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THE DISTRIBUTION OF EUROPEAN CORN BORER LARVAE *PYRAUSTA NUBILALIS* (HBN.), IN FIELD CORN*

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For many years research entomologists have realized that insect populations have a tendency to be heterogeneously distributed. This heterogeneity is present in the distribution of larval populations of the European corn borer, *Pyrausta nubilalis* (Hbn.). To the research entomologist conducting experiments on larvae of the corn borer an understanding of this heterogeneity, or "spottiness", in the distribution of the insect would be of help in the design of experiments.

Distributions may be fitted for either one of two reasons: (a) to find a transformation in order to use normal theory, for example, in performing an analysis of variance (here it does not matter if the form of distribution fitted is particularly accurate); or (b) in relating observed counts to some theory of population growth or spread (requiring forms of distributions that are biologically significant.)

The purpose of this paper is to report the results of fitting three biologically significant statistical models, the negative binomial, Neyman's type A and the Poisson binomial to entomological field data.

REVIEW [illegible] LITERATURE

Much has been written on the general application of *contagious* or *compound Poisson* distributions to plant and insect populations. For the purposes of this paper, however, only references that are concerned with the European corn borer or the Poisson binomial distribution have been included.

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Simanton *et al.* [1931] pointed out that they had never encountered homogeneous corn borer populations at any time. They said, "It seems more evident that corn borer populations are naturally *spotty.* A condition that permits large and erratic variations of adjacent plot populations from each other and from their mean."

Beall [1940] proposed to explain the observed heterogeneity in corn borer populations by fitting three mathematical distributions due to Neyman [1939] and two due to Pólya [1931] to four frequency distributions obtained by sampling plots treated alike in an experiment designed to test the efficacy of controlling the European corn borer with the parasitic fungus *Beauvaria bassiana* (Bals.).

In fitting the distributions Beall used the method of moments to estimate the parameters. First, he fitted the Neyman type A distribution to the observed frequency distributions and found that only one of them was well fitted by it. He then proceeded to smooth each of the four observed frequency distributions by eye and to the four smoothed distributions he fitted all five mathematical distributions. Of these smoothed distributions he found one to be fitted best by the Neyman type B, two by the Neyman type A, and one by the negative binomial.

Bliss [1953], using Beall's observed data and estimating the parameters of the distributions by the method of maximum likelihood, concluded that the negative binomial was the appropriate mathematical distribution for fitting corn borer data.

Finally, Evans [1953], again using Beall's original data, and estimating the parameters of the distributions by both the method of moments and the frequency of zeros and ones, and in some cases also by the method of maximum likelihood for the negative binomial, agreed with Bliss on the negative binomial as the correct distribution for fitting corn borer data.

As is evident from the above review of the work all conclusions as to the appropriate mathematical distribution are based on Beall's data. Since the empirical frequency distributions obtained by Beall were from non-contiguous plots and were based on a small number of sampled observations, it was felt that his data might have given only an approximate answer to this question of the appropriate distribution. Therefore, it was thought worthwhile to get uniformity data from more extensive experimental areas and to re-examine the fitting of the more important contagious distributions.

All of the distributions referred to are known, in general, as *contagious distributions.* Biologically speaking, the name is unfortunate. In the present case, contagion is only apparent (Feller [1943]) and may be defined as an inflation of the variance in a population which should be described by a Poisson distribution. In this instance it therefore indicates the condition of "spottiness" previously discussed. A more adequate name would be *compound Poisson*, as used by Feller [1943], since, in general, they consist of a Poisson variable compounded in a Poisson or Gamma distribution, or a binomial variable compounded in a Poisson distribution. In the authors' opinion the name *compound Poisson* is more descriptive than *contagious*.

METHODS

During the summer of 1952, all of the 3205 corn plants growing on an area located in Northwest Iowa were dissected. During the summer of 1953, three additional areas were sampled by dissecting one plant, selected at random, from each hill.

