϯϲϫͼͼϮ	ТӨСТСААӨАӨСАСӨӨС	τετοτερέρου	211
Sbjct	547	CCCCACGAAGGAGA	CCAGGGGCTCAGGC	TGCTCAAGAGCGCGCG	TCTGTCACAACTCT	606
Query	212	CTACCTCGCCATCT	ϯϲϫϯϲϫϯϲͼϲϲϫϯϲϯ	<u> </u>	ѵѧѧѧҁҁҭҁҁѧҁҁѧѧҁ	271
Sbjct	607	ctacctcgccatct.	tcgtcgtcgccAtct	gcqtcycccgyagyggg	saaacctagaggaag	666
Query	272	ϛϛϛϲϛϯϛϙϙϛϯϯϛϙ	ҁҁттҁҁҭҁѧҁҁѧҭҁҁ	тсөтсөлөөтсөтсө	σο στη τη τ	A 330
Sbjct	667	¢¢¢g¢t¢AA¢tt¢A	scctectcyecetce	tcgtccyagtcgtcya	secoceccic exercic	726
Query	331	ϙϲϙϲϙϙϯϯϲϭϭϙϭϙ	ΑGCCTGAAAACGAA T	ΑΑCAAΑΤΑΤGACTGC Ι	асттасттссааса	Г 390
Sbjct	727	AAGCAAATC-GAGA	a-cctgaaaacgaat	AAAGACGAAtaCA	gétteattéétéé-	- 779

Query	391	TGTTGGTTTCCTTCATGGAAGCTGACATGTTTTATCCTTCACATTCCGCAGTGCGG -GTTGATTTCCTTCATGGAAGGAAGCTGACATGTTTTGTCTTTCACATTCCGCAGCGCCTT	446
Sbjct	780	-&++&a+++&&++&&+&&+&&+&+&+&+++&+&+&+&+&+	838
Query	447	<u></u> АТ <u></u> Б <u></u> Б Б <u></u> Б <u></u> Б Б <u></u> Б Б <u></u> Б <u></u> B B B B B B B B B B B	506
Sbjct	839		898
Query	507	ŢĠŢĠĊ₳ĊĊĠĄĊĠĠĠŢĠĠĄĊĊĠĠĊŢŢĊĠŦĊĠĠĠġĠġŢĠĠġŢĠĄŢŢĊŢĠĠĊġġĠĊŢĊĄŢĊĊ	566
Sbjct	899	TGTGCACCGACGGGTGGACCGGCTTCGTCGGGGAGGTGGAGTGATTCTGGCAAGCTCATCC TGTGCGCCGACAGGTGGACCGGCTTCGCCGGAAGGTGGAGCGATTCTGGCAAGCTCATCC	958
Query	567	ŢÇĄŢŢÇĠŢŢĢŢĠĄŢĢÇ 582	
Sbjct	959	TCATTCGTTGTGATGC 582 TCATTC-TTGTAATGC 973	



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	
Feature	s:					
Query	92	ͼϯϟϲϲϯͼϲϲϯϲϲ	τρογο	сатттөаөөөөөөгт	сөөөсөтөрөөөс	CA 151
Sbjct	1263	<u></u> <u> </u>	tacaceacateettte	catttgaagagagag	ccaeceteaaeeac	CA 1322
Query	152	ТСССАСССАССАССАС	ΑϲϲϲϲͼͼͼͼͼτϲϫͼͼϮ	ТӨСТСААӨАӨСАСӨС	στετετερέρησησ	IC 211
Sbjct	1323	tcccaceeeee	bAcccadddddtgAddt	tgctcyygygygygy		tc 1382
Query	212			бсе⊤сассбалабо	δΑΑΑΑCCTCGAGGAA	GA 271
Sbjct	1383	64466446666446	ttrgtcAtccccAtct	ĠĊĠŦĊĂĊŦĠĂĠĂĠĠĠ	SAAAAGCTCAAGGAG	GA 1442
Query	272	CCCCCTCAACTTC		ТСӨТСӨААӨТСӨТСИ	G 316	
Sbjct	1443	6666646446446	LAACTTGCTCAGCATCG	tcgtcgyygtcgtcgtc	G 1487	

Triticum durum HKT1;4-1 mRNA, complete cds

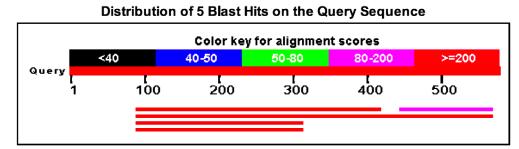
Sequence ID: **gb|KF443078.1|** Length: 1692 Number of Matches: 1 Range 1: 1269 to 1493

