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Heritability Estimates of Naupliar Length in *Artemia franciscana* Using Different Methods

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Abstract

Parent offspring regression and analysis of variance of full-sib data was used to estimate heritability (h^2) of naupliar length from two sub lines (SNS and BNS) of *Artemia franciscana* evolved from same base population. Heritabilities were estimated from each of six generations of SNS and five generations of BNS. Heritabilities pooled over generations were also estimated. The pooled estimates of h^2 from parent offspring regression in males and females were 0.2123 ± 0.0766 and 0.3885 ± 0.1108 in SNS and 0.5777 ± 0.1154 and 0.3364 ± 0.1176 in BNS. The corresponding values from full-sib data were 1.3256 ± 0.0474 and 1.1004 ± 0.0522 in SNS and 1.2580 ± 0.0583 and 1.4221 ± 0.0479 in BNS.

Introduction

Heritability is one of the most important properties of the metric characters. The concept of heritability is associated with the relative importance of heredity and environment as they influence variations in character. Although *Artemia* has already been described in the 18th century and extensively studied in the most diverse fundamental disciplines of biological sciences, there is still an apparent lack of information on its quantitative genetic aspects. Tobias et al. (1980), Wear et al. (1986) and Wanigasekera and Browne (2000) have studied the influence of salinity and temperature on the life processes of A*rtemia*. Many other works are reported on *Artemia* in the different branches of genetics such as biochemical and population genetics. Gajardo et al. (1995) have studied the genetic variability and interpopulational differentiation of seven *Artemia* samples from three South American countries (Chile, Brazil and Peru) using starch electrophoresis. Similarly Triantaphyllidis et al. (1997) have performed morphological and allometric studies with adult males and females of eleven bisexual populations of brine shrimp *Artemia* using discriminant and cluster analysis techniques, which has allowed to separate and group together the populations of great genetic similarities. Although there is an abundance of heritability estimates reported for various traits of livestocks, and to a lesser extent of fishes, there are no reports on heritability estimates for *Artemia*. Browne et al. (1984) have estimated the genetic components of a number of traits in *Artemia*, but no attempt has been made to estimate the heritability of any of the quantitative traits using the standard procedures. Hence, an attempt is made in the present work to estimate the heritability of naupliar length of *Artemia franciscana* using different methods of estimation.

Materials and Methods

Artemia franciscana, Kellogg (1906) from Great Salt Lake, Utah was used in the present investigation because of its sexual breeding behaviour and its major share in commercial use. The nauplii obtained from foundation stock cyst belonging to batch no. 425 G, 06345 of Supreme, San Francisco Bay Brand of Inve Aquaculture, Inc. were used to generate base generation. The subpopulation derived from the same base population *viz*. SNS line and BNS line under mass selection for smaller and bigger naupliar length, respectively were used for the study. Generations were raised through pair mating. The number of pairs mated and individuals measured according to sex, line and generation are given in table 1.

The heritability of the naupliar length was estimated using two standard methods *viz*. regression of offspring on parent and analysis of variance full-sib data. Heritability for each line was initially estimated within sex and within generation. These estimates were then pooled over generations, within sex and line, to provide mean estimates.

Heritability estimate from full-sib data

The variance component analysis was used to estimate sire component of variance and heritability from full-sib correlation. The linear statistical model used was:

$$Y_{ik} = \mu + S_i + e_{ik}$$

where

Y_{ik} = Observation of the kth progeny of the ith sire
μ = Overall mean
S_i = Effect of ith sire
e_{ik} = Random error attributed to individuals, assumed to be normally and independently distributed with mean zero and variance σ^2_e.

The standard error of heritability was calculated as per Swinger et al. (1964). The heritability estimates were pooled over generations, within line and sex following the procedure of Enfield et al. (1966).

Heritability by regression of offspring on parent

Heritability was also estimated from the regression of offspring on parent. Sire-Son and Dam-Daughter data were used for this purpose. The statistical model and computational formulae used in the present study are as follows:

$$Z_i = \beta X_i + e_i$$

where,

Z_i = Value of offspring of the i^{th} sire
Xi = Observation of the i^{th} sire
β = Regression coefficient of Z on X
e_i = Error associated with Zi
h^2 = $2\ b_{op}$

$$h^2 = 2\ \widehat{\text{Cov}}_{XY} / \sigma_X^2 = 2b$$

The standard error of heritability was calculated as per Klein et al. 1973.

Results

The heritability of naupliar length was estimated, sex wise from the regression of progeny values on parent (b_{op}) and also from the analysis of variance of full-sib data, for each generation (Tables 2 and 3). Though the heritability estimate showed variation from generation to generation, the estimates from b_{op} were of medium magnitude as compared to the estimates from full-sib data, which were very high in magnitude. The pooled estimates of heritability,

Table 1. Number of pairs mated and individuals measured according to sex, line and generation.

