

Additional file 1

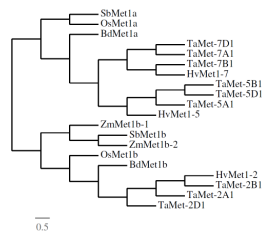
Additional file 1A: Likelihood ratio tests (LRT)

Hypothesis	<i>Lnl</i>	$2\Delta l$	<i>ddl</i>	LRT	ω_0	ω_1	ω_2	P<0.05	P<0.01
h0	-21434.8	-	-	-	0.23993	-	-	-	-
h1	-21330.6	104.1	1	0	0.17544	0.55407	-	***	***
h2	-21434.3	0.4768	1	0.0383	0.23822	0.30632	-	*	ns
h3	-21434.0	0.7571	1	0.0383	0.23567	0.26794	-	*	ns
h4	-21434.8	0.0009	1	1	0.23986	0.24225	-	ns	ns
h5	-21362.2	72.6	1	0	0.12974	0.32857	-	***	***
h6	-21434.8	-0.00004	1	1	0.23993	0.36697	-	ns	ns
h7	-21362.2	72.6	1	0	0.12974	0.32858	-	***	***
h8	-21434.6	0.2523	1	0.0617	0.21638	0.2417	-	ns	ns
h9	-21433.4	1.4	1	0.0235	0.22161	0.2512	-	*	ns
h10	-21330.6	104.1	1	0	0.17544	0.55407	-	***	***
h11	-21326.0	108.8	2	0	0.12193	0.21988	0.48706	***	***

Additional file 1B: Details of the 11 hypotheses tested in the branch model described in Fig 3B

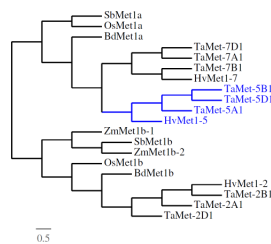
h0: all the branches evolve at the same evolution rate

(((((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1)),(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1))),((HvMet1-7,TaMet-7B1),(TaMet-7A1,TaMet-7D1))),BdMet1a),(OsMet1a,SbMet1a)));



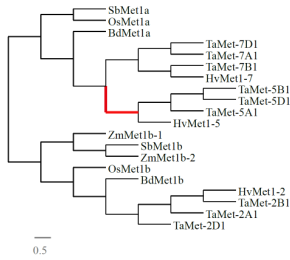
h1: the branches including group 5 homoeologs and HvMet1-5 evolve at the same rate which is significantly different from the rest of the tree

(((((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1)),(((HvMet1-5 #1,(TaMet-5A1 #1,(TaMet-5D1 #1,TaMet-5B1 #1) #1) #1),((HvMet1-7,TaMet-7B1),(TaMet-7A1,TaMet-7D1))),BdMet1a),(OsMet1a,SbMet1a)));



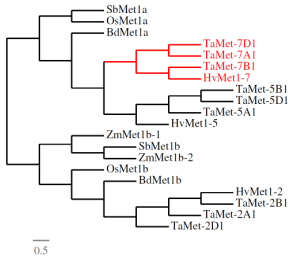
h2: evolution rate increases soon after the second duplication and return to its initial rate

(((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1)),(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1)))#1, ((HvMet1-7,TaMet-7B1),(TaMet-7A1,TaMet-7D1))),BdMet1a),(OsMet1a,SbMet1a));



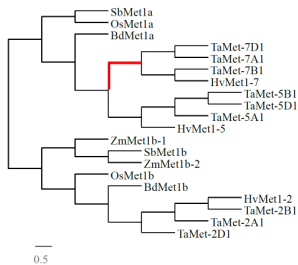
h3: the branches including group 7 homoeologs and HvMet1-7 evolve at the same rate which is significantly different from the rest of the tree

(((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1)),(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1 #1))),((HvMet1-7 #1,TaMet-7B1 #1) #1,(TaMet-7A1 #1,TaMet-7D1 #1) #1) #1),BdMet1a),(OsMet1a,SbMet1a));



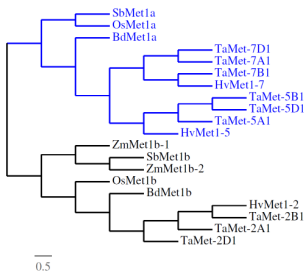
h4: evolution rate increases soon after the second duplication and return to its initial rate

(((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1)),(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1 #1))),((HvMet1-7,TaMet-7B1),(TaMet-7A1,TaMet-7D1) #1),BdMet1a),(OsMet1a,SbMet1a));

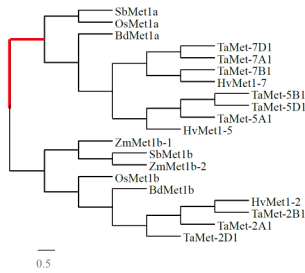


h5: the branches including MET1a lineage evolve at the same rate which is significantly different from the rest of the tree (i.e from MET1b lineage)