Each area consisted of approximately $\frac{1}{3}$ acre chosen from a different corn field. An attempt was made to select it from parts of the field on level ground so as to make it as uniform as possible. All four areas were square in shape and included 36 rows of corn. The field sampled in 1952 had 54 hills per row at intervals of 2.3 feet while the three sampled in 1953 had 36 hills per row at intervals of 3.5 feet. Each area was divided into 324 plots and a coordinate system was employed to specify the exact location of each plant in the area. The dissection of the plants in the 1952 area was completed in 4.5 days. In 1953 the plants were dissected in from 1.25 to 2.5 days per area.

In all cases the data consisted of the number of cavities, and the number of borers by stages, for each plant dissected. All information was punched on I.B.M. cards and the frequency distributions used in this paper were obtained from the cards. The original data are the property of the Iowa State Experiment Station and have been issued under the title of "Uniformity Data from European Corn Borer, *Pyrausta nubilalis* (Hbn.), Populations" as Mimeo Series No. 2, Statistical Laboratory, Iowa State College.

FITTING THE DISTRIBUTIONS

In this paper three different compound Poisson distributions are fitted to 9 observed frequency distributions from 4 sets of sampling data, (see Appendix). The three distributions are the negative binomial, the Neyman type A, and a distribution here called the Poisson binomial. This was first suggested by Neyman [1939], while Skellam [1952] fitted it to some plant data by expanding the probability generating function.

For insects in the field the assumption made by Neyman that the survival from each egg mass follows a Poisson distribution is somewhat stringent. In actuality the value of p for the European corn borer is in the range of 0.01 to 0.05, which although low does not approach sufficiently close to zero for the Poisson distribution to be more efficient than the binomial itself. In the present study the value of the parameter n in the Poisson binomial depends on the number of larvae surviving from each egg mass, at the time of dissection. A similar statement was made by Neyman [1939, page 39]. However, n does not have to be integral as long as the values of zero and one, which are points of discontinuity, are excluded, but by allowing non-integral values the biological significance as developed in Neyman's model is lost. Mathematically the Poisson binomial is quite flexible; as $n \to \infty$ it can be shown to approach the Neyman type A distribution, and if $0 < n < 1$ as $n \to 0$ it comes closer and closer to the negative binomial. As a purely graduating curve it should be quite versatile. Recurrence formulae for calculating the probabilities are presented in this paper for the first time. Fisher's [1953] method of maximum likelihood was used in fitting the negative binomial while the method of moments was used for the other two distributions.

Beall has discussed the fitting of the Neyman type A and Bliss that of the negative binomial, so that it is not deemed necessary to describe those fitting procedures here. The fitting of the Poisson binomial, however, is explained.

The probability generating function for the Poisson binomial is:

$$G(\theta) = \exp\{a[(q + p\theta)^n - 1]\} \tag{1}$$

from which the recurrence expressions for the distribution are obtained by setting $\theta = 0$ in

$$d^xG(\theta)/d\theta^x \quad \text{where} \quad d^0G(\theta)/d\theta^0 = G(\theta). \tag{2}$$

The recurrence expressions are:

$$P_0 = e^{-a(1-q^n)} \tag{3}$$

$$P_x = \frac{\mu_1'}{x!} \sum_{i=0}^{x-1} \binom{x-1}{i} (n-1)^{[x-i-1]} p^{x-i-1} q^{n-x+i} i! P_i \,, \qquad x > 0, \tag{4}$$

where $(n - 1)^{[0]} = 1$ and $(n - 1)^{[3]} = (n - 1)(n - 2)(n - 3)$, P_x is the probability of a given x $(x = 0, 1, \cdots, \infty)$ in the population and a, p, q and n are parameters of the distribution.

It has been found that the labor of fitting is lessened if the recurrence formulae are left in the form

$$F_0 = e^{-a(1-q^n)} \tag{5}$$

$$(6) \qquad F_x = \mu_1' \sum_{i=0}^{x-1} \binom{x-1}{i} (n-1)^{[x-i-1]} p^{x-i-1} q^{n-x+i} F_i \,, \qquad x > 0,$$

and the probabilities are obtained from the relation $P_x = F_x/x!$.

