

Table S1. Details regarding the primers used in this study

Gene	GenBank accession number	Primer Name	Primer sequence (5'-3')	Tm (° C)	Amplicon size (bp)	Usage
<i>Trehalase1</i> (<i>MsTre1</i>)	MN894706	<i>MsTre1</i> -F	CTCCGACGAAATGACAAA	56.8	2303	cDNA cloning
		<i>MsTre1</i> -R	CCCTCAAAAGCGTAGAAA	57.3		
<i>Trehalase2</i> (<i>MsTre2</i>)	MN894707	<i>MsTre2</i> -F	TAGTGTAGTGTTGTGCCATTG	56.8	1987	
		<i>MsTre2</i> -R	GTCGGATAACTATTTCCTCAC	56.6		
<i>Trehalase1</i> (<i>MsTre1</i>)	MN894706	<i>MsTre1</i> -q-F	TCTACTACTGGGACTCTTTCTG	55.9	127	RT-qPCR
		<i>MsTre1</i> -q-R	CTTCCGTTAGGGATGTGA	55.6		
<i>Trehalase2</i> (<i>MsTre2</i>)	MN894707	<i>MsTre2</i> -q-F	ATGTTGCCAGACACTTTGA	56.1	111	
		<i>MsTre2</i> -q-R	CGTTGAGAATGAACCACC	55.6		
<i>Trehalose-6-phosphate Synthase</i> (<i>MsTPS</i>)	MN832898	<i>MsTPS</i> -q-F	GAACAGGCGAGGAAGCT	55.0	144	
		<i>MsTPS</i> -q-R	ACTCCAGTCCAATCCGAACG	56.2		
<i>Beta-actin</i> (<i>Msβ-actin</i>)	GQ856238	<i>Msβ-actin</i> -q-F	CGTCCCAAACCAAACAC	56.2	178	
		<i>Msβ-actin</i> -q-R	TCTGACCCATACCAACCA	56.3		
<i>Glyceraldehyde-3-phosphate dehydrogenase</i> (<i>MsGAPDH</i>)	HM055756	<i>MsGAPDH</i> -q-F	GCTACAGTCGTTGCCATCAA	56.0	150	
		<i>MsGAPDH</i> -q-R	GAGGACGGAGATTTTGTTC	55.0		
<i>Chitin synthase A</i> (<i>MsCHSA</i>)	KT948989	<i>MsCHSA</i> -q-F	GGTGATACAGTTCTCCGCTATG	56.1	121	
		<i>MsCHSA</i> -q-R	CTAGCAGAGCGTCTTGAGATAAG	55.8		
<i>Chitin synthase B</i> (<i>MsCHSB</i>)	KY348776	<i>MsCHSB</i> -q-F	TCCAGGAGGAAGACCATACA	55.0	92	
		<i>MsCHSB</i> -q-R	GTCAGCCTCCTCTTGAAGTTAG	55.0		
<i>Hexokinase</i> (<i>MsHK</i>)	MT995930	<i>MsHK</i> -q-F	TCCTTGCGTTGGATTTAG	56.5	123	
		<i>MsHK</i> -q-R	CCCCTGTGCCAGTCATT	55.4		
<i>Glucose-6-phosphate isomerase</i> (<i>MsG6PI</i>)	OR933577	<i>MsG6PI</i> -q-F	CGGACAGTGGAAGGGAT	56.5	120	
		<i>MsG6PI</i> -q-R	AGCTGGTTGGCATAAAGG	55.7		
<i>Glutamine-fructose-6-phosphate aminotransferase</i> (<i>MsGFAT</i>)	OR933576	<i>MsGFAT</i> -q-F	TTGTTCCGTCTGTCCCA	56.9	186	
		<i>MsGFAT</i> -q-R	CAGACAAACGATGAATGCTA	56.8		
<i>Glucosamine-6-phosphate N-acetyltransferase</i> (<i>MsGNAT</i>)	OR933578	<i>MsGNAT</i> -q-F	TGTCGGCAATGTTACGC	56.4	165	
		<i>MsGNAT</i> -q-R	CCACGCACAGAGCAGTTAT	57.0		
<i>Phosphoacetylglucosamine</i>	OR933574	<i>MsPGM</i> -q-F	ACTCAAGGTCACGGTCAA	55.3	182	
		<i>MsPGM</i> -q-R	TCTCAGCCTCAGCATAACAC	55.8		

<i>mutase</i> (MsPGM)						
UDP-N-acetylglucosamine pyrophosphorylase (MsUAP)	OR933575	MsUAP-q-F	AAGCGTGGCGTAGAACA	55.2	148	RNA interference
		MsUAP-q-R	CGACTGCTTCACTTGGGTA	56.0		
<i>Chitinase</i> (MsCht)	MG551526	MsCht-q-F	GTATTGTGATTTTCGTGGGA	55.2	171	
		MsCht-q-R	GGATGTGACTGAGGTGGAAC	56.2		
<i>Trehalase1</i> (MsTre1)	MN894706	dsMsTre1-F	TAATACGACTCACTATAGGGGT GTCCTTTTGTAAGATGCG	57.3	244	
		dsMsTre1-R	TAATACGACTCACTATAGGGAC GGGTTTTGATTGGTG	56.2		
		dsMsTre2-F	TAATACGACTCACTATAGGGTCC GACCAAGGCTGACA	57.2		
<i>Trehalase2</i> (MsTre2)	MN894707	dsMsTre2-R	TAATACGACTCACTATAGGGCG ACCACCAGGCACAAT	56.8	264	
		dsGFP-F	TAATACGACTCACTATAGGGAG TGCTTCAGCCGCTAC	57.0		
<i>Green fluorescent protein (GFP)</i>	MK558050	dsGFP-R	TAATACGACTCACTATAGGGCA CCTTGATGCCGTTCT	57.8	284	