Line	Sex	Generations						
		S0	S1	S2	S3	S4	S5	S6
Lower	Pairs	61	55	63	50	39	39	30
	Male	239	223	246	226	102	95	116
	Female	255	195	275	202	154	190	118
	Total	494	418	521	428	256	285	234
Higher	Pairs	61	43	48	37	26	33	-
	Male	239	187	215	162	65	78	-
	Female	255	171	186	153	91	168	-
	Total	494	358	401	315	156	246	-

-No pair was mated in higher line of S6 generation which are considered to be more reliable than individual estimates, also exhibited a similar trend. The heritability of pooled estimates from regression of progeny on parent when pooled over the generations was 0.2123 ± 0.0766 and 0.3885 ± 0.1108 for males and females of SNS line. The corresponding figures in BNS line were 0.5777 ± 0.1154 and 0.3364 ± 0.1176 respectively.

While the heritability estimates from analysis of variance of full-sib data, when pooled over generations, were 1.3256 ± 0.0474 and 1.1004 ± 0.0522 for males and females respectively in SNS line, the corresponding estimates in BNS line were 1.2580 ± 0.0583 and 1.4221 ± 0.0479 respectively. Though the standard errors associated with individual estimates were generally high, pooled estimates were of lower magnitude.

Table 2. Heritability estimates for naupliar length in SNS and BNS lines by parent-offspring regression.

Generation	Heritability ± S.E.			
	SNS		BNS	
	Male offspring on male parent	Female offspring on female parent	Male offspring on male parent	Female offspring on female parent
0	0.5851 ± 0.2153	0.3766 ± 0.1899	0.5851 ± 0.2153	0.3766 ± 0.1899
1	0.3770 ± 0.2305	0.3249 ± 0.2337	0.2558 ± 0.2097	0.0210 ± 0.2238
2	0.1836 ± 0.2460	0.6866 ± 0.2955	0.0760 ± 0.3120	0.3120 ± 0.3153
3	-0.1262 ± 0.3470	0.2989 ± 0.4299	0.6902 ± 0.4717	0.2186 ± 0.4781
4	0.4601 ± 0.4320	0.1162 ± 0.3817	1.1806 ± 0.5280	1.0798 ± 0.4993
5	0.1034 ± 0.6839	0.3857 ± 0.4384	1.3522 ± 0.2834	0.9488 ± 0.4454
6	0.3791 ± 0.3393	0.4577 ± 0.4577	-	-
Pooled heritability	0.2123 ± 0.0766	0.3885 ± 0.1108	0.5777 ± 0.1154	0.3364 ± 0.1176
b ± S.E.	-0.0317 ± 0.0480	-0.0073 ± 0.01083	0.2064 ± 0.0854	0.1698 ± 0.0748

Table 3. Heritability estimates for naupliar length in SNS and BNS lines from full-sib analysis.

Generation	Heritability ± S.E.			
	SNS		BNS	
	Male	Female	Male	Female
0	1.4669 ± 0.0921	1.3877 ± 0.1001	1.4669 ± 0.0921	1.3877 ± 0.1001
1	1.4146 ± 0.1027	1.1054 ± 0.1426	1.0412 ± 0.1541	1.1672 ± 0.1442
2	1.1034 ± 0.1263	1.0561 ± 0.1246	0.9996 ± 0.1445	1.2382 ± 0.1338
3	1.1297 ± 0.1315	1.1099 ± 0.1422	1.2696 ± 0.1416	1.3709 ± 0.1302
4	1.2898 ± 0.1740	0.8401 ± 0.1768	1.2007 ± 0.2368	1.4979 ± 0.1441
5	1.3153 ± 0.1731	1.1078 ± 0.1479	1.1155 ± 0.2300	1.6253 ± 0.0895
6	1.3635 ± 0.1490	0.3928 ± 0.1955	-	-
Pooled heritability	1.3256 ± 0.0474	1.1004 ± 0.0522	1.2580 ± 0.0583	1.4221 ± 0.0479
b ± S. E.	-0.0115 ± 0.0279	-0.1141 ± 0.0365**	-0.0288 ± 0.0435	0.0661 ± 0.0300*

* and **indicate the significance of the b at $P<0.001$ and $P<0.005$ respectively

The regression of heritability estimates on generation numbers, which indicate the change in heritability over the generations, were of low magnitudes.

Discussion

The heritability estimates of naupliar length from regression of offspring on parent were of medium magnitude and well within the theoretical limits, in both sexes of both lines, while those from full-sib data were very high and generally beyond 1.00. This is so because the heritability estimates from regression of offspring on parent is in the narrow sense the heritability, which include mostly additive genetic variance as against the estimates from full-sib data which is heritability in the broad sense.

Heritability in the broad sense is the ratio of the total genetic variance to the total phenotypic variance, wherein the total genetic variance includes additive genetic variance, variance due to dominance deviation and epistatic interaction. Thus. the high heritability values recorded from full-sib data, *vis-à-vis* the parent offspring regression, may be due to a substantial quantum of dominance deviation and/or epistatic interaction in the population under study.

