

Supplementary Material

Regulation of Cell Fate Determination by Single-repeat R3 MYB Transcription Factors in Arabidopsis

Shucaai Wang¹ and Jin-Gui Chen^{2, *}

¹ Key Laboratory of Molecular Epigenetics of MOE and Institute of Genetics & Cytology,
Northeast Normal University, Changchun, China

² Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, USA

* Correspondence:

Biosciences Division

Oak Ridge National Laboratory

1 Bethel Valley Rd

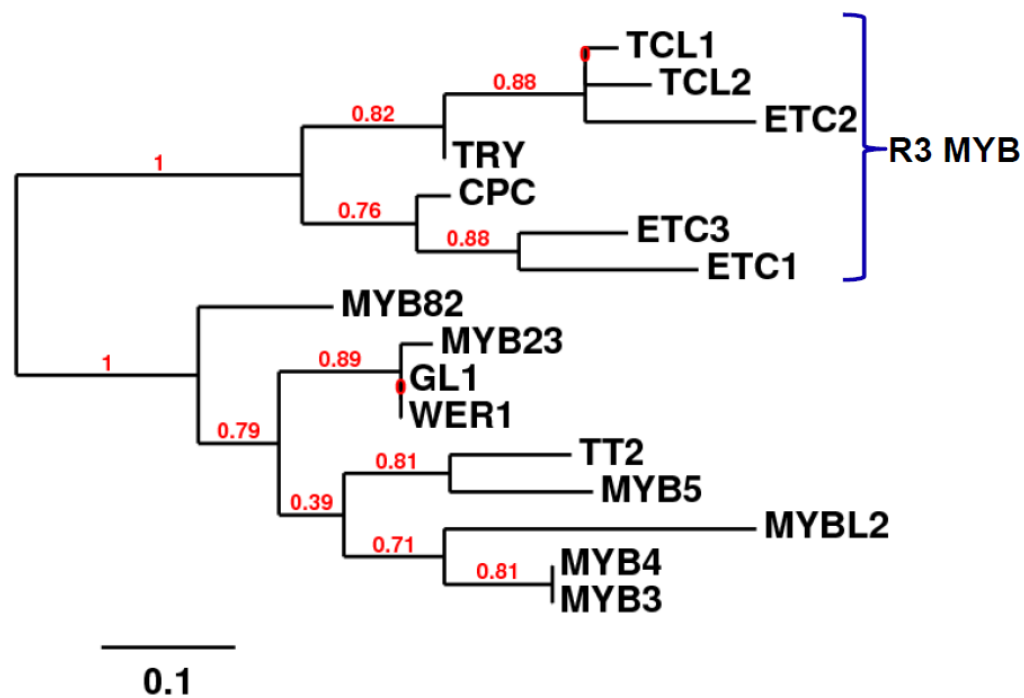
Oak Ridge, TN 37831

USA

Email: chenj@ornl.gov

TRY	1	-----MDNTDR-----RRRRK-----QHKIALH--DSEEVSSIEWE-FIN-----	32
CPC	1	-----MFRSDKAEK-----MDKRR-----RRQSKAKASCSE--EVSSIEWE-AVK-----	37
ETC1	1	-----MNTQR-----KSMHL-----KTNPATIVASSSE--EVSSIEWE-EIA-----	33
ETC2	1	-----MDNTNR-----LRLRGPSLRQTKFTRSRYSSEEVSSIEWE-FIS-----	39
ETC3	1	-----MDNHR-----RTKQP-----KTN-SIVTSSSEGTEVSSIEWE-VVN-----	34
TCL1	1	-----MDNTNR-----LRLRH--CHKQPKFTH--SSQEVSSMKWE-FIN-----	34
TCL2	1	-----MDNTNR-----LRHLR--SRKQSKFTIG--DTAEVNSVWE-FIN-----	35
MYBL2	1	-----MNKTR-----LRALSPPSGMOHR-KRCRLRGNYVRPEVKQRN	37
MYB4	1	-----MGRSPCCEKAHTNKGAWTKEEDERLVAYIKAHGEGGWRSLPKAAGLIRCGKSCRLRWNYLRPDLKRG	69
MYB3	1	-----MGRSPCCEKAHMNKGAWTKEEDQLVDYIRKHGEGGWRSLPRAAGLIRCGKSCRLRWNYLRPDLKRG	69
MYB5	1	MMSCGGKPVSKTTPCCTKMGMRGHWITVEEDEILVSFIKKEGEGWRSLPKRAGLIRCGKSCRLRWNYLRPSVKRGG	80
GL1	1	-----MR--IRRDEKENQYKKGLWITVEEDNILMDYVLNHGTCWNRIVRKTGLIRCGKSCRLRWNYLRPNVNRGN	71
TT2	1	-----MG--KRATTSVRREELNRGAWTIDHEDKILRDYITTHGEGWSTLPNQAGLIRCGKSCRLRWNYLRPGIKRG	71
MYB23	1	-----MR--MTRDGKE--HEYKKGHWITVEEDKILMDYVVRHGGGWNRIAKKTIGLIRCGKSCRLRWNYLRPNVNRGN	69
MYB82	1	-----MECKREEGKSIVKRGHWITVEEDMILKSYVETHGGGWADISRRSGLIRCGKSCRLRWNYLRPNIKRGS	69
WER1	1	-----MRKKVSSSGDEGNNEYKGLWITVEEDKILMDYVKAHGEGWNRIAKKTIGLIRCGKSCRLRWNYLRPNVNRGN	73
TRY	33	MTEQEEDLIERMYRLVGDWRDLIAGFVPGROPETIERYWIMRNSGEGFADKRRQLHSSSHKHTKPHR-----PRFSIY	104
CPC	38	MSEEEEDLIERMYKIVGDWRDLIAGFIPGRTPEETIERYIMKHGVVFANRRRDFR-----	94
ETC1	34	MAQEEEDLIERMYKIVGDWRDLIAGFIPGRTAETIERYVWMKN-----HRRSQLR-----	83
ETC2	40	MTEQEEDLIERMYRLVGNRDLIAGFVVGKANEIERYWIMRNSDYFSHKRRRLNNSPFFSTSPLN-----IQENLK	111
ETC3	35	MSQEEEDLIERMYKIVGDWRDLIAGFIPGRTAGEETIERYVWMKN-----	77
TCL1	35	MTEQEEDLIERMYRLVGDWRDLIAGFVVGREAKEETIERYWIMRNCDFYFSHK-----	84
TCL2	36	MTEQEEDLIERMYRLVGDWRDLIAGFVVGREAKEETIERYWIMRNCDFYFSHK-----	100