The moments of the distribution are:

$$(7) \qquad \begin{aligned} \mu_1' &= apn \\ \mu_2 &= apn[1 + (n-1)p] \\ \mu_3 &= apn[1 + 3(n-1)p + (n-1)(n-2)p^2]. \end{aligned}$$

The parameters of the distribution may be estimated by the method of moments using the relations,

$$(8) \qquad \hat{a} = \frac{(n-1)\bar{x}^2}{n(s^2 - \bar{x})}\,, \qquad \hat{p} = \frac{(s^2 - \bar{x})}{(n-1)\bar{x}} \text{ and } \hat{q} = (1 - \hat{p}),$$

where $\bar{x}$ is the sample estimate of the mean and s^2 is the sample estimate of the variance. For clearness in the biological interpretation of the distributions only integral values of n greater than 1 were considered and, since with an increase in n the Poisson binomial approaches the Neyman type A, in order to get the maximum difference between the two curves the value of n to be used in the distribution was determined from the relation for estimating p in (8) above. The authors chose the smallest value of n such that $p = 1$. Neither maximum likelihood nor minimum chi square methods of fitting the parameters a and p are known under these conditions. In general if non-integral values of n are to be allowed the criterion

$$(9) \qquad R = \frac{K_{[1]} K_{[3]}}{K_{[2]}^2}$$

as described by Skellam [1952] may be used as an aid in determining which type of distribution to fit, and for the Poisson binomial n may be estimated by

$$(10) \qquad n = \frac{R-2}{R-1}.$$

In Equation (9) above $K_{[i]}$ is a factorial cumulant which may be derived from the factorial moments in the same manner as the cumulants are derived from the moments. In general, a useful value of n may be expected to be between 2 and 4 since the Poisson binomial approaches the Neyman type A quite rapidly.

Distribution 9, Table 1, has been chosen as an example of the actual fitting of this distribution.

The first two moment estimates, using six decimals for all computation which may be rounded off, are $\bar{x} = 0.648\ 148$ and $s^2 = 0.845\ 334$, hence, substituting in Equations (6) with $n = 2$,

$$\hat{a} = (n - 1)\bar{x}^2/n(s^2 - \bar{x}) = (0.648\ 148)^2/(2)\ (0.197\ 186) = 1.065\ 227,$$

$$\hat{p} = (s^2 - \bar{x})/\bar{x}(n - 1) = (0.197\ 186)/(0.648\ 148) = 0.304\ 229$$

$$\hat{q} = (1 - \hat{p}) = 0.695\ 771.$$

In order to compute P_0 the value of $\hat{q}^n$ is needed.

$$\hat{q}^n = \hat{q}^2 = (0.695\ 771)^2 = 0.484\ 097.$$

Since $(s^2 - \bar{x})/\bar{x}$ is less than one we may allow n to be 2. With $n = 2$, only two multipliers are required. These are

$$\hat{q}^{n-1} = \hat{q} = 0.695\ 771 \quad \text{and} \quad (n - 1)\hat{p}\hat{q}^{n-2} = (1)\hat{p}(1) = 0.304\ 229.$$

Using the above values for the parameters and multipliers, the required F_x values are next calculated to be

$$F_0 = e^{-a(1-\hat{q}^n)} = e^{-0.549\ 554} = 0.577\ 207,$$

$$F_1 = \bar{x}\hat{q}^{n-1}F_0 = (0.648\ 148)(0.695\ 771)(0.577\ 207) = 0.260\ 299,$$

$$\begin{aligned} F_2 &= \bar{x}[(n - 1)\hat{p}\hat{q}^{n-2}F_0 + \hat{q}^{n-1}F_1] \\ &= (0.648\ 148)[(0.304\ 229)(0.577\ 207) + (0.695\ 771)(0.260\ 299)] \\ &= 0.231\ 202, \end{aligned}$$

$$\begin{aligned} F_3 &= \bar{x}[2(n - 1)\hat{p}\hat{q}^{n-2}F_1 + \hat{q}^{n-1}F_2] \\ &= (0.648\ 148)[2(0.304\ 229)(0.260\ 299) + (0.695\ 771)(0.231\ 202)] \\ &= 0.206\ 918 \end{aligned}$$

etc. Hence, the required probabilities are:

$$P_0 = F_0/0! = 0.577\ 207,$$

$$P_1 = F_1/1! = 0.260\ 299,$$

$$P_2 = F_2/2! = 0.115\ 601,$$

$$P_3 = F_3/3! = 0.034\ 486$$

and so on. The expected frequencies are obtained by multiplying the probabilities in turn by the total frequency (324).

