

Supplementary Materials

Table S1. GLMM null and full model for positive controls. Response variables (var) are glucose titer (glu), trehalose titer (tre) and hsp70AB gene expression (hsp). n/f – null or full model, AIC – Akaike Information Criterion, df_R – degrees of freedom for Residuals, var. – variance, s.d. – standard deviation, est. - estimate, s.e. – standard error, t – t-value, p – p-value for fixed effect, ANOVA – for comparison of models, df – degrees of freedom for the model, p – p-value for model comparison.

ANOVA															
Random effects					Fixed effects										
var	n/f	model	AIC	df _R	name	var.	s.d.	name	est.	s.e.	t	p	df	Chi²	p
glu	null	1+ (1 cage)	0.2	35	cage	1.83	1.35	(intercept)	0.364	0.004	93.73	<2E-16	3		
					resid	0.05	0.22								
	full	treatment + (1 cage)	-3.5	34	cage	0.25	0.50	(intercept)	0.366	0.048	7.64	2.1E-14	4	5.71	0.017
					resid	0.04	0.20	group	-2.585	0.742	-3.48	4.9E-4			
tre	null	1+ (1 cage)	-42.3	35	cage	0.51	0.71	(intercept)	-0.045	0.041	-1.10	0.27	3		
					resid	0.02	0.13								
	full	treatment + (1 cage)	-46.1	34	cage	0.05	0.21	(intercept)	-0.043	0.041	-1.06	0.29	4	5.83	0.016
					resid	0.01	0.12	group	-1.552	0.268	-5.80	6.7E-9			
hsp	null	1+ (1 cage)	345.2	37	cage	735.4	27.1	(intercept)	3.547	0.114	31.17	2.0E-16	3		
					resid	152.0	12.3								
	full	treatment + (1 cage)	324.5	36	cage	0.0	0.0	(intercept)	3.564	0.110	32.27	2.0E-16	4	22.7	1.8E-6
					resid	152.0	12.3	group	-2.205	0.589	-3.75	1.8E-4			

Table S2. GLMM null and full model for cages with varying group size. Response variables (var) are glucose titer (glu), trehalose titer (tre) and hsp70AB gene expression (hsp). n/f – null or full model, AIC – Akaike Information Criterion, df_R – degrees of freedom for Residuals, var. – variance, s.d. – standard deviation, est. - estimate, s.e. – standard error, t – t-value, p – p-value for fixed effect, ANOVA – for comparison of models, df – degrees of freedom for the model, p – p-value for model comparison. Table is continued on next page.

					Random effects			Fixed effects				ANOVA				
var	n/f	model	AIC	df _R	name	var.	s.d.	name	est.	s.e.	t	p	df	Chi²	p	
glu	null	1+ (1 cage) + (1 trial)	65.3	124	cage	0.06	0.26	(intercept)	-0.875	0.120	-7.3	2.9E-13	4			
					trial	0.00	0.00									
					resid	0.09	0.30									
	full	group + (1 cage) + (1 trial)	67.2	123	cage	0.07	0.26	(intercept)	-0.833	0.170	-4.9	9.6E-7	5	0.11	0.74	
					trial	0.00	0.00	group	-0.003	0.010	-0.3	0.742				
					resid	0.09	0.30									
tre	null	1+ (1 cage) + (1 trial)	-82.3	124	cage	0.05	0.24	(intercept)	-1.200	0.135	-8.9	2.0E-16	4			
					trial	0.003	0.05									
					resid	0.028	0.17									

	full	group + (1 cage) + (1 trial)	-80.4	123	cage	0.059	0.24	(intercept)	-1.180	0.167	-7.1	1.6E-12	5	0.04	0.85
					trial	0.002	0.05	group	-0.002	0.010	-0.2	0.856			
					resid	0.028	0.17								
	hsp	1 + (1 cage) + (1 trial)	-128.7	32	cage	0.104	0.32	(intercept)	-3.863	0.834	-4.6	3.6E-6	4		
					trial	0.139	0.37								
					resid	0.001	0.04								
	full	group + (1 cage) + (1 trial)	-126.9	31	cage	0.092	0.30	(intercept)	-3.667	0.943	-3.9	1.0E-4	5	0.15	0.70
					trial	0.136	0.37	group	-0.008	0.021	-0.4	0.691			
					resid	0.001	0.04								

