

Supplementary Materials

Table S1. List of primers and amplicons for sequencing the coding regions of the barley *Msh* genes.

Gene/ Locus-Amplicon	Forward Primer	Reverse Primer	Amplicon Size (bp)
<i>Msh1</i> / HORVU2Hr1G087660.5 ^a	E1F3 CGACTCAATCCTCCGGCG	E10R GAACCATCAAACCAGTCAAAGGA	924
	E10F TCTTGTGGGGAGAGTGCAAC	E20R AGCGCATACTGACATCGTTCA	1326
	E20F TGCAGGATTATAGTACTGAAGAAAGC	E22R TGGCTTCTCCAGAGGTTACAG	1222
<i>Msh2</i> / HORVU1Hr1G030930.2 ^a	E1F TTTGCACACATTTGCGCGAG	E6R AGCACAGCCAAATCAGGAGA	1496
	E6F ACAGCCATTGACCTCGATCA	E13R GGGATTACTGGCTGCGTCTT	1452
<i>Msh3</i> / HORVU2Hr1G085940.3 ^{a,e}	E1F CCAGAAGAGGGGAGCAGGTA	E7R TGGTAGTTTCGATCAGGTAAGCTG	1302
	E6F GCTGACCAGTTCCCGAG	E12R AGCTTCCCCTGTGCCATCC	1249
<i>Msh4</i> / HORVU2Hr1G031870.3 ^a	It was not amplified nor sequenced		
<i>Msh5</i> / HORVU1Hr1G066830 ^b	It was not amplified nor sequenced		
<i>Msh6</i> / HORVU5HrG1061020 ^{c,e}	E1F1 CTGTGCAGGAGGATGAGGAT	E8R TTGAAAATAGCAATGGCACCT	1669
	E8F1 TGAATCATTGTGTTACTGGATTG	E13R1 GACACCAACCGTCTCCACTT	838
	E13F1 CTGCCGGTACTGGACACC	E17R1 CCTGGCACGCATCTGTACT	1114
<i>Msh7</i> / HORVU3Hr1G021520 ^d	E1F1 CAGCAGCAGTCCATCCTCTC	E5R CCTCTAACTTTCGCCTGTGC	1460
	E5F ATGGAATCTGCAGCACAGG	E12R TCATCAAGAGAGCTCAGGGTTG	1085
	E11F CTTGGACGAGTCAGATCCAC	E16R1 TGGGCGACACAGAACATC	1313

- The numbers after the dots correspond to the splice variant producing the most probable protein isoform, which was used to design the primers.
- In this locus, the splice variant producing the most probable protein isoform does not correspond to any of the variants shown in Ensembl Plants database. Actually, it is a mixture of those producing isoforms 28 and 9.
- In this locus, the splice variant producing the protein isoform that was used to design the primers does not correspond to any of the variants shown in Ensembl Plants database. Actually, it is a mixture of those producing isoforms 32 and 11.
- In this locus, the splice variant producing the protein isoform that was used to design the primers does not correspond to any of the variants shown in Ensembl Plants database. Actually, it is a mixture of those producing isoforms 35 and 20.
- The proteins encoded in these loci lack the first part in comparison to the *A. thaliana* protein.

Table S2A. Prediction of the subcellular location of barley MSH proteins with TargetP-1.1.

Protein	Mitochondrial transfer peptide	Chloroplast transfer peptide	Signal peptide to secretory pathway	Any other location	Location
MSH1	0.791	0.620	0.004	0.006	Mitochondria Chloroplast
MSH2	0.122	0.068	0.044	0.952	-
MSH3*	0.122	0.041	0.030	0.968	-
MSH4	0.175	0.103	0.051	0.865	-
MSH5	0.503	0.020	0.232	0.499	Mitochondria
MSH6*	0.045	0.075	0.025	0.939	-
MSH7	0.571	0.299	0.008	0.076	Mitochondria

*These proteins lack the first part in comparison to the *A. thaliana* protein.

Table S2B. Prediction of the subcellular location of barley MSH proteins with TargetP-2.0.

Protein	Mitochondrial transfer peptide	Chloroplast transfer peptide	Thylakoid luminal transfer peptide	Signal peptide to secretory pathway	Any other location
MSH1	0.4146	0.3796	0.0023	0.0240	0.2010
MSH2	0	0	0	0	1
MSH3*	0	0	0	0.0001	0.9999
MSH4	0	0	0	0.0002	0.9998
MSH5	0.0001	0	0	0.0005	0.9994
MSH6*	0	0	0	0	1
MSH7	0.0001	0	0	0.0005	0.9985

*These proteins lack the first part in comparison to the *A. thaliana* protein.