RESULTS

The results of fitting the three mathematical distributions to three observed frequency distributions from the 1952 field and to two frequency distributions from each of the three 1953 fields are given in Table 1.

In most cases the difference between the various fitted distributions is slight, and in some cases, for practical purposes, no distinction would be made between two or even all three of them. Had more efficient methods of estimation, consistent with the selected tests of goodness-of-fit, been available, the Poisson binomial distribution might perhaps have been fitted more closely, but even using the above estimating procedures, this model gave on the whole closer approximations to the data than did the negative binomial, as measured by an ordinary chi-square goodness-of-fit test.

All three compound Poisson distributions were fitted to the nine observed distributions. In six cases the Poisson binomial gave the best fit. The negative binomial fitted best in three cases (Table 1). The fitting indicates that for these data the Poisson binomial and the negative binomial are the appropriate graduating curves in that order. An interesting question presenting itself is whether or not sampling a population of corn borer larvae enhances the skewness of the resulting frequency distribution and thus makes the negative binomial the appropriate distribution.

DISCUSSION AND SUMMARY

It has been shown that data from an area on which total larvae counts of the European corn borer, *Pryausta nubilalis* (Hbn.) made, giving Distributions 2 and 3 (see Appendix), were best fitted by the Poisson binomial distribution. On the other hand when the corn borer population was sampled, as was done in the areas from which Distributions 4 to 9 (see Appendix) originated, the appropriate distribution was the negative binomial, provided the mean was above one. However, when the mean was less than one, it seemed that sampling made little difference and the best fitting distribution was again the Poisson binomial.

Completely random samples from a population of known distribution will tend to reproduce the parent distribution. Why then would sampling make so much difference in the observations from compound Poisson populations? A possible explanation may be deduced from the assumptions underlying the three distributions fitted. The assumption underlying the negative binomial is that there are many values of a Poisson mean which are distributed as a modified chi-square distribution. On the other hand the assumptions underlying the Neyman type A and Poisson binomial distributions are; (1) that eggs are laid in masses of N eggs each, (2) that these egg masses are laid at random over the field,

TABLE 1

OBSERVATIONAL UNIT, ESTIMATED MEAN AND VARIANCE, DEGREES OF FREEDOM AND GOODNESS OF FIT OF THE NEGATIVE BINOMIAL, NEYMAN TYPE A AND POISSON BINOMIAL FREQUENCY FUNCTIONS FOR EACH OF NINE OBSERVED DISTRIBUTIONS

Observed distribution*	Type of observational unit	Mean	Variance	Degrees of freedom	Goodness of fit					
					Negative binomial		Neyman type A		Poisson binomial	
					χ^2	p	χ^2	p	χ^2	p
1**	Total borers/plant	2.591	3.298	9	34.52	0.001	27.49	0.010	25.52	0.010
2**	Pupae & 5th instar larvae/plant	2.032	2.704	7	15.48	0.035	10.02	0.187	7.07	0.420
3**	Total borers/plot	25.633	82.368	24	17.03	0.843	16.22	0.877	15.79	0.894
4	Total borers/plant	1.307	1.856	5	0.71	0.952	2.63	0.792	17.47	0.005
5	Total borers/plot	5.228	10.621	11	14.60	0.202	16.17	0.135	17.53	0.063
6	Total borers/plant	0.410	0.512	2	1.94	0.385	1.24	0.535	0.61	0.740
7	Total borers/plot	1.642	2.594	5	3.26	0.658	5.05	0.410	18.90	0.003
8	Total borers/plant	0.164	0.192	2	1.35	0.510	0.40	0.820	0.05	0.980
9	Total borers/plot	0.648	0.845	3	2.36	0.505	1.28	0.735	1.06	0.785

*The observed frequency distributions are given in the appendix.

**All plants in experimental area were dissected. Distributions 4 to 9 came from sampled fields. A 33% sample was taken, comprising one plant from each hill.