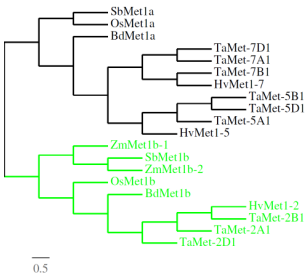
(((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1)),(((HvMet1-5 #1,(TaMet-5A1 #1,(TaMet-5D1 #1,TaMet-5B1 #1) #1) #1,((HvMet1-7 #1,TaMet-7B1 #1) #1,(TaMet-7A1 #1,TaMet-7D1 #1) #1) #1),BdMet1a #1),(OsMet1a #1,SbMet1a #1) #1) #1);



h6: evolution rate increases soon after the first duplication and return to its initial rate
 (((((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1)),(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1))),((HvMet1-7,TaMet-7B1),(TaMet-7A1,TaMet-7D1))),BdMet1a),(OsMet1a,SbMet1a)) #1);

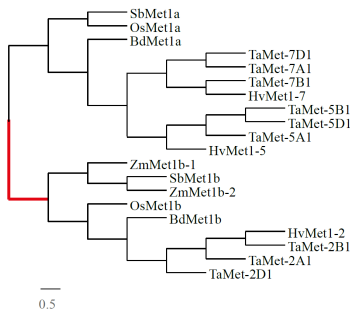


h7: the branches including MET1b lineage evolve at the same rate which is significantly different from the rest of the tree (i.e from MET1a lineage)
 (((((TaMet-2D1 #1,(TaMet-2A1 #1,(TaMet-2B1 #1,HvMet1-2 #1) #1) #1),BdMet1b #1),OsMet1b#1) #1,((ZmMet1b-2 #1,SbMet1b #1) #1,ZmMet1b-1 #1) #1),(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1))),((HvMet1-7,TaMet-7B1),(TaMet-7A1,TaMet-7D1))),BdMet1a),(OsMet1a,SbMet1a));



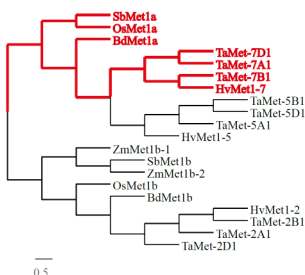
h8: evolution rate increases soon after the first duplication and return to its initial rate

(((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1) #1,(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1))),((HvMet1-7,TaMet-7B1),(TaMet-7A1,TaMet-7D1))),BdMet1a),(OsMet1a,SbMet1a));



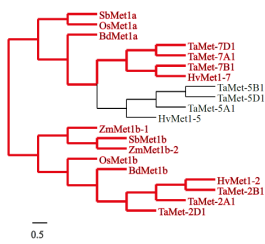
h9: the branches including MET1a lineage except group 5 homoeologs and HvMet1-5 evolve at the same rate which is significantly different from the rest of the tree

(((TaMet-2D1,(TaMet-2A1,(TaMet-2B1,HvMet1-2))),BdMet1b),OsMet1b),((ZmMet1b-2,SbMet1b),ZmMet1b-1),(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1))),((HvMet1-7 #1,TaMet-7B1 #1) #1,(TaMet-7A1 #1,TaMet-7D1 #1) #1) #1),BdMet1a #1),(OsMet1a #1,SbMet1a #1) #1);



h10: all branches except group 5 homoeologs and HvMet1-5 evolve at a different rate which is significantly different from group 5 homoeologs and HvMet1-5 (reciprocal to h1)

(((TaMet-2D1 #1,(TaMet-2A1 #1,(TaMet-2B1 #1,HvMet1-2 #1) #1) #1,BdMet1b #1) #1,OsMet1b#1) #1,((ZmMet1b-2 #1,SbMet1b #1) #1,ZmMet1b-1 #1) #1,(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1))) ,((HvMet1-7 #1,TaMet-7B1 #1) #1,(TaMet-7A1 #1,TaMet-7D1 #1) #1) #1) #1,BdMet1a #1) #1,(OsMet1a #1,SbMet1a #1) #1) #1);



h11: 3 evolution rates are observed, one for branches including group 5 homoeologs and HvMet1-5, one for group 7 homoeologs and HvMet1-7 and one for the MET1b lineage

(((TaMet-2D1 #2,(TaMet-2A1 #2,(TaMet-2B1 #2,HvMet1-2 #2) #2) #2,BdMet1b #2),OsMet1b #2) #2,((ZmMet1b-2 #2,SbMet1b #2) #2,ZmMet1b-1 #2) #2,(((HvMet1-5,(TaMet-5A1,(TaMet-5D1,TaMet-5B1))) ,((HvMet1-7 #1,TaMet-7B1 #1) #1,(TaMet-7A1 #1,TaMet-7D1 #1) #1) #1) #1,BdMet1a #1) #1,(OsMet1a #1,SbMet1a #1) #1) #1);

