

# Insect Distribution in Bulk-stored Wheat in Relation to Detection or Estimation of Abundance<sup>1</sup>

DAVID W. HAGSTRUM, GEORGE A. MILLIKEN,<sup>2</sup> AND MERRILEE S. WADDELL

U.S. Grain Marketing Research Laboratory, Agricultural Research Service, U.S. Department of Agriculture, Manhattan, Kansas 66502

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**ABSTRACT** A stratified sampling plan demonstrated that pattern of distribution of insects among nine regions of a bin (center and edge or midway in four compass directions) differed between bins of wheat. Within a bin, variation between two samples taken at a site was generally the largest, followed by variation between regions and then variation within a region between two sites 30 cm apart. The five most common species were most abundant in the center of the bin and another four species were most common along the bin wall. The negative binomial best described distribution of all species and variance increased more rapidly than the mean. Probability of detection increased with density, although progressively more slowly as density increased. Increase in number of samples with insects as a function of increasing density was apparently reduced by a disproportionate increase in number of insects per sample as density increased. Sampling effort required for detection or estimation of abundance was modeled as a function of insect density, sample-to-sample variation, and acceptable accuracy or confidence levels.

WHEN SAMPLING TO detect or estimate insect populations, the distribution and abundance components are so interrelated that an accurate assessment of insect presence or absence and estimations of abundance are only possible when distribution patterns are considered. Most surveys of insects infesting stored grain have recognized this unevenness by taking several samples, but have then pooled samples and ignored sample-to-sample variation (Storey et al. [1983] and references cited therein are examples). Studies of populations in commercial-size storage bins such as those by Smith (1978) and Meagher (1982) have characterized the large-scale distribution pattern of insects within a bin, but have not determined statistical distribution of insects among samples. For laboratory populations of two species, *Sitophilus granarius* (L.) and *Plodia interpunctella* (Hübner), analyses of statistical distributions have quantified the degree of unevenness (Andersen 1965, Arbogast and Mullen 1978).

Detection/estimation models relating necessary sampling effort to insect abundance are derived here from an analysis of insect distribution in bulk-stored wheat. These analyses identify primary sources of sample-to-sample variation, characterize insect distribution, and model the relationships between insect abundance, probability of a sample

containing an insect, and the number of samples needed.

### Materials and Methods

The numbers of each insect species in 0.5-kg samples of wheat taken with a grain trier (Seedboro 1.27-m open-end spiral probe) from the top meter of four bins (5.8 or 6.4 m diam) of 82-122 t capacity (3,000-4,500 bushels) were determined on two farms, one near Enterprise, Kans. (bins A and B), and the other near Manhattan, Kans. (bins C and D). Insects were separated from the wheat with an oblong-hole grain sieve (0.18 by 1.27 cm, Seedboro) and removed from the sievings with aid of a dissecting microscope. On three occasions, sets of 36 samples each were taken from the same 18 sites within each bin between 22 October 1983 and 6 January 1984. Nine regions located in three concentric zones with one in the center of the bin, four at compass points along the bin wall (edge) and four at compass points midway between center and edge zones were sampled at two sites from each of which two samples 30 cm apart were taken.

The Statistical Analysis System (SAS Institute, Inc. 1982) was used to calculate and compare means, calculate frequencies of association, estimate variance components, and fit regression equations. Models in Fig. 1 were compared using model comparison procedures of Draper and Smith (1981). A FORTRAN program from Gates and Ethridge (1972) was used to fit frequency distri-

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<sup>2</sup> Statistics Dept., Kansas State Univ., Manhattan, KS 66502.

