CITRUS RUST MITE (ACARI: ERIOPHYIDAE) COUNTS ON FRUIT AND THE NEGATIVE BINOMIAL DISTRIBUTION

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ABSTRACT

Count data for the number of citrus rust mites per cm² on fruit across a 4-ha (10-acre) area of orange trees followed the negative binomial probability distribution 79% of the time based on chi-square tests. A correlation of r = 0.993 was found between observed counts and counts projected based on the distribution. A common k of 0.149 was computed but generally appeared more suitable for mean densities of 3.0 to 55.0 than 0.5 to 3.0 citrus rust mites per cm². For mean densities of from 0.5 to 55 citrus rust mites per cm², the parameter k of the negative binomial was related to the mean density (x): k = 0.081 + 0.1139*(log₁₀ x). Estimated k-values were used to draw expected count data profiles for several mean densities ranging from 1 to 40 citrus rust mites per cm². Due to the skewness of the count data, the number of mites per cm² expected in most individual samples was always considerably smaller than the average density. Based on the negative binomial, mean rust mite densities could be estimated from the percentage of samples with at least one mite. Results of the study provide a means to predict the relative frequency histogram of densities associated with a mean density of citrus rust mites per cm² across an area of trees.

Key Words: citrus rust mite, Phyllocoptruta oleivora, sampling, negative binomial distribution

RESUMEN

Los datos del número de Phyllocoptruta oleivora por cm² en frutos de naranja en un área de 4 ha (10 acres) siguieron una distribución de probabilidad binomial negativa en el 79% de los casos, basada en pruebas de chi-cuadrada. Fue encontrada una correlación de r = 0.993 entre los conteos observados y los proyectados sobre la base de la distribución. Una k común de 0.149 fue computada, aunque en general parecía ser más adecuada para densidades medias de 3.0 a 55.0 que para densidades de 0.5 a 3.0 ácaros por cm². Para densidades promedio de 0.5 a 55 por cm², el parámetro k de la binomial negativa estuvo relacionado con la densidad promedio (x): k = 0.081 + 0.1139*(log₁₀ x). Los valores estimados de k fueron usados para calcular los perfiles de los datos de conteo esperados para varias densidades medias en el rango de 1 a 40 ácaros por cm². Debido a la desviación de los datos de los conteos, el número de ácaros por cm² esperado en la mayoría de las muestras individuales fue siempre considerablemente menor que la densidad promedio. Tomando como base la binomial negativa, las densidades medias de ácaros podrían ser estimadas a partir del porcentaje de muestras con al menos un ácaro. Los resultados del estudio proveen medios para predecir
Average densities of the citrus rust mite (CRM) \( [\text{Phyllocoptruta oleivora} \text{ (Ashmead)}] \) per \( \text{cm}^2 \) on fruit across an area of orange trees can be estimated from counts of the number of mites present within a one-\( \text{cm}^2 \) surface area per fruit (Hall et al. 1994). The number of fruit and trees that must be sampled depends upon both the desired precision of estimates and the density of mites at which this precision is required.

If the probability distribution (e.g., see Gomez & Gomez 1984) associated with CRM count data is known, the frequency histogram of individual counts associated with a particular mean density can be projected. This would be useful for projecting damage by a CRM population and for establishing control levels. Histograms of CRM counts taken within individual trees usually followed the negative binomial probability distribution (Hall et al. 1991). No information was available on probability distributions describing CRM count data from fruit over an area of trees.

We had a considerable amount of CRM count data from fruit samples taken across 4-ha (10-acre) areas of ‘Hamlin’ and ‘Valencia’ orange trees in Florida (Hall et al. 1994). Previous analyses of the data indicated that the counts usually followed an aggregated distribution (Hall et al. 1994). Because aggregated dispersions often follow the negative binomial probability distribution (Southwood 1978), and because CRM count data from individual trees usually followed the negative binomial, we evaluated this distribution for projecting the frequency histograms of our count data.

