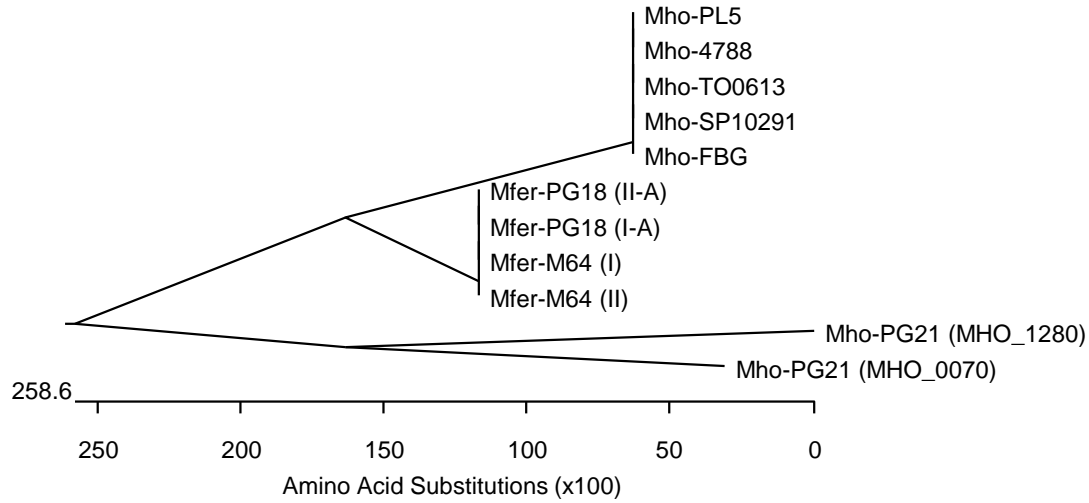


# CDS6-Homologues

## A. Phylogenetic Tree



## B. Sequence Distances

		Percent Identity												
		1	2	3	4	5	6	7	8	9	10	11		
Divergence	1	█	100.0	100.0	100.0	32.3	32.3	32.3	32.3	32.3	11.3	14.5	1	Mfer-PG18 (II-A)
	2	0.0	█	100.0	100.0	32.3	32.3	32.3	32.3	32.3	11.3	14.5	2	Mfer-PG18 (I-A)
	3	0.0	0.0	█	100.0	32.3	32.3	32.3	32.3	32.3	11.3	14.5	3	Mfer-M64 (I)
	4	0.0	0.0	0.0	█	32.3	32.3	32.3	32.3	32.3	11.3	14.5	4	Mfer-M64 (II)
	5	146.6	146.6	146.6	146.6	█	100.0	100.0	100.0	100.0	11.1	11.1	5	Mho-FBG
	6	146.6	146.6	146.6	146.6	0.0	█	100.0	100.0	100.0	11.1	11.1	6	Mho-SP10291
	7	146.6	146.6	146.6	146.6	0.0	0.0	█	100.0	100.0	11.1	11.1	7	Mho-TO0613
	8	146.6	146.6	146.6	146.6	0.0	0.0	0.0	█	100.0	11.1	11.1	8	Mho-PL5
	9	146.6	146.6	146.6	146.6	0.0	0.0	0.0	0.0	█	11.1	11.1	9	Mho-4788 (MhoE)
	10	430.0	430.0	430.0	430.0	430.0	430.0	430.0	430.0	430.0	█	16.7	10	Mho-PG21 (MHO_1280)
	11	339.0	339.0	339.0	339.0	447.0	447.0	447.0	447.0	447.0	296.0	█	11	Mho-PG21 (MHO_0070)
		1	2	3	4	5	6	7	8	9	10	11		