butions. The number of samples ( $n$ ) required to estimate mean ( $\bar{x}$ ) population densities was calculated as suggested by Ruesink and Kogan (1975) using:

$$n = \left(\frac{100}{c}\right)^2 t_{\alpha}^2 a \bar{x}^{b-2} \quad (1)$$

where  $c$  = accuracy as percentage of mean,  $t$  = value of  $t$  distribution for confidence limits  $\alpha$ , and  $a$  = antilogarithm of intercept and  $b$  = slope of the regression of logarithm of variance against logarithm of mean.  $n$  needed to be 95% confident that the mean is below a specified level was calculated from the binomial distribution:

$$P = (1 - q)^n \quad (2)$$

where  $P$  = probability that none of the samples has insects and  $q$  = probability that a sample will have at least one insect by solving equation 2 for  $n$ , setting  $P = 0.05$  and substituting the model involving  $K$  from Fig. 2 for  $q$ :

$$n = \frac{\log 0.05}{\log \left[ \left( \frac{1.31}{x + 1.31} \right)^{1.31} \right]} \quad (3)$$

**Results**

A sampling plan with redundancy at each of five levels of stratification was used to partition sample-to-sample variation and identify primary sources of variation. The densities of most species differed significantly between bins (Table 1) and these differences contributed 0-78.6% (mean = 28.9%) of the variance (Table 2). The significant contribution of bin-region and bin-set-region interactions to overall variance indicates that the pattern of distribution of insects among regions generally differed between bins and in three cases even between sets of samples from the same bin. Within a bin, the variation between two samples taken at a site was generally the largest, followed by variation between regions and then between areas within a region. The disturbance of taking first sample at a site must not have affected the second, since for each of the bins the overall mean numbers of a species in the second samples taken from sites did not differ significantly at 1% level from that for first samples. The reduction in variance that might be achieved by increasing the number of samples in any one of the strata can be estimated using the equation,

$$\text{var} = \text{Total } \hat{\sigma}^2 \left[ \frac{\text{bin } \%}{S} + \frac{\text{set } \%}{SR} + \frac{\text{region } \%}{R} + \frac{\text{bin-region } \%}{R} + \frac{\text{set-region } \%}{SR} \right]$$

**Table 1. Variation between bins or zones in the insect population densities in bulk-stored wheat**

Species <sup>a</sup>	# no. of insects per 0.5 kg of wheat <sup>b</sup>																			
	Bin A		Bin B		Bin C		Bin D		Center zone <sup>c</sup>		Midway zone <sup>c</sup>		Edge zone <sup>c</sup>							
	$\bar{x}$	SE	$\bar{x}$	SE	$\bar{x}$	SE	$\bar{x}$	SE	$\bar{x}$	SE	$\bar{x}$	SE	$\bar{x}$	SE						
<i>Cryptolestes ferrugineus</i> (Stephens)	2.53b	0.60	8.75a	1.83	3.49b	0.78	0.69c	0.085	19.37a	4.13	2.26b	0.20	1.59c	0.15						
<i>O. surinamensis</i> (L.)	0.0093d	0.0093	0.54c	0.11	41.60a	6.74	1.83b	0.29	38.77a	14.86	4.83b	0.60	10.22b	1.70						
<i>Rhizopertha dominica</i> (F.)	0.19c	0.065	2.06a	0.64	1.55a	0.30	1.68a	0.23	6.33a	1.32	1.10b	0.17	0.41c	0.094						
<i>Tribolium castaneum</i> (Herbst)	0.14c	0.048	0.37b	0.086	6.99a	1.97	0.39b	0.060	15.21a	4.16	0.33b	0.041	0.31b	0.049						
<i>A. advena</i> (Walt)	0.69a	0.11	0.34b	0.067	0.065c	0.027	0.0089c	0.0093	0.29a	0.089	0.14b	0.046	0.41a	0.062						
<i>T. stercorea</i> (L.)	2.02a	0.38	0.41b	0.087	0.093c	0.031	0c	—	0.27b	0.068	0.24b	0.098	1.11a	0.21						
<i>P. interpunctella</i> (Hübner)	0.58a	0.10	0.49a	0.10	0.88a	0.15	0.39a	0.068	0.23b	0.095	0.25b	0.045	1.02a	0.11						
<i>Trogoderma glabrum</i> (Herbst)	0c	—	1.06a	0.20	0.31b	0.067	0.055c	0.022	0.021b	0.021	0.099b	0.025	0.70a	0.12						
Hymenoptera <sup>d</sup>	0.25c	0.067	0.84b	0.22	8.82a	0.94	0.43b	0.061	9.27a	2.04	2.29b	0.31	1.21b	0.17						
Total	6.41c	0.76	14.87b	2.65	63.81a	9.43	5.46c	0.39	89.77a	20.69	11.54b	0.98	16.96b	1.82						

<sup>a</sup> Counts for *P. interpunctella* and *T. glabrum* represent larvae; those for other species represent adults.