**Materials and Methods**

Count data were obtained on the number of CRM per \( \text{cm}^2 \) on fruit across 32 4-ha blocks of ‘Hamlin’ and ‘Valencia’ orange trees using a transect sampling plan (Hall et al. 1994). This plan consisted of 192 1-\( \text{cm}^2 \) samples per block - two samples per fruit, four fruit per tree (1 from each compass quadrant), 12 trees along one transect between the northeast and southwest corners of the block, and 12 trees along a second transect between the northwest and southeast corners of the block. All CRM except eggs within a 1-\( \text{cm}^2 \) sample were counted using a 10X magnifier fitted with a 1-\( \text{cm}^2 \) grid of 25 equal-sized subdivisions. In cases where \( >35 \) CRM per \( \text{cm}^2 \) were present, the number of mites was sometimes estimated by counting the number of mites in a diagonal row of five grid subdivisions and multiplying by 5. The block samples were taken during May through December within several different citrus growing areas in Florida. The only treatment applied to the blocks during the study was a summer spray of copper and oil. No samples were taken until at least 6 wk after this treatment.

The negative binomial probability distribution is characterized by two parameters, the mean (\( \bar{X} \)) and a coefficient \( k \) (Johnson & Kotz 1969). The value of the \( k \) parameter defines the shape of the negative binomial distribution and serves as a general indicator of aggregation, with smaller values of \( k \) indicating increased aggregation (Southwood 1978). An iterative solution was used to manually estimate \( k \) for each block averaging at least 0.5 CRM per \( \text{cm}^2 \) (25 blocks):

\[
N \cdot \log_e \left( 1 + \frac{3}{k} \right) = \sum \left[ \frac{A_i}{k + x} \right]
\] (1)
Hall et al.: Citrus Rust Mite & the Negative Binomial

with \( N \) = total number of samples, \( \log_e \) = natural logs, and \( Ax \) = the sum of all frequencies of sampling units containing more than \( x \) individuals (Bliss & Fisher 1953, Southwood 1978).

The 25 \( k \) estimates were then evaluated using regression procedures presented by Bliss & Owen (1958) and Bliss (1958) to determine if a single, common \( k \) \((k_c)\) existed. This involved regressing two statistics for each block, \( y' = s^2 - \bar{x} \) on \( x' = \bar{x} - (s^2/N) \), where \( \bar{x} \) was the mean, \( s^2 \) the variance and \( N \) the number of individual counts per block. The regression was forced through the origin, and \( k \) was estimated from the inverse of the slope of the regression. The adequacy of this \( k \) estimate was evaluated using a regression analysis of \( 1/k \) on \( \log_{10}(x) \): a trend between these variables discards the suitability of a single \( k_c \) (Bliss & Owen 1958, Southwood 1978).

One way to write negative binomial probabilities is:

\[
p_x = \frac{(x+k-1)!}{x!(k-1)!} \left( \frac{k}{k+x} \right)^k \left( \frac{x}{k+x} \right)^x \quad x = 0, 1, 2, \ldots \tag{2}
\]

where \( p_x \) is the probability of a sample having \( x \) mites (Williamson & Bretherton 1963). To determine the histogram of CRM counts expected in each block according to the negative binomial, we used observed mean densities and estimates of \( k \) in the following iterative probability formula:

\[
p_{x+1} = \frac{k+x}{x+1} \left( \frac{x}{k+x} \right) p_x \quad x = 0, 1, 2, \ldots \tag{3}
\]

with the probability of no mites \((x=0)\) being

\[
p_{x=0} = \left[ \frac{k}{k+x} \right]^x
\]

where \( p_{x=0} \) is the probability of a sample containing \( x \) mites. Equation (3) was obtained by writing successive terms for \( p_0, p_1, p_2, \ldots \) from equation (2) and noting the common multiplier. Using this iterative method avoids brute force calculation of the combinatorials which often cause computer overflow for large values of \( x \). We programmed SAS (SAS Institute Inc. 1990) software to compute the successive probabilities. Chi-square tests \((a = 0.05)\) according to guidelines presented by Gomez & Gomez (1984) and correlation analyses were used to test the fit of the observed CRM counts to those expected under the negative binomial based on estimated \( k \)-values.

