Relationships between RNA content and egg production rate in *Acartia bifilosa* (Copepoda, Calanoida) of different spatial and temporal origin

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Unfortunately, the presentation of Table 1, with caption, and the figure caption of Fig. 2 are incorrect. The correct Table 1 and Fig. 2 are given below.

Fig. 2 *A. bifilosa*. Observed vs. predicted egg production rate (EPR, eggs female⁻¹ day⁻¹). The overall correlation is statistically significant (Spearman rank correlation test, $r = 0.67$, $P < 0.0001$, $N = 89$). Study periods: A1 (filled square)—Askö, spring ($N = 19$); A2 (plus sign)—Askö, summer ($N = 20$); T1 (open circle)—Tvärminne, spring ($N = 19$); T2 (filled circle)—Tvärminne, summer ($N = 18$); G2003 (open triangle)—data from Gorokhova 2003 ($N = 13$) collected in August 1998 east of Gotland (57°36'N, 19°21'E and 57°16'N, 20°05'E). The predicted values of EPR were calculated using formula: $EPR = 14.74 + 106.17 \times RNA - 43.79 \times PL + 0.24 \times T$ (Table 1d). The line represents observed $EPR =$ predicted EPR

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Table 1 *A. bifilosa*: results of multiple linear regression analysis

Variable	Beta $\pm$ SE	Partial corr.	<i>P</i> level	R^2	Adjust R^2	SE estimate
(a) $\text{RNA} = -0.321 + 0.721 \times \text{PL} + 0.003 \times \text{EPR} - 0.026 \times \text{season}$				0.88	0.88	0.02
Intercept			0.0000			
PL	0.85 ± 0.06	0.87	0.0000			
EPR	0.31 ± 0.05	0.61	0.0000			
Season	-0.20 ± 0.05	-0.42	0.0002			
(b) $\text{RNA} = -0.254 + 0.655 \times \text{PL} + 0.003 \times \text{EPR} - 0.002 \times T$				0.87	0.86	0.02
Intercept			0.0000			
PL	0.78 ± 0.05	0.87	0.0000			
EPR	0.31 ± 0.05	0.59	0.0000			
<i>T</i>	-0.12 ± 0.05	-0.30	0.0087			
(c) $\text{EPR} = 24.57 + 113.05 \times \text{RNA} - 56.81 \times \text{PL} + 2.98 \times \text{season}$				0.53	0.51	4.22
Intercept			0.0052			
RNA	1.21 ± 0.18	0.61	0.0000			
PL	-0.72 ± 0.21	-0.37	0.0011			
Season	0.25 ± 0.11	0.26	0.0256			
(d) $\text{EPR} = 14.74 + 106.17 \times \text{RNA} - 43.79 \times \text{PL} + 0.24 \times T$				0.51	0.49	4.30
Intercept			0.0418			
RNA	1.14 ± 0.18	0.59	0.0000			
PL	-0.56 ± 0.19	-0.32	0.0049			
<i>T</i>	0.14 ± 0.09	0.18	0.1235			

All regressions are significant ($P < 0.0001$, $n = 76$)

Four models were tested: (a) $\text{RNA} = b_0 + b_1 \text{PL} + b_2 \text{EPR} + b_3 \text{station} + b_4 \text{season}$, (b) $\text{RNA} = b_0 + b_1 \text{PL} + b_2 \text{EPR} + b_3 T$, (c) $\text{EPR} = b_0 + b_1 \text{RNA} + b_2 \text{PL} + b_3 \text{station} + b_4 \text{season}$, and (d) $\text{EPR} = b_0 + b_1 \text{RNA} + b_2 \text{PL} + b_3 T$. The factors, for which data are presented above, contributed significantly with explanatory values and were selected by forward stepwise selection procedure

PL is prosome length (mm), *RNA* – RNA content in female ($\mu\text{g RNA female}^{-1}$), *EPR* – egg production rate ($\text{eggs female}^{-1} \text{day}^{-1}$), and *T* – ambient surface temperature during sampling ($^{\circ}\text{C}$). *Beta* $\pm$ *SE* is beta weights with standard errors, *partial corr* – partial correlations, and SE estimate – standard error of value estimated from the regression equation