(3) that the hatching larvae will move away from the location of the mass equally in all directions, (4) that the number of survivors from each egg mass follows either a Poisson or a binomial law, and finally, (5) that there is only a limited distance (small relative to the size of the plot) over which any larva move from the egg mass. It seems logical to assume therefore that the important factor in both the Neyman type A and the Poisson binomial distributions is the area over which the larvae from a certain number of egg masses will interact. By taking all the information available, a complete census, this area interaction is reflected in the type of distribution obtained. When a sample of one plant per hill is taken only the varying Poisson populations are measured by the sample, the area interactions may not be observed and the resulting distribution is therefore closer to the negative binomial than to the Neyman type A or Poisson binomial distributions.

One other point should be discussed. If this sampling favors the negative binomial, why should a distribution with a low mean be fitted best by the Poisson binomial if the larval population was sampled? In the cornfield with a low larval population the infested hills will be found in localized areas with many surrounding non-infested hills. If one plant from each hill is dissected, as was done in the case of the three areas studied in 1953, then the sample is sufficient to show the true distribution of the insect since the larvae will tend to remain on the plants in a hill. In other words, less information is lost in thus sampling from a population with a low larval density than in sampling from a population with a high larval density. The area over which the larvae travel may vary directly with the population density.

In summary, then, it has been shown for the data analyzed that with complete information on the corn borer population in a large area of corn, at least $\frac{1}{3}$ acre, the appropriate mathematical distribution to describe the population of larvae seems to be the Poisson binomial. When, on the other hand, the information was incomplete, based on a restricted random sample, the appropriate distribution seems to be the negative binomial for fields with a high density and the Poisson binomial for fields with a low density. It must be pointed out, however, that even for the sampled fields with the low densities the negative binomial may be an excellent approximating distribution.

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APPENDIX

Frequency Distributions Observed and Computed from Fitted Negative Binomial (NB), Neyman Type A (NTA) and Poisson Binomial (PB) Functions

Observational units as specified in Table 1. Brackets indicate groupings adopted for goodness of fit tests.

DISTRIBUTION 1
$N = 3205$

Count per plant	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 2$)
0	355	324.30	331.79	341.84
1	600	660.37	654.44	644.37
2	781	734.06	734.77	728.03
3	567	610.45	608.67	609.14
4	441	408.82	411.61	415.60
5	245	236.54	239.64	242.72
6	135	122.49	124.09	125.17
7	42	58.12	58.44	58.20
8	17	25.68	25.45	24.76
9	⎧ 11	10.70	10.41	9.75
10	⎩ 11	4.47	5.69	5.42

Distribution 2

$N = 3205$

Count per plant	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 2$)
0	588	553.18	568.14	587.85
1	807	845.72	829.36	799.38
2	741	750.81	742.53	741.12
3	479	506.58	509.95	515.08
4	328	287.83	293.57	299.67
5	159	145.14	148.37	150.76
6	67	67.01	67.71	67.74
7	22	28.89	28.43	27.64
8	5	11.80	11.13	10.39
9	7	4.61	4.11	3.63
10	2	2.76	1.92	1.74

Distribution 4

$N = 1296$

Count per plant	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 2$)
0	423	426.60	419.40	461.53
1	414	406.36	405.33	349.79
2	253	248.65	257.06	259.29
3	117	123.91	128.39	129.54
4	53	54.71	54.70	60.14
5	22	22.30	20.75	23.34
6	4	8.58	7.15	8.45
7	5	3.16	2.29	2.75
8	3	1.13	0.69	0.84
9	2	0.60	0.27	0.32

