Estimating Gypsy Moth (Lepidoptera: Lymantriidae) Fecundity in the Field: Comparison of Data from North America and Sardinia, Italy

CLIVE G. JONES, MARC K. STEININGER,[1] PIETRO LUCIANO,[2]
AND KAREN E. B. MOORE

Institute of Ecosystem Studies, New York Botanical Garden,
Mary Flagler Cary Arboretum, Millbrook, New York 12545

ABSTRACT   Regression equations for estimating fecundity of gypsy moth, *Lymantria dispar* (L.), from egg mass length were compared for a North American population and one from Sardinia, Italy. There was no significant difference in slopes and intercepts of the two data sets, indicating that the relationship between egg mass length and fecundity was the same for these two populations. A combined linear regression function was developed ($\log_{10}$ number of eggs per mass = 1.48 $\log_{10}$, egg mass length + 0.44, $r^2 = 0.71$, $P < 0.0001$). If subsequent comparisons of this regression with data from other populations reveal the same general relationship, measurement of egg mass length may be of general use as a simple, rapid, noninvasive field estimator of gypsy moth fecundity.

KEY WORDS   Insecta, *Lymantria dispar*, fecundity, egg mass length

POPULATIONS OF GYPSY MOTH, *Lymantria dispar* (L.), fluctuate substantially in density. Because fecundity can vary by nearly two orders of magnitude (Leonard 1981, Luciano & Prota 1981, Moore & Jones 1987), monitoring of population trends for research and management purposes requires estimation of the number of eggs per mass as well as number of egg masses. We recently reported a simple, nondestructive field method for estimating fecundity from egg mass length, based on data combined from a New York population over 2 yr and a Connecticut population over 1 yr (Moore & Jones 1987) (hereinafter referred to as North American data). These data showed variation in fecundity (58-fold) and density (15-fold) within and between years. Here we compare the regression developed for North American data with fecundity and egg mass length measurements from data collected at two sites in Sardinia, Italy, that varied in fecundity (22-fold) and density (nearly 9 × 10³-fold) over the period 1972–1979 (Luciano & Prota 1981) (hereinafter referred to as Sardinian data). We wished to see if the same fecundity estimation equation could be used for both data sets.

Materials and Methods

The North American data on egg mass length (measured on intact masses in the field) and number of eggs per mass (subsequently determined in

the laboratory) were from populations in forests dominated by chestnut oak (*Quercus prinus* L.) at the Mary Flagler Cary Arboretum, New York (1981, number of egg masses, $n = 138$; 1982, $n = 57$) and those dominated by white oak (*Q. alba* L.) at N. Stonington, Conn. (1984, $n = 12$). These populations varied in density (248–3,596 egg masses per ha), fecundity (26–1,509 eggs per mass), and egg mass length (8–54 mm). Data from New York were deliberately sampled evenly across a wide fecundity range to maximize variance in this parameter. Data from both years in New York and Connecticut sites were combined because previous analysis showed there was no significant difference in the fecundity–egg mass length relationship in the three data subsets (Moore & Jones 1987). Sardinian data were from two cork oak (*Q. suber* L.) sites near Tempio Pausania (Cusseddu, $n = 122$; Nuchis, $n = 100$; separated by 1 km) that varied in density (1–8,875 egg masses per ha), fecundity (63–1,379 eggs per mass), and egg mass length (10–65 mm) over the period 1972–1979. Egg mass length was measured in the laboratory on intact masses attached to pieces of cork oak bark removed from the tree. Data from these sites were pooled across years and across sites as in the original study by Luciano & Prota (1981).

Linear regressions of egg mass length and number of eggs per mass were carried out on raw data and $\log_{10}$-transformed data (SAS Institute 1985). Regressions and residuals were examined to detect nonlinearity, lack of independence of error terms, lack of constancy and normality in error variance, omission of key variables, and presence of outlier values (Neter & Wasserman 1974). A Bartlett's test

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[1] Current address: 792 Hot Springs Road, Santa Barbara, Calif. 93108.