## C. Multiple Sequence Alignment

	10										20										30										40										50										60																
1	M	K	R	Y	F	Y	R	I	R	-	V	K	K	N	L	E	S	K	K	T	K	S	Y	A	V	C	S	-	N	F	N	E	A	D	K	I	A	N	E	I	I	E	K	G	D	Y	G	-	-	W	V	Q	V	E	R	V	E	K	I	K	H	Y	F	K	E	V	Mfer-PG18 (II-A)
1	M	K	R	Y	F	Y	R	I	R	-	V	K	K	N	L	E	S	K	K	T	K	S	Y	A	V	C	S	-	N	F	N	E	A	D	K	I	A	N	E	I	I	E	K	G	D	Y	G	-	-	W	V	Q	V	E	R	V	E	K	I	K	H	Y	F	K	E	V	Mfer-PG18 (I-A)
1	M	K	R	Y	F	Y	R	I	R	-	V	K	K	N	L	E	S	K	K	T	K	S	Y	A	V	C	S	-	N	F	N	E	A	D	K	I	A	N	E	I	I	E	K	G	D	Y	G	-	-	W	V	Q	V	E	R	V	E	K	I	K	H	Y	F	K	E	V	Mfer-M64 (I)
1	M	K	R	Y	F	Y	R	I	R	-	V	K	K	N	L	E	S	K	K	T	K	S	Y	A	V	C	S	-	N	F	N	E	A	D	K	I	A	N	E	I	I	E	K	G	D	Y	G	-	-	W	V	Q	V	E	R	V	E	K	I	K	H	Y	F	K	E	V	Mfer-M64 (II)
1	M	S	K	Y	F	Y	R	L	R	G	S	Q	S	T	G	K	N	A	K	T	Y	S	F	G	S	A	Q	-	Q	Y	N	K	A	L	I	M	A	Q	D	A	I	S	K	N	Q	F	K	-	-	E	V	Q	I	E	R	I	Q	V	I	K	I	I	K	Q	N	S	Mho-FBG
1	M	S	K	Y	F	Y	R	L	R	G	S	Q	S	T	G	K	N	A	K	T	Y	S	F	G	S	A	Q	-	Q	Y	N	K	A	L	I	M	A	Q	D	A	I	S	K	N	Q	F	K	-	-	E	V	Q	I	E	R	I	Q	V	I	K	I	I	K	Q	N	S	Mho-SP10291
1	M	S	K	Y	F	Y	R	L	R	G	S	Q	S	T	G	K	N	A	K	T	Y	S	F	G	S	A	Q	-	Q	Y	N	K	A	L	I	M	A	Q	D	A	I	S	K	N	Q	F	K	-	-	E	V	Q	I	E	R	I	Q	V	I	K	I	I	K	Q	N	S	Mho-TO0613
1	M	S	K	Y	F	Y	R	L	R	G	S	Q	S	T	G	K	N	A	K	T	Y	S	F	G	S	A	Q	-	Q	Y	N	K	A	L	I	M	A	Q	D	A	I	S	K	N	Q	F	K	-	-	E	V	Q	I	E	R	I	Q	V	I	K	I	I	K	Q	N	S	Mho-PL5
1	M	S	K	Y	F	Y	R	L	R	G	S	Q	S	T	G	K	N	A	K	T	Y	S	F	G	S	A	Q	-	Q	Y	N	K	A	L	I	M	A	Q	D	A	I	S	K	N	Q	F	K	-	-	E	V	Q	I	E	R	I	Q	V	I	K	I	I	K	Q	N	S	Mho-4788 (MhoE)
1	M	P	K	M	K	T	K	S	G	-	L	K	K	R	I	S	I	T	E	S	G	K	V	K	R	G	Q	-	A	F	R	S	H	L	A	Q	N	K	T	T	K	Q	K	R	H	A	R	-	-	K	A	T	T	L	S	S	S	D	F	K	R	Y	K	E	Mho-PG21 (MHO_1280)		
1	M	P	G	R	D	Q	L	T	G	-	Q	K	A	L	S	G	N	K	R	S	H	A	L	N	T	A	K	R	T	F	D	L	N	L	Q	K	V	T	V	L	T	E	T	G	S	K	K	T	V	R	V	T	A	K	N	A	R	T	L	K	K	Y	G	L	V	A	Mho-PG21 (MHO_0070)