Score		Expect	Identities	Gaps	Strand	Frame
311 bits	s(168)	1e-80()	206/225(92%)	0/225(0%)	Plus/Plus	
Feature	S:					
Query	92	ͼ ϯϙϲϲϯͼϲϲϯϲϲ	<u></u> ΑΤΑ ΓΑ ΓΕΑΓΕΑΤΑΓΑΤΑΓΑ	сатттеребрерс	<mark>ГСӨӨӨСӨТӨААӨӨА</mark>	CCA 151
Sbjct	1269	etycstercty	Atacacgacgtggtttc	catttgaagagagc	łęcęęcętcyłęcy	CCA 1328
Query	152	ΤϹϹϹΑϹϾϾΑϾϾΑ	ассссаааатсааат	Тестсалелесасе	^{ͻϲ} ϯϲϯϙϯϲϙϙϲϯ	CTC 211
Sbjct	1329	ACCCAGGGAGGAG	sacccadddddtcaddc	ϯͼϲϯϲϥϥͼϥͼϲϥϲͼͼ	сттстбтсүсүүс	ctc 1388
Query	212	CTACCTCGCCAT(CTTCATCATCGCCATCT	GCGTCACCGAAAGGG	ΓΑΑΑΑCCTCGAGGA	AGA 271
Sbjct	1389	64466466666446	tttgtcAtcGccAtct	dcatcaccdagaddd	SAAAAGCTCAAGGA	GGA 1448
Query	272	CCCCCTCAACTTC	AGCTTGCTCAGCATCG	ТСӨТСӨААӨТСӨТСИ	AG 316	
Sbjct	1449	6666646446446	ŁAACTTGCTCAGCATCG	tçetçeyyetçetç	G 1493	

HKT1;4-HD-2329

RID	UNUYUR6X01R (Expires on 08-11 16:54 pm)		
Query ID Description Molecule type Query Length	nucleic acid	•	nr Nucleotide collection (nt) 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)	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%	<u>HQ696002.1</u>
Triticum durum HKT1;4-2 mRNA, complete cds	300	300	38%	3e-77	91%	<u>KF443079.1</u>
Triticum durum HKT1;4-1 mRNA, complete cds	300	300	38%	3e - 77	91%	<u>KF443078.1</u>
Triticum monococcum putative sodium transporter HKT7-A2 (HKT7-A2) mRNA, complete cds	172	172	21%	6e-39	91%	<u>EF062819.1</u>

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	s:					
Query	91	ͼ ϯ ϙ ϲϲϯͼϲϲϯϲϲϙϯ		атттөдөөдөөстс	өөөсө лөөөөөсс	A 150
Sbjct	1	649664966466944	<u> </u>	A+++&A&&A&&&+&	ҁҁҁҁѧҭҁүүҫҁүҁҁ	A 60

В

Query	151		210
Sbjct	61	tcccacgqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	120
Query	211		270
Sbjct	121	ĊŦĂĊĊŦĊĠĊĊĂŦĊŦŦĊĂŦĊĠĊĊĂŦĊŦĠĊĠŦĊĂĊĊĠĂĠĂĠĠĠĂĂĂĂĊĊŦĊĠĂĠĠĂĂĂĂ	180
Query	271		330
Sbjct	181	¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿¿	240
Query	331	CGCaaatcaaaaaagccagaaaacgaataaaaaaTATGACTGCTTCTTACTTCCGGCGTT CGCAAATCAAGAAAGCCTGAAAAACGAATAACAAATATGACTGCAACTTAGTTCCGGCATT	390
Sbjct	241	¿ĠĊĂĂÆĊĂĂĠĂĂĂĠĊĊŦĠĂĂĂĂĂĊĠĂĂŦĂĂĊĂĂĂŦĂĬĠĂĊŦĠĊĸĸĊŦŦĂĠŦŦĊĊĠĠĊĸŦŦ	300
Query	391	GTTGGTTTCCTTCATGGAAGATGACATGTTT 421	
Sbjct	301	attggtttccttcatggaaggctgacatattt 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 964