<sup>b</sup> Means for a species across bins or zones followed by the same letter were not significantly different ( $P = 0.05$ ; Duncan's multiple range test). Each bin mean is the average for 108 samples and means for center, midway, and edge zones represent 48, 192, and 192 samples, respectively. To eliminate the correlation between mean and variance (Fig. 1), a cubed-root transformation was necessary before analysis, but the untransformed means are presented in the table.

<sup>c</sup> Data combined for all bins.

<sup>d</sup> Combines bethylid and pteromalid parasites of storage pests, including *Cephalonomia waterstoni* Gahan, *C. tarsalis* (Ashmead), and *Anisopteromalus calandrae* (Howard).

**Table 2. Partitioning of sample-to-sample variation in the insect population densities in bulk stored wheat among five levels of stratification**

Species	% contribution to variation <sup>a</sup>									
	Bin	Set	Bin-Set	Region	Bin-Region	Region-Set	Bin-Region-Set	Area	Site	Total
<i>C. ferrugineus</i>	27.7 <sup>a</sup>	0.4	0	19.4 <sup>a</sup>	11.7 <sup>a</sup>	0	0.6	3.1	37.1	0.795
<i>O. surinamensis</i>	78.6 <sup>a</sup>	0	0.03	1.8	4.2 <sup>a</sup>	0	3.4	2.3	9.7	2.373
<i>R. dominica</i>	6.6	0	0.09	10.9	48.4 <sup>a</sup>	2.1	0	11.5	20.3	0.566
<i>T. castaneum</i>	4.9	0.03	0.3	1.5	57.5 <sup>a</sup>	0.9	4.8	5.3	24.7	0.583
<i>A. advena</i>	16.1 <sup>a</sup>	1.0	0	1.5	5.6	10.3 <sup>a</sup>	18.1 <sup>a</sup>	0	47.3	0.379
<i>T. stercorea</i>	26.1 <sup>a</sup>	0.5	0	8.7 <sup>a</sup>	4.2	0	33.5 <sup>a</sup>	1.1	26.0	0.233
<i>P. interpunctella</i>	0	0.2	0	11.1 <sup>a</sup>	13.7 <sup>a</sup>	0	7.8	0	67.3	0.335
<i>T. glabrum</i>	15.3 <sup>a</sup>	0	0.1	2.0	43.0 <sup>a</sup>	0.8	0	0	38.8	0.235
Hymenoptera	62.6 <sup>a</sup>	0.02	0.07	5.9 <sup>a</sup>	8.6 <sup>a</sup>	0	2.9	1.7	18.2	0.919
Total	51.6 <sup>a</sup>	0	0.02	13.3 <sup>a</sup>	11.8 <sup>a</sup>	0.9	5.3 <sup>a</sup>	1.4	15.6	1.587
$\bar{x}$	28.9	0.21	0.061	7.6	20.9	1.5	7.6	2.6	30.5	0.801
SD	26.6	0.33	0.093	6.1	20.4	3.2	10.5	3.5	17.4	0.687

<sup>a</sup> Variance component significant at the 1% level after cubed-root transformation. Analysis is based upon all 432 samples.

$$+ \left[ \frac{\text{bin-set-region \%}}{SR} + \frac{\text{area \%}}{SRA} + \frac{\text{site \%}}{SRAN} \right] \quad (4)$$

where S, R, A, and N represent the number of samples for sets, regions, areas, and sites within an area. Increasing S or R sampled would reduce the largest number of variance components but increasing the number of regions sampled would be most effective at reducing the most influential variance components.