MYBL2	38	ESKDEEDLIERMYRLVGNRDLIAGFIPGRTDNEVRIETIERYVWMKN-----RRHLH	109
MYB4	70	ETEEDEDLIERMYRLVGNRDLIAGFIPGRTDNEIKNYWNTIIRKLLINRGIDPTSHRPIQESSASQDSKPTOLEPVTN	149
MYB3	70	ETEEDEDLIERMYRLVGNRDLIAGFIPGRTDNEIKNYWNTIIRKLLINRGIDPTSHRPIQESSASQDSKPTOLEPVTN	145
MYB5	81	ITSEDEDLIERMYRLVGNRDLIAGFIPGRTDNEIKNYWNTIIRKLLINRGIDPTSHRPIQESSASQDSKPTOLEPVTN	152
GL1	72	ETEEDEDLIERMYRLVGNRDLIAGFIPGRTDNEIKNYWNTIIRKLLINRGIDPTSHRPIQESSASQDSKPTOLEPVTN	140
TT2	72	ISSDEEDLIERMYRLVGNRDLIAGFIPGRTDNEIKNYWNTIIRKLLINRGIDPTSHRPIQESSASQDSKPTOLEPVTN	143
MYB23	70	ETDQEEDLIERMYRLVGNRDLIAGFIPGRTDNEIKNYWNTIIRKLLINRGIDPTSHRPIQESSASQDSKPTOLEPVTN	139
MYB82	70	MSQEEEDLIERMYRLVGNRDLIAGFIPGRTDNEIKNYWNTIIRKLLINRGIDPTSHRPIQESSASQDSKPTOLEPVTN	141
WER1	74	ETEEDEDLIERMYRLVGNRDLIAGFIPGRTDNEIKNYWNTIIRKLLINRGIDPTSHRPIQESSASQDSKPTOLEPVTN	141
TRY	105	PS-----	106
CPC	94	-----	94
ETC1	83	-----	83
ETC2	112	L-----	112
ETC3	77	-----	77
TCL1	84	-----	84
TCL2	100	-----	100
MYBL2	110	SSHKEHETKIIISQSSSVSESGVITLPIPTSTNCSEDSTSTGRSHLPDLNIGLIPAVTSLPALC-----	173
MYB4	150	TINISFTSAPKVFTHESISFPGKSEKISMLTFEKEEKDECPQVEKFDLNLRLSLPDDVDRLQGHGKSTTPRCFKCSL	229
MYB3	146	TIHLDFSGPVKPEPVREEIGMVNNCESSTGTTSEKDYGN-----EEDWVLNLELSVGPSYRYESTR-----KV	207
MYB5	153	SGGQRYPLEPISSHTDDTTVNGGDSKNSINVFGEHGYEDFGFCYDDKFSFSLNLSINDVG-----	216
GL1	141	ITAA--TPSSCHHQENIYENIAKSFNGVVSASVYEDKPKQE--LAQKDVLMATNDPSHYGN-----	199
TT2	144	TKARCSKTLFLSLQKKSSTSLPLKEQEMDQGGSSSLMGDLDFDRIHSEFHFDPDLMDFDG-----	208
MYB23	140	IT----TTSSSHQEIISGKNSITLRFDTLVDESKLKPKSKLV--HATPTDVEVAATVPNLFD-----	194
MYB82	142	ELRR--SHGEGGEEESN-----TWMEETNHFG-----YDVHVGSPPLISHYP-----	182
WER1	142	NP----TETSEETKISN-----IVNNNIIIG-----DEIQEDHQGSNYLS-----	177
TRY	106	-----	106
CPC	94	-----	94
ETC1	83	-----	83
ETC2	112	-----	112
ETC3	77	-----	77
TCL1	84	-----	84
TCL2	100	-----	100
MYBL2	173	-----LQDSSESSTNGSTGQETLLLF-----	195
MYB4	230	GMINGMECRGMRCDVVGSSSKGSDMSGDFDLGLAKKETTSLLGFRSLEMK-----	282
MYB3	208	SVVDSAESTR-RWGSELF--AHESDAVCLCCRIGLFRNESCRNCRVSDVRTH-----	257
MYB5	216	-----DPFGNIIPIS--QPLQMDCKDGIAGSSSSSLGHD-----	249
GL1	199	-----NALWVHDDF--ELSSLV--MMNFASGDVEYCL-----	228
TT2	208	-----LDCGNVTSLVSSNEILGELVPAQGNLDLNR-FTSCHHRGDDDEDLWLDFTC-----	258
MYB23	194	-----TFWVLEDDF--ELSSLT--MDFTNG--YCL-----	219
MYB82	182	-----DNTLVDFPCF--SFTDFPFL-----	201
WER1	177	-----SLWVHEDEF--ELSTLTNMMDFIDG--HCF-----	203