Maternal effects and genetic differences among families can also result in an inflated heritability estimate from full-sib data by Lester (1988). The higher estimates obtained in the present study are on similar lines to those reported by Lester (1988) for early growth in a penaeid *Penaeus stylirostris*. The heritability of early growth estimated from full-sib data by Lester, 1988 in Experiments I and II respectively were 1.31 ± 0.62 and 1.27±0.53 for protozoea I, 1.09 ± 0.81 and 0.64 ± 0.58 for Mysis I and 0.84 ± 0.79 and 1.02 ± 0.60 for Post larvae I. He concluded that heritability estimates from full-sibs data were most likely to be affected by maternal effects and genetic differences among families and there was no way that the two causative factors could be separated when dealing with full-sibs.

Another point, which needs to be underscored is that *Artemia* is a primitive animal with lower phylogenic position i.e. less evolved compared to higher vertebrates in which heritability estimates are always within the theoretical range. Aquatic animals are ectothermic and lack sophisticated endogenous homeostasis like mammals and birds (Wickins 1981). Such an environment has a profound effect on their phenotypic expression. This may be one of the reasons why the estimated heritability values are higher than the normal limits. In the present study, heritability was estimated from animals, which were maintained in very similar environment and management practices under laboratory conditions except for the temperature of the culture media. This was so because the experimental period was spread over all the seasons *viz.* summer, monsoon and winter. Since the heritability estimates from full-sib data were affected by environment, the above factor might have also contributed to its higher magnitude, as compared to those estimated from parent-offspring regression, which were free from environmental effects. Experimental evidence for the variations in heritability estimates emanating from environmental factors like temperature are also available in copepod groups. McLaren (1976) estimated the heritability of adult size of copepod (*Eurytemora herdmany)* as 0.0 for male at 10°C and 0.97 at 15°C. This shows that heritability estimates of growth character are influenced a lot by environmental factors like temperature. Malecha et al. (1984) estimated heritability in a broad sense for growth of the juveniles of the prawn *Macrobrachium rosenbergii* as 0.35 for females and 0.0 for males, and concluded that the heritability estimates for growth have sex-linkage.

The effect of environment on estimates of heritability has already been proven by Hedgecock et al. (1976) and Hedgecock and Nelson (1978) in the American lobsters, wherein the estimates were 0.30 without environmental treatment, but 0.38 with temperature treatment. Fairfull et al. (1981) reported heritabilities ranging from 0.15 to 0.62 for size at specific moult over different diet treatments in the American lobster.

In the present study, although the generation-wise and sex-wise estimates of heritability indicated variations, they do not seem to follow any specific trend, as already reported by Dempster and Lerner (1951), Dempster et al. (1952), Falconer (1955) and Friars et al. (1962). This was true for both sexes, irrespective of the method of estimation used.

The regression of heritability estimates on generation number, which is known to indicate mean change in heritability per generation, also did not reveal any specific trend. Evidence of change in the genetic variations within the populations under selection, as manifested by changes in heritability estimates, was reported to be positive by Scosseroli (1957) in *Drosophila malanogaster*. On the other hand, workers like Yamada et al. (1958), Gowe (1970), Poggenpoel and Erasmus (1978) and others have reported decreasing trends. Fairly constant estimates of heritability over the generations for other terrestrial animals were reported by geneticists like Dempster and Lerner (1951); Dempster et al. (1952); Falconer (1955) and Friars et al. (1962). Changes in genetic variance, due to selection pressure appear to be controlled by specific genetic constitution of population at the commencement of selection.

Compared to very high heritability of 0.98 for body weight in the copepod *Pseudocalanus*, estimated by McLaren and Corkett (1978) using parent-offspring regression, the heritabilities in *Artemia* nauplii estimated in the present study using the same method were of medium magnitude.

As mentioned earlier, pooled heritability estimates for naupliar length of both SNS and BNS lines by parent-offspring regression were within normal limits, and of medium magnitude, unlike the estimates from full-sib data. This is very much on the expected lines, since heritability estimates from parent-offspring regression is heritability in the narrow sense, which includes mostly additive genetic variance, very little epistatic variance and no dominance variance. Further, these estimates were not much affected by sources of covariance, since the parent and offspring were usually measured over different time periods. Hence, the estimate from regression of offspring on parent is bound to be more reliable than the estimates from the full-sib data. There are no reports on heritability values of naupliar length that can be compared with the present study.

Conclusion

Medium and high magnitude heritability estimates for naupliar length from regression of offspring on parent and full-sib data analysis point towards the high level of genetic variance in the population.

It also indicates that a substantial portion of the variance in the population is due to additive genetic variance, which can be exploited through a simple mass selection. The higher estimates of full-sib heritability highlight the importance of non-additive genetic factors that contribute to variability.

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