The distribution pattern differed among species and locations. For the five most abundant species and total insects, densities were significantly higher in the center zone than elsewhere, but for the other species, densities were highest in the edge zone (Table 1). Adult *Oryzaephilus surinamensis* (L.) occurred more frequently than expected by chance in samples containing the other four most abun-

dant species, and *Ahasverus advena* (Waltl) occurred more than expected with the other fungus feeder, *Typhaea stercorea* (L.) (Table 3). In nine cases, mainly with the most abundant species, the numbers of one species present were correlated with the numbers of another. Furthermore, live and dead insects were generally found together and in proportional numbers.

The distribution patterns of each of the nine species or all insects disregarding species can be further characterized for each of four bins by fitting statistical frequency distributions to the numbers of insects of that species in each of the 108 samples taken from a bin. The negative binomial distribution most consistently fit the data with *k* ranging from 0.075-5.49 (mean = 1.18) (Table 4). Of the 40 possible distributions, 9 could not be fitted because they had 4 or fewer frequency classes and another 5 (*O. surinamensis* in bin C or total insects for each of four bins), because there were too few observations in each frequency class.

**Table 3. Percentage of samples from bulk-stored wheat that have both species present of a pair being compared or both live and dead insects of a single species**

Species	Live vs dead	Species									
		<i>C. ferrugineus</i>	<i>O. surinamensis</i>	<i>R. dominica</i>	<i>T. castaneum</i>	Hymenoptera	<i>P. interpunctella</i>	<i>T. glabrum</i>	<i>A. advena</i>	<i>T. stercorea</i>	
<i>C. ferrugineus</i>	40 <sup>a</sup>	—	37 <sup>a</sup>	27 <sup>a</sup>	26 <sup>a</sup>	36 <sup>a</sup>	24	18	18	22	
<i>O. surinamensis</i>	45 <sup>a</sup>	37 <sup>a</sup>	—	32	31 <sup>a</sup>	53 <sup>a</sup>	23 <sup>a</sup>	15	5 <sup>a</sup>	4	
<i>R. dominica</i>	35 <sup>a</sup>	27 <sup>a</sup>	32	—	27	33	11	4	7	6	
<i>T. castaneum</i>	11	26 <sup>a</sup>	31 <sup>a</sup>	27	—	25 <sup>a</sup>	18	18	7	9	
Hymenoptera	—	36 <sup>a</sup>	53 <sup>a</sup>	33	25 <sup>a</sup>	—	21	13	9	11	
<i>P. interpunctella</i>	13	24	23 <sup>a</sup>	11	18	21	—	23	20	27	
<i>T. glabrum</i>	29 <sup>a</sup>	18	15	4	18	13	23	—	16	15	
<i>A. advena</i>	—	18	5 <sup>a</sup>	7	7	9	20	16	—	34	
<i>T. stercorea</i>	—	22	4	6	9	11	27	15	34	—	

If insects were randomly distributed, one would expect 25% of samples not to have insects, 50% to have one of two species, and 25% to have both of these two species. Therefore, coincidence of any species pair in more than 25% of the samples in which either was present could represent a species association. Percentages calculated for 73-384 samples which had at least one species of a pair being compared present.

<sup>a</sup> A significant (*P* < 0.01) correlation between the numbers of one species present and the number of the other or between live and dead of the same species exists. Comparisons are based upon 11-153 samples.