Table S3. GLMM null and full model for cage vs colony. Response variables (var) are glucose titer (glu), trehalose titer (tre) and hsp70AB gene expression (hsp). n/f – null or full model, AIC – Akaike Information Criterion, dfr – degrees of freedom for Residuals, var. – variance, s.d. – standard deviation, est. - estimate, s.e. – standard error, t – t-value, p – p-value for fixed effect, ANOVA – for comparison of models, df – degrees of freedom for the model, p – p-value for model comparison. Table is continued on next page.

var	n/f	model	AIC	dfr	Random effects			Fixed effects				ANOVA			
					name	var.	s.d.	name	est.	s.e.	t	p	df	Chi ²	p
glu	null	1 + (1 cage) + (1 trial)	80.5	144	cage	0.063	0.25	(intercept)	-0.812	0.005	-165.5	2E-16	4		
					trial	0.002	0.04								
					resid	0.092	0.30								
	full	source + (1 cage) + (1 trial)	81.6	143	cage	0.067	0.26	(intercept)	-0.890	0.155	-5.7	8.8E-9	5	0.88	0.35
					trial	0.003	0.06	group	0.174	0.182	0.9	0.339			
					resid	0.092	0.30								
tre	null	1 + (1 cage) + (1 trial)	-72.9	144	cage	0.075	0.27	(intercept)	-0.865	0.243	-3.5	3.8E-4	4		
					trial	0.018	0.13								
					resid	0.032	0.18								
	full	source + (1 cage) + (1 trial)	-79.6	143	cage	0.050	0.22	(intercept)	-1.246	0.237	-5.3	1.4E-7	5	8.71	0.003
					trial	0.013	0.12	group	0.405	0.131	3.1	0.002			
					resid	0.031	0.18								
hsp	null	1 + (1 cage) + (1 trial)	-212.1	58	cage	0.164	0.40	(intercept)	-3.836	0.592	-6.5	9.4E-11	4		
					trial	0.087	0.29								
					resid	0.002	0.04								

full	source + (1 cage) + (1 trial)	-218.1	57	cage	0.061	0.25	(intercept)	-3.559	0.719	-4.9	7.5E-7	5	8.01	0.005
				trial	0.132	0.36	group	-1.167	0.571	-2.0	0.041			
				resid	0.001	0.04								

Table S4. Welch t-test for positive controls and cage vs colony. Response variables (var) are glucose titer (glu), trehalose titer (tre) and hsp70AB gene expression (hsp). Means are derived from log-transformed data. T – t-value, df – degrees of freedom, P - p-value. Significant values indicated by bold letters.

positive control	var	mean_{control}	mean_{stressor}	t	df	P
	glu	0.34	-2.08	15.04	34.0	2.2E-16
	tre	-0.06	-1.63	11.72	29.4	1.3E-12
	hsp	-3.33	-1.32	-8.37	9.8	8.8E-6
cage vs colony	var	mean_{cage}	mean_{colony}	t	df	P
	glu	-1.06	-0.95	-0.61	25.4	0.55
	tre	-1.36	-0.90	-3.33	33.0	0.002
	hsp	-3.67	-4.23	2.69	59.2	0.009

Table S5. Samples and sample size for different experiments. N – total sample size setup for experimental period of 7 days. N_{experiments} – available number of individuals for subsequent physiological marker analysis.

	Replicate 1		Replicate 2		Total	
Group size	N	N_{experiments}	N	N_{experiments}	N glucose/trehalose experiment	N hsp70 gene expression
1	10	8	10	4	12	6
10	10	9	10	9	18	6
10	10	8	10	10	18	6
10	10	10	10	10	20	6
30	30	10	30	10	20	6
30	30	10	30	10	20	6
30	30	10	30	10	20	6
colony	10	10	10	10	20	20
total	140	75	140	73	148	62