[2] Istituto di Entomologia Agraria, Università Degli Studi di Sassari, Via Enrico De Nicola, Sassar, Sardinia, Italy.
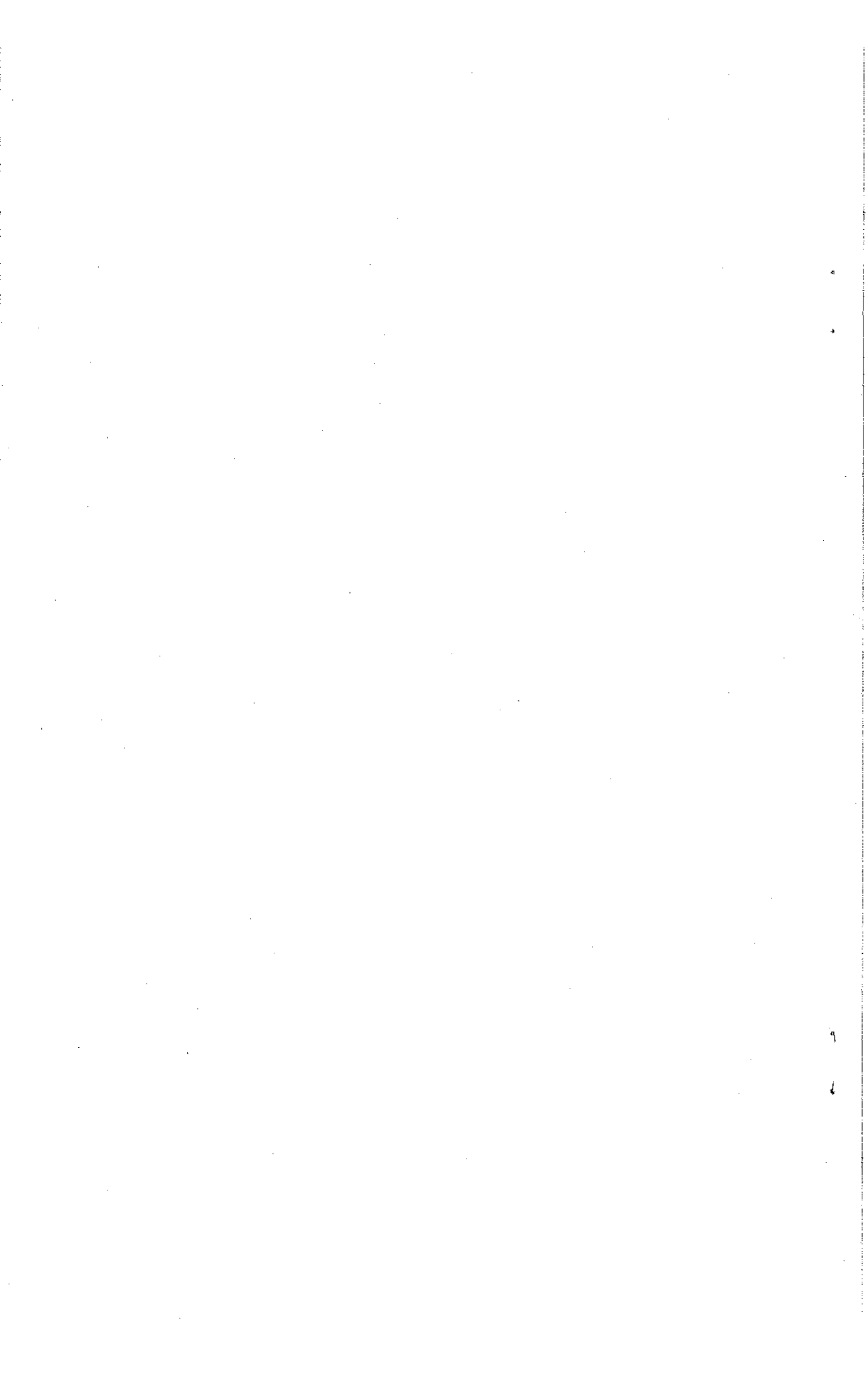
for homogeneity of regression error variance for the two data sets was used. Slopes and intercepts of the two regressions were compared using an F ratio test (Neter & Wasserman 1974).