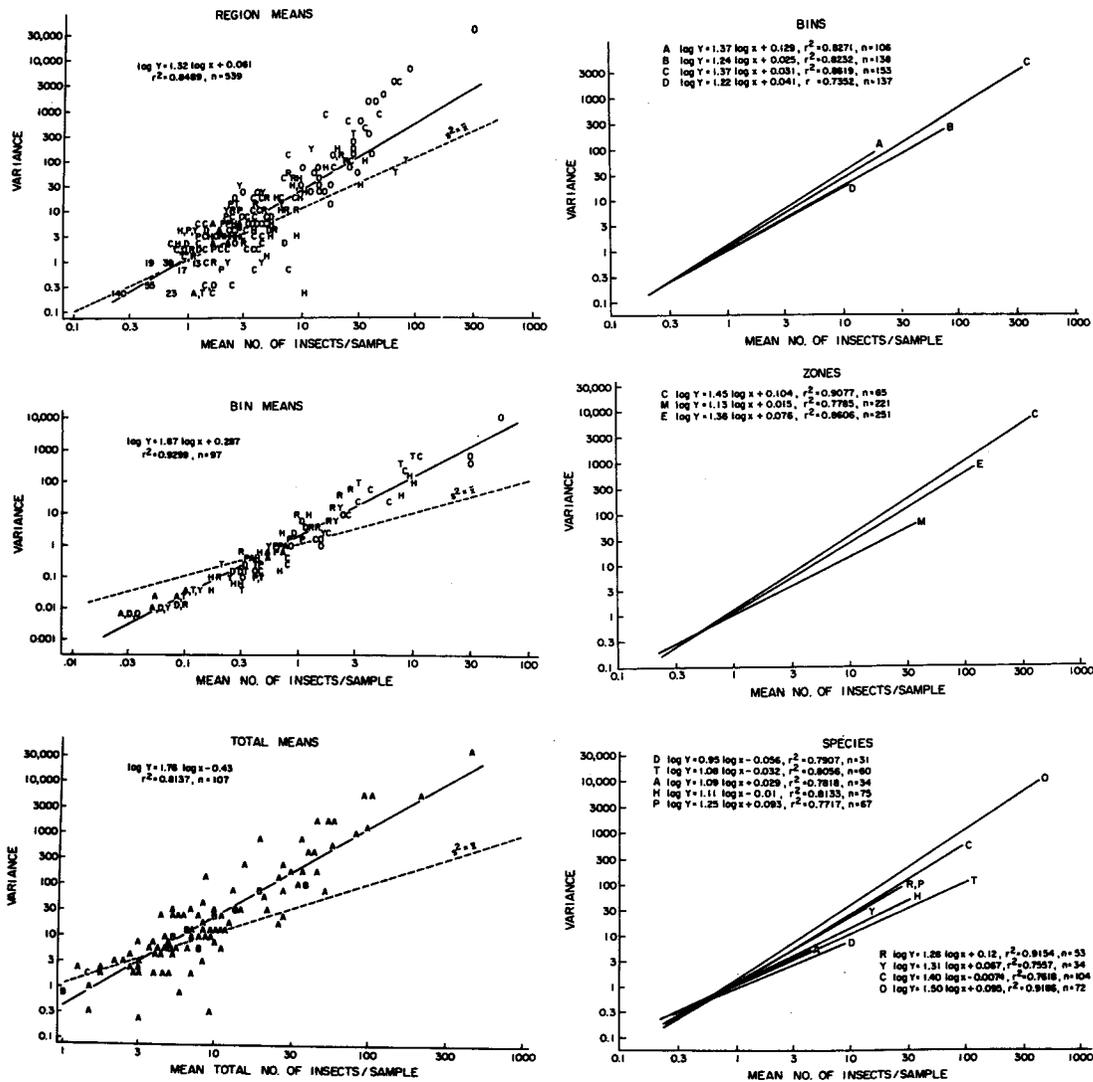


Fig. 1. Regression of logarithm of variance (Y) against logarithm of mean ( $\bar{x}$ ) numbers of insects in samples from bulk-stored wheat. For region or bin means and species, letters on graphs are generally coded by the first letter of genus or order name of species they represent except for *T. glabrum* (D) and *T. stercorea* (Y), but where large numbers of points have the same coordinates, the numbers of points are given. For total means, A, B, and C represent one, two, or three data points at coordinates. The models differed significantly between bins ( $F = 1.12$ ;  $df = 532, 538$ ;  $P < 0.005$ ) zones, ( $F = 10.4$ ;  $df = 534, 538$ ;  $P < 0.005$ ), and species ( $F = 4.6$ ;  $df = 522, 538$ ;  $P < 0.005$ ).