Score		Expec	ct Identities	Gaps	Strand	Frame
453 bits	(245)	2e-123	3() 409/487(8	34%) 15/487(3	%) Plus/Plus	
Feature	S:					
Query	91	GTACCTOCC	ŢĊĊĄŢĄĊĄĊĊĄĊĄŢ	ĠĠŢŢŢĊĊĄŢŢŦĠĄĠĠĄĠ	ΑĠĊŢĊĠĠĠĊĠĂĠĂĂĠĠĂ	CCA 150
Sbjct	487	644664666	tccatacacat	ddtttccaddd	ΑἀἀτέςατέἀτἀσςαἀΑ	CCA 546
Query	151	TCCCACGGAC	зеаеассссеееее 			CTC 210
Sbjct	547	CCCCACGAA	GGAGACCCAGGGGG	CTCAGGCTGCTCAAGAGC	GCGCTTCTGTCACAACT	СТС 606
Query	211		ς ΑΤς ΤΤς ΑΤς ΑΤς Α Ι Ι Ι Ι Ι Ι Ι Ι Ι	ЗССАТСТОСОТСАССОАА 	AGGGAAAACCTCGAGGA	AAA 270 III
Sbjct	607	ĊŦĂĊĊŦĊĠĊ	cAtcttcgtcgtcd	ĠĊĊĂŦĊŦĠĊĠŦĊĂĊĊĠĂĠ	AGGGGAAACCTAGAGGA	
Query	271		СТТСАВСТТВСТСИ		GTCAGGCAAGCCCC-TT	СТА 329
Sbjct	667	CCCGCTCAA	CTTCAGCCTGCTCA	AGCGTCGTCGTCCAAGTC	GTCAGGCACGCCCCACT	ČCA 726
Query	330		aaaaaagccagaaa	acgaataaa-aaaTATG	ACTGCTTCTTACTTCCG	GCG 388
Sbjct	727	AAGCAAATC				GC - 779 GCG 444
Query Sbjct	389 780					GCT 837
Query	445	GATGGAAAT	GGGGGCTTCTCCA	IGGGCTACGGTTGCAATT	GACAGATCAGCCCGGAC	
Sbjct	838	ТАСССАААТ				CGG 897
Query	505	CTGTGCACC	GACGGGTGGACCG	GCTTCGTCGGGAGGTGGA		
Sbjct	898	GTGTGCGCC	GACAGGTGGACCG	LITTCGCCGGAAGGTGGA	LLLL++++++++++++++++++++++++++++++++++	ATC 957
Query	565	CTCATTC	571			
Sbjct	958	6468446	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	ͼϯϙϲϲϯͼϲϲϯϲϲ	<u></u> ΑΤΑ <u>Γ</u> ΑΓ <u>Α</u> ΓΑ	сатттаабаабаба	ҁҁҁҁҁҁѧҁѧѧҁҁѧ	CA 150	
Sbjct	1263	ϐϯΫϚϚϯϲϚϚϯϚϚ	Atacaccacated ttt	:catttgaagagagag	ссадсдтдддддд	CA 1322	
Query	151	ТСССАСБЕАБЕА	зассссееееетсаеет	Тестсалелесасее	στετατερερατικά	TC 210	
Sbjct	1323	ϯϲϲϲΫϲϨͼϩϩͼͼ	sacccagggggtggggt	ϯͼϲϯϲϥϥͼϥͼϲϥϲͼϲ	сттстбтсАсААсто	tc 1382	
Query	211		;ϯϯϲͽϯϲϙϯϲϙϲϙϯϲϯ		δΑΑΑΑCCTCGAGGA/	AA 270	
Sbjct	1383	6446644666446	tttgtcAtcGccAtct	ĠĊĠ†ĊĂĊŦĠĂĠĂĠĠĠ	GAAAAGC†CAAGGAG	GA 1442	
Query	271	CCCCCTCAACTT(ТССТССААСТССТСА	G 315		
Sbjct	1443	66666464A6446	ĊĂĂĊŦŦĠĊŦĊĂĠĊĂŦĊĠ	itcdtcdAAdtcdtcA	d 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	ͼ ϯ ϙ ϲϲϯͼϲϲϯϲϲ	Ϟϯϙϲϙϲϲϙϲϫϯϙϙϯϯϯ	ссатттөабөөөөст	ҁҁҁҁҁҁѧҁѧѧҁҁѧҁ	CA 150
Sbjct	1269	\$ 1 7777777	\tACACGACGtGGttt	ccatttgaagagagct	ссеесетстерее	CA 1328
Query	151	тсссасбабеа	ҕѧҫҫҫҫҫѳѳѳѳҭҫѧҩҩ	ттөстсаабабсасбе	ͼϯϲϯϙϯϲϙϲϙϲϯϲ	TC 210
Sbjct	1329	acccaeeeeee	bACCCAGGGGGGTCAGG	ctectcaaeeecoc	ттстеренски	tc 1388
Query	211	CTACCTCGCCAT	;ϯϯϲͽϯϲϙϯϲϙϲϲ	Төсөтсассөллөөө	ΑΑΑΑCCTCGAGGAA	AA 270
Sbjct	1389	6476646666744	Litteleverse	tecatcacceaeeee	AAAAGCTCAAGGAG	GA 1448
Query	271	ϛϛϛϛϛϯϛϙϙϛϯϯ	ΑΘΕΤΤΘΕΤΕΑΘΕΑΤΕ	GTCGTCGAAGTCGTCA	G 315	
Sbjct	1449	666646446446	LAACTTGCTCAGCATC	etçetçeyyetçetçe	G 1493	