Figure S1. Alignment of *H. vulgare*, *cpm* and control MSH1 proteins. Mismatch-recognition, ATPase and endonuclease domains are indicated by red, blue and green boxes, respectively.

<i>H. vulgare</i>	MQRLLASSIVAATPWLPLADSIILRRRRPRRSPLPILLFNRSWSKPTKVSRISIMVSSKA	60
control	MQRLLASSIVAATPWLPLADSIILRRRRPRRSPLPILLFNRSWSKPTKVSRISIMVSSKA	60
<i>cpm</i>	MQRLLASSIVAATPWLPLADSIILRRRRPRRSPLPILLFNRSWSKPTKVSRISIMVSSKA	60
<i>H. vulgare</i>	NKQGDLCNEGMLSHIMWKKERMESCRKSSVQLTQRLVYSNIGLDSTLRNGSLKDGTLN	120
control	NKQGDLCNEGMLSHIMWKKERMESCRKSSVQLTQRLVYSNIGLDSTLRNGSLKDGTLN	120
<i>cpm</i>	NKQGDLCNEGMLSHIMWKKERMESCRKSSVQLTQRLVYSNIGLDSTLRNGSLKDGTLN	120
<i>H. vulgare</i>	MEMLQFKSKFPREILLCRVGFYEAIGFDACILVEHAGLNPFGLRSDSI PKAGCPIMNL	180
control	MEMLQFKSKFPREILLCRVGFYEAIGFDACILVEHAGLNPFGLRSDSI PKAGCPIMNL	180
<i>cpm</i>	MEMLQFKSKFPREILLCRVGFYEAIGFDACILVEHAGLNPFGLRSDSI PKAGCPIMNL	180
<i>H. vulgare</i>	RQTLDDLTRCGYSVCIVEEIQGPTQARARKGRFISGHAHPGSPYVFGLAEDHDLEFPDP	240
control	RQTLDDLTRCGYSVCIVEEIQGPTQARARKGRFISGHAHPGSPYVFGLAEDHDLEFPDP	240
<i>cpm</i>	RQTLDDLTRCGYSVCIVEEIQGPTQARARKGRFISGHAHPGSPYVFGLAEDHDLEFPDP	240
<i>H. vulgare</i>	MPVVGISRSAGYCLISVLEMTKTYSAEGLTEEAUVTKLRICRYHLYLHSSLRNNSG	300
control	MPVVGISRSAGYCLISVLEMTKTYSAEGLTEEAUVTKLRICRYHLYLHSSLRNNSG	300
<i>cpm</i>	MPVVGISRSAGYCLISVLEMTKTYSAEGLTEEAUVTKLRICRYHLYLHSSLRNNSG	300
<i>H. vulgare</i>	TSRWGEFGEGLLWGEANGKSFDFWFGSPIDEILLCKVREIYGLDEKTSFRNVTISLEGRP	360
control	TSRWGEFGEGLLWGEANGKSFDFWFGSPIDEILLCKVREIYGLDEKTSFRNVTISLEGRP	360
<i>cpm</i>	TSRWGEFGEGLLWGEANGKSFDFWFGSPIDEILLCKVREIYGLDEKTSFRNVTISLEGRP	360
<i>H. vulgare</i>	QPLYLTATQIGVITPTEGIPSLPKMLLPNCAGLPSMYIRDLLNPPSFDVASAIQACR	420
control	QPLYLTATQIGVITPTEGIPSLPKMLLPNCAGLPSMYIRDLLNPPSFDVASAIQACR	420
<i>cpm</i>	QPLYLTATQIGVITPTEGIPSLPKMLLPNCAGLPSMYIRDLLNPPSFDVASAIQACR	420
<i>H. vulgare</i>	IMCSITCSIPEFTCIPSALVKLESKEVNHIEFCRIKVLDEIMLMNGNTELSAIQNK	480
control	IMCSITCSIPEFTCIPSALVKLESKEVNHIEFCRIKVLDEIMLMNGNTELSAIQNK	480
<i>cpm</i>	IMCSITCSIPEFTCIPSALVKLESKEVNHIEFCRIKVLDEIMLMNGNTELSAIQNK	480
<i>H. vulgare</i>	LEPASVVTGLKVDADILIKECRFISKRIGEVISLAGESDQAISSEYIPKEFFNDMESSW	540
control	LEPASVVTGLKVDADILIKECRFISKRIGEVISLAGESDQAISSEYIPKEFFNDMESSW	540
<i>cpm</i>	LEPASVVTGLKVDADILIKECRFISKRIGEVISLAGESDQAISSEYIPKEFFNDMESSW	540