Another 6 of the remaining 26 fit only after being truncated to omit samples with  $>15$  insects per sample. Aggregations of  $>15$  insects per 0.5-kg sample of wheat occurred at only 1.9% of the sites sampled, and 81% of these were in the center, representing one of seven sites.

Another way of characterizing insect distribution patterns is the regression of the logarithm of variance against the logarithm of the mean number of insects per sample. The within-region variances increased more rapidly than the regional means and this relationship varied between bins,

zones, and species (Fig. 1). The scatter of points was reduced and the slope and intercept increased when regional means were used to calculate means and variances for each of three sets of samples from each of the four bins. Ignoring species when calculating regional means and variances also increased the slope, but reduced intercept. These changes in the slopes and intercepts were a consequence of lower variances below 0.3 and 10 insects per 0.5 kg, respectively. The slopes calculated by species and bin were not significantly correlated with  $k$  ( $r^2 = 0.0112$ ,  $n = 26$ ,  $P = 0.61$ ) (Table

Table 4. Variation between species in the fit between observed data and various models

Species	No. of bins fitting distribution							
	Negative binomial	Logarithmic w/zero	Neyman type A	Thomas	Poisson binomial	Poisson w/zero	Poisson	Positive binomial
<i>C. ferrugineus</i>	4	3	4	3	3	1	1	1
<i>T. castaneum</i>	3	3	3	3	3	3	4	3
Hymenoptera	3	3	3	3	1	2	1	1
<i>P. interpunctella</i>	4	4	3	3	3	3	0	0
<i>O. surinamensis</i>	2	2	1	0	0	0	0	0
<i>A. advena</i>	2	2	1	1	1	1	0	1
<i>T. glabrum</i>	2	2	1	1	1	1	0	1
<i>R. dominica</i>	4	3	2	1	1	1	0	0
<i>T. stercorea</i>	2	1	1	1	1	1	1	0
Total	26	23	19	16	14	13	7	7

<sup>a</sup> Slope of the regression of logarithm of variance against logarithm of mean.

4), but both were significantly correlated at the 5% level with means ( $r^2 = 0.2340$  and  $0.1885$ ,  $n = 26$ ,  $P = 0.027$  and  $0.012$ ) (Table 1).

The probability of detecting an infestation equals the fraction of samples with that species present. This increased with density, although progressively more slowly as density increased (Fig. 2). Two models shown in Fig. 2 each fit the data for the nine species in the three concentric zones of each of the four bins. The models indicate that a species was present in 1, 5, 10, 25, 50, 75, and 90% of samples when densities averaged 0.01, 0.05, 0.1,

0.3, 0.9, 2.6, and 5.4 insects per 0.5-kg sample of wheat.

Discussion

A model of the sampling effort required as a function of insect density, sample-to-sample variation and acceptable accuracy or confidence levels is presented in Fig. 3. The numbers of samples required for detection or estimation were inversely related to insect density. Utilization of regional means to calculate bin average at densities below