RESULTS AND DISCUSSION

The mean density of CRM observed in the 25 blocks ranged from 0.5 to 112.5 per \( \text{cm}^2 \). A regression analysis indicated that the maximum density of CRM \((y)\) observed in each block could be estimated from the mean density \((\bar{x})\):

\[
y = 32.5 + 17.3x \quad r^2 = 0.85, \quad F = 123.1, \quad PR > F = 0.0001, \quad \text{d.f.} = 23.
\]

Individual estimates of the negative binomial \( k \) ranged from 0.0199 to 1.58 \((R = 0.2147, s = 0.3025)\) (Fig. 1). With respect to investigations into \( k \), an initial plot of \( y' \) on \( x' \) indicated that one data point clearly deviated from the main trend of the regression (Fig. 2). This data point, which was associated with a mean density of 112.5 CRM per \( \text{cm}^2 \) and a \( k \) value of 1.58, was excluded from further investigations into \( k \), but indicated that CRM aggregation may substantially decrease as population densities increase to as high as 100 or more CRM per \( \text{cm}^2 \).
Among the 24 sets of count data retained for $k$ determination, mean densities ranged from 0.5 to 54.9 CRM per cm$^2$ ($\bar{x} = 12.96$ per cm$^2$, $s = 16.9$). The individual $k$ estimates for the blocks varied from 0.0199 to 0.3580 ($\bar{k} = 0.158$, $s = 0.1052$). A $k$ of 0.149 was calculated ($F = 141.7$, Pr $> F = 0.0001$, $r^2 = 0.86$, d.f. = 24) ($r^2$ corrected for the mean $= 0.83$, d.f. = 23) (Fig. 2). A statistically insignificant relationship ($\alpha = 0.05$) was found between $1/k$ and $\bar{x}$ number CRM per cm$^2$, but a weak relationship ($r^2 = 0.395$) was found between $1/k$ and $\log_{10}(x)$ number CRM per cm$^2$ (Fig. 3), which indicated the $k$ of 0.149 may not have been a suitable substitute for all of the individual $k$-values. A similar problem was reported with respect to determining a $k$, associated with a set of wireworm counts (Bliss & Owen 1958). Variability in individual $k$-values associated with small mean CRM densities (e.g., 0.5 to 3.0 CRM per cm$^2$) was responsible for this trend; no significant trend was found between $1/k$ and $\log_{10}(x)$ number CRM per cm$^2$ among mean densities of from 3 to 55 CRM per cm$^2$ ($N = 15$), and the same $k$ (0.149) was calculated across these densities.

Because $k$ tended to be a poor substitute for individual $k$-values at mean densities below around 3.0, as an alternative to $k$, we conducted a regression analysis and determined an equation for estimating $k$ across different mean densities ($\bar{x}$): $k = 0.081 + \ldots$

Fig. 1. Negative binomial $k$-values associated with observed mean densities of citrus rust mites (crm) per cm$^2$ on fruit across 4-ha areas of orange trees.
0.1139*(log_{10}x); F = 27.11; Pr > F = 0.0001; r^2 = .55; d.f. = 23. A comparison of some histograms generated from individual, common and regressed k-values is presented in Fig. 4.

Chi-square tests indicated that CRM counts across a 4-ha area of trees followed the negative binomial distribution in 19 of 24 (79%) areas based on individual k-values and in 16 of 24 (67%) areas based on either k or regressed k-values. Among the observed count histograms that did not follow the negative binomial based on chi-square tests, these histograms visually resembled the distribution (e.g., Fig. 4). Over all 24 sets of CRM count data, the correlation between observed counts and counts projected using the negative binomial was 0.993 based on individual k-values, 0.976 based on regressed k-values, and 0.965 based on the k estimate. Among the 24 count sets, the lowest correlation between observed counts and counts expected under the negative binomial was 0.929, 0.921 and 0.872 based on individual k-values, regressed k-values and k, respectively.