<i>H. vulgare</i>	KGRVKRVHAEFESFNVDAQAALSTAVTEDFLPIIVRVKSVMSHGSSKGEISYAKEHGA	600
control	KGRVKRVHAEFESFNVDAQAALSTAVTEDFLPIIVRVKSVMSHGSSKGEISYAKEHGA	600
<i>cpm</i>	KGRVKRVHAEFESFNVDAQAALSTAVTEDFLPIIVRVKSVMSHGSSKGEISYAKEHGA	600
<i>H. vulgare</i>	VWFKGRRFTPNVWANTPGEEQIKQLKPAIDSKGRVGEWFTTTKVENALARYHEACDNA	660
control	VWFKGRRFTPNVWANTPGEEQIKQLKPAIDSKGRVGEWFTTTKVENALARYHEACDNA	660
<i>cpm</i>	VWFKGRRFTPNVWANTPGEEQIKQLKPAIDSKGRVGEWFTTTKVENALARYHEACDNA	660
<i>H. vulgare</i>	KGKVLLELLRGLSSELQDKINILVFCSTLLIITKALFGHVSEGLRRGWLPPIYPLSKDYS	720
control	KGKVLLELLRGLSSELQDKINILVFCSTLLIITKALFGHVSEGLRRGWLPPIYPLSKDYS	720
<i>cpm</i>	KGKVLLELLRGLSSELQDKINILVFCSTLLIITKALFGHVSEGLRRGWLPPIYPLSKDYS	720
<i>H. vulgare</i>	TEESSEMDDLGLFPYWLNTNQGNAILNDVSMRSLFILTGPNGGGKSSMLRSVCAALLG	780
control	TEESSEMDDLGLFPYWLNTNQGNAILNDVSMRSLFILTGPNGGGKSSMLRSVCAALLG	780
<i>cpm</i>	TEESSEMDDLGLFPYWLNTNQGNAILNDVSMRSLFILTGPNGGGKSSMLRSVCAALLG	780
<i>H. vulgare</i>	VCGLMVPAASAVIPHFDSIMLHMAYDSPADGKSSFIEMSEIRSLVSRATGRSLVLIDE	840
control	VCGLMVPAASAVIPHFDSIMLHMAYDSPADGKSSFIEMSEIRSLVSRATGRSLVLIDE	840
<i>cpm</i>	VCGLMVPAASAVIPHFDSIMLHMAYDSPADGKSSFIEMSEIRSLVSRATGRSLVLIDE	840
<i>H. vulgare</i>	ICRGITETAKGTCIAGSIIERLDDAGCLGIVSTHLHGFIDLPLSLNNTDFKAMGTEWVNGY	900
control	ICRGITETAKGTCIAGSIIERLDDAGCLGIVSTHLHGFIDLPLSLNNTDFKAMGTEWVNGY	900
<i>cpm</i>	ICRGITETAKGTCIAGSIIERLDDAGCLGIVSTHLHGFIDLPLSLNNTDFKAMGTEWVNGY	900
<i>H. vulgare</i>	IQPTWRLMDGICRESLAFQTARKEGMPDLIIKRAEELYLNMSRNKHTSLTLHPIVANS	960
control	IQPTWRLMDGICRESLAFQTARKEGMPDLIIKRAEELYLNMSRNKHTSLTLHPIVANS	960
<i>cpm</i>	IQPTWRLMDGICRESLAFQTARKEGMPDLIIKRAEELYLNMSRNKHTSLTLHPIVANS	960
<i>H. vulgare</i>	SVNGGLVDRPDGLNGLEPPTGSFGLLRKDVEISIVTAICEDKLLDLNKRISIEQVEVVC	1020
control	SVNGGLVDRPDGLNGLEPPTGSFGLLRKDVEISIVTAICEDKLLDLNKRISIEQVEVVC	1020
<i>cpm</i>	SVNGGLVDRPDGLNGLEPPTGSFGLLRKDVEISIVTAICEDKLLDLNKRISIEQVEVVC	1020
<i>H. vulgare</i>	VIVGAREQPPSTVGRSSIIYIIIRDNKLYVGQTDLLVGRGLGAHRSKEGMQDATILYIVV	1080
control	VIVGAREQPPSTVGRSSIIYIIIRDNKLYVGQTDLLVGRGLGAHRSKEGMQDATILYIVV	1080
<i>cpm</i>	VIVGAREQPPSTVGRSSIIYIIIRDNKLYVGQTDLLVGRGLGAHRSKEGMQDATILYIVV	1080
<i>H. vulgare</i>	PGKSVACQLETLLINQLPSKGFKLTKADGKHNFMSVTSGEAMAAH	1128
control	PGKSVACQLETLLINQLPSKGFKLTKADGKHNFMSVTSGEAMAAH	1128
<i>cpm</i>	PGKSVACQLETLLINQLPSKGFKLTKADGKHNFMSVTSGEAMAAH	601