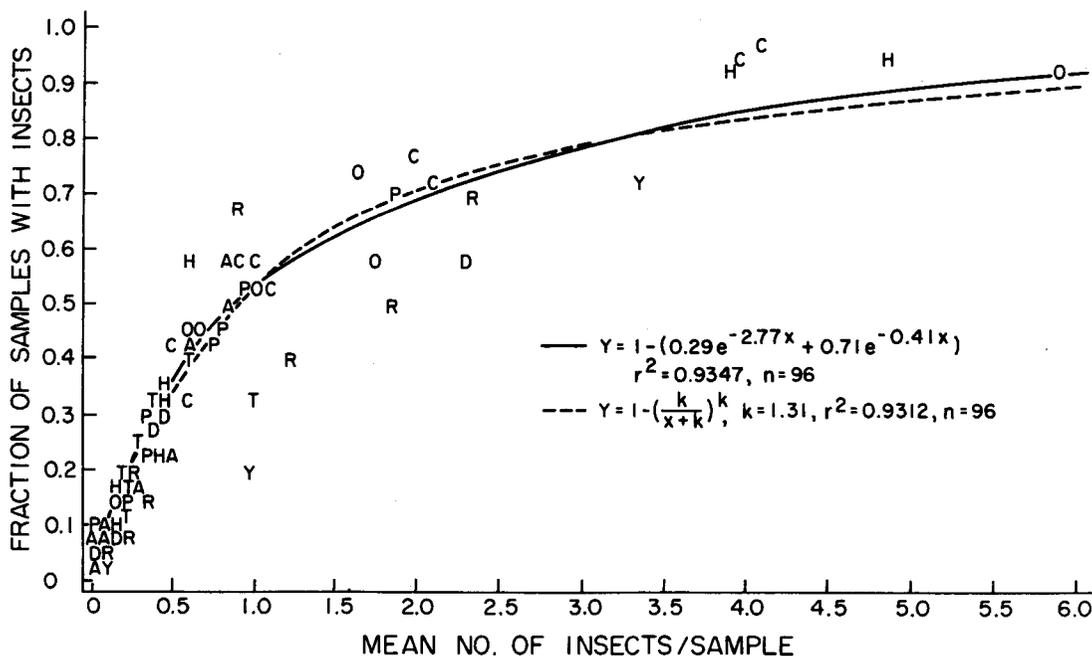


Fig. 2. Increase in fraction of samples from bulk-stored wheat with insects (Y) as a function of the mean number of insects per 0.5-kg sample (x). Letters on graphs are generally coded by the first letter of genus or order name of species, except for *T. glabrum* (D) and *T. stercorea* (Y), and each point represents the mean of samples from one of three zones in one of four bins.

Table 4. Continued

Bin A			Bin B			Bin C			Bin D		
No. of samples	k	Slope <sup>a</sup>	No. of samples	k	Slope <sup>a</sup>	No. of samples	k	Slope <sup>a</sup>	No. of samples	k	Slope <sup>a</sup>
105	1.27	1.69	98	4.29	1.79						
108	0.21	1.36	108	4.21	1.34	102	1.41	1.38	108	5.49	0.91
108	0.29	1.29	108	0.27	1.22	96	1.47	1.16	—	—	—
108	0.65	1.11	108	0.45	1.16	86	3.86	1.30	—	—	—
—	—	—	108	0.45	1.34	108	0.38	1.45	108	1.09	1.05
108	0.71	1.19	108	0.69	0.83	—	—	—	108	0.94	1.50
—	—	—	108	0.30	0.94	—	—	—	—	—	—
108	0.13	1.23	101	0.075	1.41	108	0.50	1.24	—	—	—
—	—	—	—	—	—	108	0.21	1.16	108	0.63	1.34
108	0.39	1.50	108	0.33	0.93	—	—	—	—	—	—

0.3 insects per 0.5 kg of wheat (in practice taking larger samples) or total numbers of insects ignoring species below 10 insects per 0.5 kg of wheat reduced the number of samples needed by reducing the sample-to-sample variation. Equation 4 indicates that sampling more regions also would reduce variation and, thus, the number of samples needed more than increasing the number of samples within a region. The unpredictable distribution of insects among regions also favors sampling more regions and the significant differences among zones favors allocating sampling effort among zones in proportion to their area. More accurate esti-

mates within 10 or 4% of mean can be attained by increasing 4- or 25-fold, respectively, the number of samples suggested in Fig. 3 for 20% accuracy. Decreasing the number of samples 4- to 25-fold will give estimates accurate within 40 or 100% of the mean, respectively. The number of samples required to be 95% confident of detection at specified density dropped off more rapidly than the other curves for estimation of insect density. Detection of infestations above 0.3 insects per 0.5 kg (17 insects per bushel) should require only 11 samples, representing only 0.02% of 900 bushels (24,489 kg) of wheat, roughly the amount stored in the top