Results and Discussion

Egg mass length was significantly correlated with the number of eggs per mass in the Sardinian data ($y = 16.26x - 11.86$; $r^2 = 0.51$, $F_{1,220} = 228$, $P < 0.0001$). However, error variance of the raw data was not constant, as was the case with the North American data (Moore & Jones 1987), so the Sardinian data were also $\log_{10}$-transformed to meet this requirement for linear regression. The transformed regression for the Italian data accounted for 55% of the variance in number of eggs per mass ($\log_{10}y = 1.20 \log_{10}x + 0.87$; $F_{1,220} = 274$, $P < 0.0001$). A Bartlett's test showed that regression error was homogenous for the Sardinian and North American data ($B = 3.45$, $\chi^2 [1 - \alpha = 0.95; 1$ df], $H_o = 3.84$), and slopes and intercepts of the two regressions were not significantly different ($F = 0.98 [1 - \alpha = 0.95; 2, \propto$ df], $H_o = 3.00$). Because the slopes and intercepts of the two data sets did not differ, the lower r^2 of the Sardinian data (0.55) compared with the North American data ($r^2 = 0.71$; Moore & Jones 1987) was most probably a reflection of the lower overall variance in egg mass length and fecundity; the low fecundity values found in North American data did not occur in the Sardinian data set over the time period that sampling occurred (See *Materials and Methods* and Fig. 1). This conclusion is substantiated by the r^2 value of a final combined regression equation for the two data sets (Fig. 1) ($r^2 = 0.71$), which is the same as the r^2 value for North American data alone. We suspect that if the Sardinian data had been sampled to maximize variance in fecundity (i.e., by adding masses with low fecundity to the sample), the r^2 of the Sardinian data would have been similar to the r^2 of the North American data.

The lack of a significant difference in the regression equations for the two data sets indicates that, in these cases, variance in egg size or density of eggs packed into a mass of given size either did not occur (see Campbell 1967, Capinera & Barbosa 1976, Capinera et al. 1977, Richerson et al. 1978) or at least was small enough so that it did not affect the strong underlying relationship between egg mass length and number of eggs per mass. Nevertheless, the overall r^2 of the final equation (0.71) indicates that some independent variance in egg size, packing density (eggs per unit mass volume), or mass size itself remains to be accounted for.

The equation we have developed for the two data sets permits comparison of fecundity between these populations within and between years, and confidence intervals for estimation have been developed (see Moore & Jones [1987] for details). Because the final equation was derived from populations varying nearly four orders of magnitude in
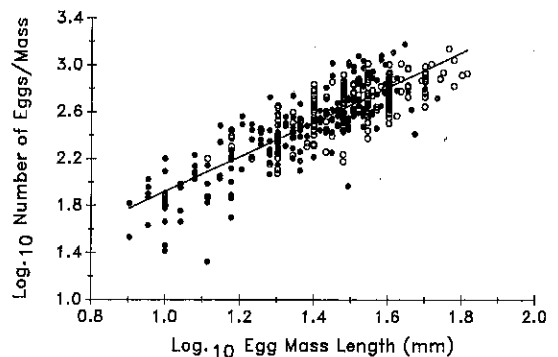

Fig. 1. Combined $\log_{10}$-transformed regression function for estimating number of eggs per mass (y) from egg mass length (x): $\log_{10}y = 1.48 \log_{10}x + 0.44$ ($r^2 = 0.71$, $F_{1,427} = 1,043$, $P < 0.0001$). ●, North American data (number of masses, $n = 207$); ○, Sardinian data ($n = 222$). Some observations are hidden where points are overlaid.

density, it also is possible to examine relationships between gypsy moth density and fecundity across this density range (C.G.J. & K.E.B.M., unpublished data). Although gypsy moth density can vary by over four orders of magnitude (Leonard 1981), the equation we have developed may be applicable across this entire density range because the fecundity values we sampled in New York (28–1,509 eggs per mass) span the entire range of fecundities that have been reported in the literature from low- to high-density populations (Campbell 1967, DeGroff 1969, Richerson et al. 1978, Leonard 1981, Luciano & Prota 1981, Moore & Jones 1987).

The fact that the relationship between egg mass length and fecundity does not significantly differ between these two data sets (derived from sites widely separated in space and time) suggests that this relationship may be generally robust and potentially applicable as a simple, rapid, noninvasive field estimator of gypsy moth fecundity. However, the extent to which this equation may hold true for other gypsy moth populations can be ascertained only by further independent validations. We would be delighted to make our raw data sets available to other researchers for further validation.

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