Overall, counts of the number of CRM per cm^2 on fruit across a 4-ha area of trees appeared to be at least reasonably described by the negative binomial distribution when mean densities were in the range of 0.5 to 55 per cm^2. The distribution in con-

**Fig. 2.** Regression analysis used to calculate a single, common k (k_c) for a negative binomial distribution describing the number of citrus rust mites per cm^2 on fruit across 4-ha areas of orange trees. The open circle represents a data point excluded from the regression; this data point was associated with a mean of 112.5 mites/cm^2 and a k of 1.58.
Junction with the k parameter could therefore be used to project the frequency histogram of CRM densities at any mean density within this range, which in turn could be used in combination with models projecting how much surface damage to fruit a given density of CRM will cause (e.g., see Allen 1976, Yang et al. 1995) for an overall estimate of damage a CRM population will cause. The distribution could also be used to develop a sequential sampling plan (Southwood 1978), which might reduce the cost of sampling CRM. While histograms projected based on \( k \) were similar to those based on regressed \( k \) values, overall our analyses favored histograms based on the regressed estimates. As a word of caution, \( k \) values and the goodness-of-fit of the negative binomial distribution could be negatively influenced by extraneous factors that affect mite dispersion in a grove (e.g., chemical applications).

Expected profiles of CRM counts for a number of mean densities ranging from 1 to 40 mites per cm\(^2\) were projected based on the negative binomial using regression estimates of \( k \) in formula #3 (Fig. 5). Differences were relatively small between means of 1 to 40 mites per cm\(^2\) with respect to the projected probability of any individual count in the range of 5 to 15 mites per cm\(^2\). Due to the skewness of CRM count data, the number of mites per cm\(^2\) expected in most individual samples was always considerably smaller than the average density. For example, at an average density of 5 CRM per cm\(^2\), fewer than 5 mites per cm\(^2\) were expected to be present in around 80% of the individual samples across a 4-ha area. This information would be important to a citrus grower who might mistakenly assume that an average density based on scouting data reflects the midpoint of densities present. As the mean density increased, the probability increased that any particular large count would be observed. For example, the expected percentage of counts above 30 mites per cm\(^2\) increased from about 4% at a mean of 5 mites per cm\(^2\) up to about 18% at a mean of 20 mites per cm\(^2\). The skewness of CRM count data supported contentions made by McCoy et al. (1976), namely that a control threshold should take into consideration the frequency histogram of mite counts.

Given that count data follow the negative binomial and \( k \) is known, expected mean densities can be estimated from the percentage of samples containing at least one an-
Fig. 4. Probability (proportion) of observed counts of citrus rust mites per cm² compared to counts projected from negative binomial (NB) distributions derived from individual, common and regressed k-values (largest observed counts shown, probabilities below 0.0001 or above 0.15 not shown). An asterisk (*) indicates the observed histogram followed the projected histogram based on a chi-square test ($\alpha = 0.05$).
The relationship between mean CRM density and the percentage of infested samples based on the negative binomial is presented in Fig. 6. Similar relationships between percentages of infested samples and mean CRM densities have been observed without the use of a probability distribution (Knapp & Fasulo 1983, McCoy et al. 1976). The percentage of samples infested became increasingly poorer as an indicator of mean density as CRM densities increased. Benefits and precautions associated with using the percentage of infested samples as an indicator of mean CRM densities have been discussed (McCoy et al. 1976).

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Fig. 6. Relationship between the mean density of citrus rust mites per cm² on fruit across a 4-ha area of trees and the percentage of 1-cm² samples with at least one rust mite. Parameter estimates (standard error) associated with the hyperbola were 80.94 (1.166) and 3.994 (0.1905). A 95% confidence interval is given by the dotted lines. Percent samples infested (x) can be estimated from the mean number of mites/cm² (y) by:

\[ x = \frac{80.94 \times y}{3.99 + y} \]