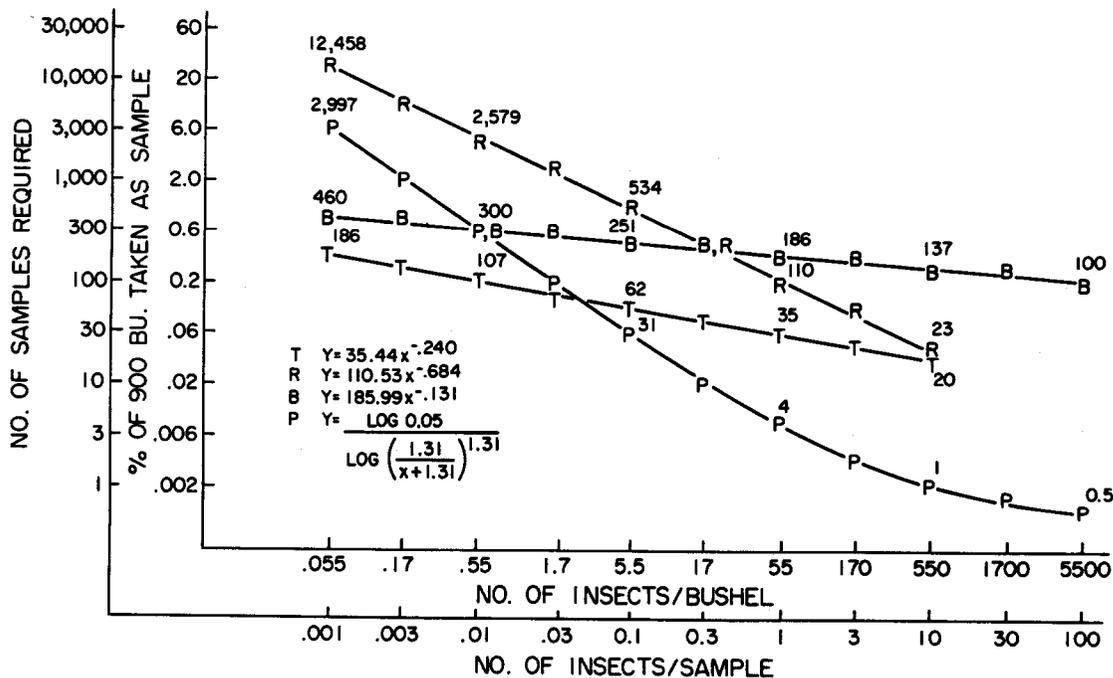


Fig. 3. Model of sampling effort required (Y) for detection or estimation of insects in bulk-stored wheat as a function of the mean number of insects per 0.5-kg sample (x̄). The four curves are based upon bin (B), regional (R), or total (T) mean models from Fig. 1 or the detection model (P) from Fig. 2. The numbers above selected points on each curve represent the number of samples required.

meter of the bins sampled. However, with 10- to 70-fold increase per month population growth rates possible (Howe 1965), wheat must either be sampled often or populations must be discovered at lower densities.

Insect densities can be estimated on the basis of presence or absence (Gerrard and Chiang 1970) by solving for the mean in the equations given in Fig. 2, but such estimates are practical over only a narrow range of densities. At low densities too many samples are required and at high densities the fraction of samples with insects increases progressively more slowly, resulting in poor resolution above one insect per 0.5 kg of wheat. The tendency for the fraction of samples to increase progressively more slowly as density increases may be explained by a purely probabilistic increase in the chance of more than one insect being present in a 0.5-kg sample of wheat. Thus, with the double logarithmic model, the logarithmic increase in the number of samples with insects as a function of increasing density is reduced by the logarithmic increase in the number of samples containing additional insects as density increases. The logarithmic increase in the number of samples with more than one insect also results in the variance increasing faster than the mean. Like the second logarithmic term in the double logarithmic model,  $k$  in the formulation of the 0 term of the negative binomial distribution also makes adjustments for the progressively slower increases in the number of samples with insects as density increases. The  $k$  of 1.31 in Fig. 2 is similar to the mean  $k$  of 1.18 for fitted distributions in Table 4. With the above mechanism, no habitat-selecting behavior is necessary to explain the majority of statistical aggregation, although such behavior may explain the high degree of aggregation at 1.9% of sites omitted in fitting some of the negative binomial distributions.

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