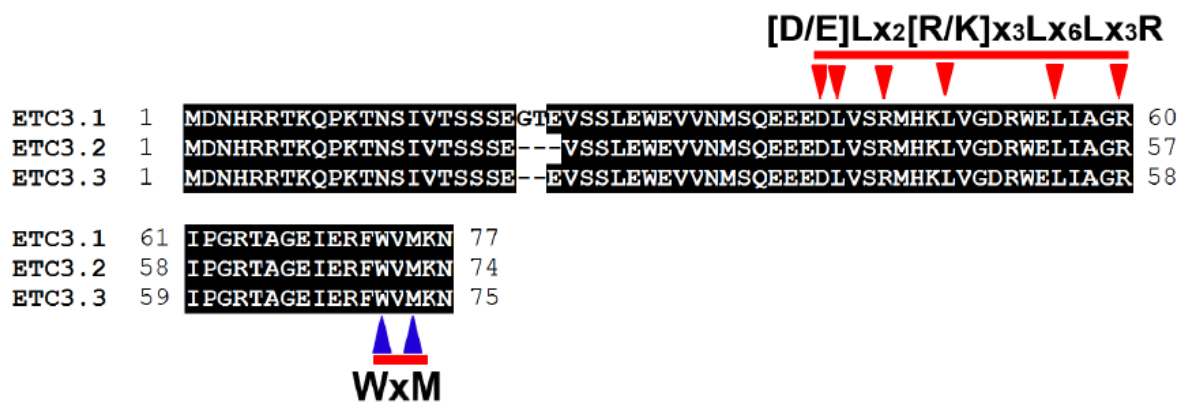
Supplemental Figure S1. Amino acid sequence alignment of R3 MYBs with other MYBs. Identical and similar amino acids are shaded in black and gray respectively. The amino acids of [D/E]Lx₂[R/K]x₃Lx₆Lx₃R signature that is required for interaction between MYBs and R/B-like bHLH transcription factors are indicated by red arrowheads on the top of amino acids. The amino acids of WxM motif that is crucial for cell-to-cell movement are indicated by blue arrowhead on the top of amino acids. The pattern of primary structure of MYB repeat, Mx₁₈Wx₁₈W, is indicated by arrows on the bottom of amino acids.