DISTRIBUTION 3

$N = 311$

Count per plot	Observed frequency	Theoretical frequency			Count per plot	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 4$)			NB	NTA	PB ($n = 4$)
0	0	0.00	0.01	0.06	30	8	11.08	11.37	11.53
1	0	0.00	0.03	0.03	31	11	10.24	10.58	10.74
2	0	0.02	0.08	0.12	32	6	9.39	9.95	9.91
3	0	0.05	0.16	0.27	33	8	8.54	8.91	9.07
4	0	0.12	0.29	0.37	34	9	7.72	8.07	8.22
5	1	0.26	0.50	0.55	35	5	6.92	7.26	7.39
6	1	0.49	0.80	0.97	36	9	6.17	6.47	6.59
7	1	0.84	1.20	1.34	37	7	5.47	5.73	5.83
8	0	1.34	1.71	1.77	38	7	4.82	5.03	5.12
9	5	2.01	2.36	2.47	39	3	4.22	4.39	4.46
10	2	2.85	3.12	3.26	40	4	3.68	3.81	3.85
11	5	3.84	4.01	4.02	41	1	3.19	3.28	3.31
12	6	4.97	4.99	4.98	42	5	2.75	2.80	2.82
13	8	6.21	6.06	6.08	43	2	2.36	2.38	2.38
14	3	7.50	7.18	6.93	44	3	2.02	2.01	2.00
15	7	8.81	8.32	8.18	45	0	1.72	1.69	1.67
16	15	10.08	9.44	9.28	46	1	1.46	1.41	1.39
17	12	11.25	10.50	10.27	47	0	1.23	1.17	1.14
18	10	12.30	11.48	11.22	48	2	1.03	0.96	0.94
19	10	13.19	12.35	12.16	49	0	0.87	0.79	0.76
20	12	13.89	13.07	12.87	50	1	0.72	0.65	0.62
21	11	14.38	13.63	13.43	51	0	0.60	0.53	0.50
22	14	14.67	14.01	13.87	52	1	0.50	0.42	0.40
23	11	14.75	14.21	14.14	53	0	0.41	0.34	0.32
24	13	14.64	14.24	14.18	54	0	0.34	0.27	0.25
25	17	14.35	14.09	14.08	55	0	0.28	0.22	0.20
26	17	13.90	13.79	13.84	56	1	0.23	0.17	0.16
27	15	13.33	13.35	13.43	57	0	0.19	0.14	0.12
28	15	12.65	12.78	12.88	58	0	0.15	0.11	0.09
29	18	11.89	12.11	12.25	59	1	0.12	0.08	0.07
					60+	0	0.99	3.34	2.85

Distribution 5
$N = 324$

Count per plot	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 3$)
0	10	8.92	12.41	16.20
1	18	22.96	23.14	19.87
2	39	35.37	33.50	33.34
3	33	42.32	39.74	38.43
4	42	43.34	41.41	40.46
5	56	39.92	39.16	39.27
6	36	34.01	34.28	34.54
7	26	27.31	28.17	28.74
8	19	20.92	21.94	22.51
9	19	15.42	16.32	16.74
10	7	11.02	11.65	11.93
11	4	7.66	8.03	8.15
12	4	5.21	5.06	5.37
13	4	3.47	3.47	3.42
14	2	2.27	2.19	2.11
15	1	1.47	1.35	1.27
16	2	0.94	0.81	0.74
17	1	0.59	0.48	0.42
18	0	0.20	0.28	0.23
19	0	0.12	0.16	0.13
20	0	0.08	0.09	0.07
21	0	0.05	0.05	0.04
22	0	0.03	0.03	0.02
23	0	0.02	0.01	0.01
24	0	0.01	0.01	0.004
25	1	0.41	0.01	0.004

Distribution 6
$N = 1296$

Count per plant	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 2$)
0	907	902.85	900.89	904.44
1	275	288.86	288.76	279.42
2	88	78.07	82.00	89.09
3	23	19.81	19.34	18.63
4	3	6.42	5.02	4.31

Distribution 7

$N = 324$

Count per plot	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 2$)
0	89	89.53	89.01	100.97
1	96	91.85	88.63	69.66
2	57	64.34	66.29	72.09
3	44	38.10	40.41	38.69
4	16	20.49	21.53	23.83
5	11	10.36	10.38	10.65
6	7	5.01	4.62	5.01
7	3	2.34	1.93	1.94
8	1	1.98	1.20	1.16

Distribution 8

$N = 1296$

Count per plant	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 2$)
0	1117	1114.98	1116.97	1116.39
1	149	154.51	150.44	150.47
2	27	22.51	24.75	26.21
3	3	3.99	3.84	2.92

Distribution 9

$N = 324$

Count per plot	Observed frequency	Theoretical frequency		
		NB	NTA	PB ($n = 2$)
0	188	185.79	187.99	197.02
1	83	89.28	85.02	84.34
2	36	32.99	34.52	37.45
3	14	10.97	11.65	11.17
4	2	3.45	3.51	3.11
5	1	1.52	1.30	0.91