Supplemental Figure S2. Phylogenetic analysis of R3 MYBs with other MYBs. The entire amino acid sequences of single repeat R3 MYB transcription factors were used for phylogenetic analysis using tool on www.phylogeny.fr with default settings.

	TRY	CPC	ETC1	ETC2	ETC3	TCL1	TCL2	MYBL2	MYB4	MYB3	MYB5	GL1	TT2	MYB23	MYB82	WER1
TRY		48.6	45.0	60.2	40.7	57.4	60.6	21.9	14.9	15.6	17.3	19.3	15.9	19.1	23.3	18.7
CPC	67.0		54.3	46.1	52.5	46.3	42.2	16.0	15.9	15.1	17.6	17.8	15.1	17.7	20.9	18.1
ETC1	58.5	67.0		40.7	65.9	51.8	39.0	16.3	9.9	11.7	13.9	13.6	13.2	13.7	18.9	15.3
ETC2	74.1	62.5	57.1		36.6	59.8	62.5	23.4	14.2	14.8	17.7	18.8	16.7	17.8	20.9	18.1
ETC3	56.6	66.0	81.9	51.8		50.0	38.0	13.8	10.6	10.9	13.3	14.5	12.4	13.7	17.4	13.8
TCL1	65.1	66.0	69.0	66.1	71.4		68.0	15.7	11.7	11.7	14.5	14.2	12.8	14.5	14.9	15.8
TCL2	74.5	68.0	62.0	75.0	59.0	74.0		18.6	13.1	13.2	17.7	15.4	14.7	18.3	16.9	16.3
MYBL2	32.8	28.2	24.6	34.4	21.5	26.2	31.3		29.8	31.0	29.7	26.9	27.4	27.6	27.1	26.7
MYB4	22.0	22.7	18.1	24.8	17.4	18.1	19.9	44.7		52.1	39.7	31.4	34.6	34.4	31.0	33.2
MYB3	24.1	23.7	19.5	26.1	17.5	20.6	21.8	47.9	62.4		38.0	34.0	36.9	35.1	35.4	35.2
MYB5	26.5	25.3	20.1	28.5	19.7	21.3	27.3	46.2	56.7	58.8		34.8	37.5	38.2	38.6	40.2
GL1	27.2	25.9	20.6	29.4	21.1	21.9	25.0	42.5	50.7	50.2	50.2		33.6	63.8	40.3	55.6
TT2	27.5	26.0	19.0	25.6	19.4	22.1	26.7	42.6	54.6	58.5	54.7	49.6		35.5	36.3	35.5
MYB23	27.4	24.7	21.5	29.7	21.9	24.7	26.5	44.3	50.0	49.8	53.8	77.2	51.6		43.7	58.9
MYB82	31.3	29.9	27.4	34.3	25.9	27.4	30.8	48.8	42.9	49.8	52.6	55.3	48.1	59.4		43.8
WER1	31.0	29.1	23.6	30.0	23.6	28.6	24.6	49.8	47.5	50.6	56.2	68.4	50.0	73.1	63.1	

Supplemental Figure S3. Amino acid similarity and identity of R3 MYBs and other MYBs.



Supplemental Figure S4. Amino acid sequence alignment of ETC3 variants. Identical and similar amino acids are shaded in black and gray, respectively. The amino acids of [D/E]Lx₂[R/K]x₃Lx₆Lx₃R signature that is required for interaction between MYBs and R/B-like bHLH transcription factors are indicated by arrowheads on the top of amino acids. The amino acids of WxM motif that is crucial for cell-to-cell movement are indicated by arrowheads on the bottom of amino acids.