HANDBOOK ON STATISTICS

IN SEED TESTING

Revised version

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CONTENT

1. INTRODUCTION

The qualification of seed lots should be evaluated on the basis of their characteristics which can be examined on small representative samples drawn from them. Data collected on such small samples can then be useful for the entire lot following the application of appropriate mathematical statistical methods. The role of this Handbook on Statistics is to supply the user with basic knowledge enabling seed experts to apply properly the most important statistical procedures. Assuming accordance with sampling and testing prescriptions of the ISTA Rules, this guide presents tools for the adequate inference from the measurements on seed lot properties. In order to obtain practical primary, composite and submitted samples, as well as working samples good enough to represent the lot, recommendations in this Handbook on Seed Sampling should be followed.

The handling of the necessary knowledge is to go out from the principles of probability and statistics and serve to explain the most important probability distributions, sampling procedures and statistical tests. In order to make clear the development of the application of statistical methods in seed testing, a short historical survey stands at disposal.

Application: tolerances for different purposes, heterogeneity and compatibility tests, fixed size, and sequential sampling plans, different statistical methods and tables are presented along with examples for the use of one-sided and two-sided test procedures. The role of the user's choice with respect to the strictness of significance levels to be applied is also explained.

A Glossary of statistical terms is provided.

2. POPULATIONS, SAMPLES AND VARIABLES

A population contains a group of elements (e.g. seeds or data) taken into account in a study.

A sample is a subgroup of elements taken randomly from a population in order to represent it. A good sample for seed testing must be representative of the lot.

A variable is a numerical measurement made on a population member, or a sample member. Variables are of two types: discrete and continuous.

A discrete variable is one which is restricted to a number of admitted values only and involves counting (e.g. the number of germinated seeds in the sample).

A continuous variable is one which can represent any value in a given range and involves measurement (e.g., seed moisture).

The expected value is the mean of a population E(x).

The expected value can be estimated by the mean value of sample data:

$$\bar{x} = \frac{\sum x}{N},$$

where N= the number of sample elements and Σ means sum of the values.

A homogeneous population is one in which seed lot values (quality values) are dispersed around expected value of the population within acceptable limits.

The variance is the most important measure of dispersion around the expected value of the population V(x).

The variance of the lot can be estimated by

$$V = \frac{N\sum x^2 - (\sum x)^2}{N(N-1)}.$$

The standard deviation is also a measure of dispersion around the expected value of population; it is the square root of the variance, SD(x)= $\sqrt{V(x)}$.

The range is another measure of dispersion, indicating the maximum difference between the observed values within the lot.

$$R = x_{max} - x_{min}$$

The above parameters of a lot can be estimated by the measured data from a sample. It should be noted that the estimation of lot parameters on the basis of sample data is not reliable unless the lot is genuinely homogeneous (within acceptable limits). A sample taken from a heterogeneous lot is unlikely to be representative. The probability is low that an estimate based on such a sample will be satisfactory .

3. PROBABILITY DISTRIBUTIONS

A discrete probability distribution for a random variable describes how the probabilities are distributed over the values of the random variable, x.

The probability function f(x) gives the probability for each value of the random variable. It is to be noted that

$$f(x) \geq 0,$$

$$\sum f(x) = 1.$$

The expected value is

$$E(x) = \sum x f(x).$$

The variance is

$$V(x) = \sum [x - E(x)]^2 f(x).$$

4. THE MOST IMPORTANT DISCRETE PROBABILITY DISTRIBUTIONS

4.1. The binomial probability distribution

The binomial distribution can be applied when a population consists of two different types of elements (e.g., healthy and not healthy, germinated and not germinated).

Suppose that the probability of showing a special characteristic of any single member of the population is p and therefore q=(1-p) is the probability of not showing it. It is important that p and q are proportions and not percentages. E.g., for germination, this definition implies that p=0 only when no seeds have germinated, and p=1 only when all seedlings have germinated. The p is constant during an experiment.

Assume a random sample of size n from the whole population and denote with x the number of observations having the special characteristic out of n. In this case x is a discrete random variable with possible values 0, 1, 2, ...n which are not equally likely. The binomial probability function f(x) shows the probability of different x values. The n and p values are characterising parameters of the binomial distribution.

$$f(x) = \binom{n}{x} p^x (1-p)^{n-x} \ .$$

Expected value and variance of the binomial distribution are:

$E(x)=np$, $V(x)=npq$, where $q=1-p$.

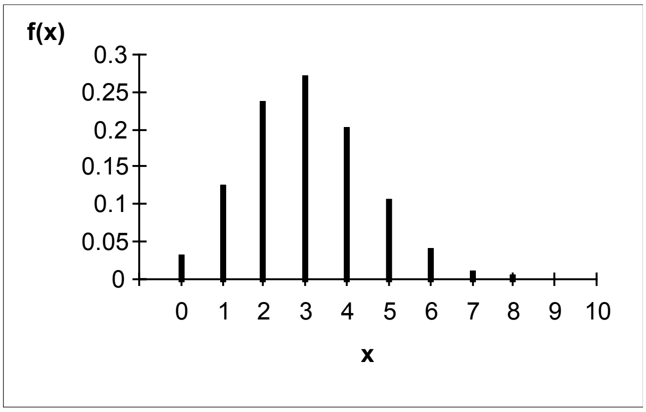

Figure 1

Binomial probability function, n=10 p=0.3.

4.2. The Poisson distribution

The Poisson distribution gets its name after the French mathematician who first studied and applied it. He showed that the Poisson distribution is the marginal case of the binomial distribution when the parameter p tends to zero and simultaneously n tends to infinite. So this distribution can be applied when a population contains only a very small number of members of a special characteristic but a large sample has to be examined, e.g. other seeds by number in a seed lot.

$p \to 0$, $n \to \infty$ and np= constant (denoted with λ).

This distribution is also a discrete one, and gives the probability of x which shows the occurrence of a rare event in a large sample. The possible values of x are 0,1,2,3,4,... (no upper limit).

The probability function f(x) of the parameter λ is given:

$$f(x) = \frac{\lambda^{x}}{x!} e^{-\lambda} \quad \text{where } x = 0,1,2,3...$$

x!=x(x-1)...1 product and e≈ 2.7183.. , is an irrational number which is the base of the natural logarithm. It can be proved that the expected value and the variance both equal λ. This value is the single characterising parameter of the Poisson distribution.

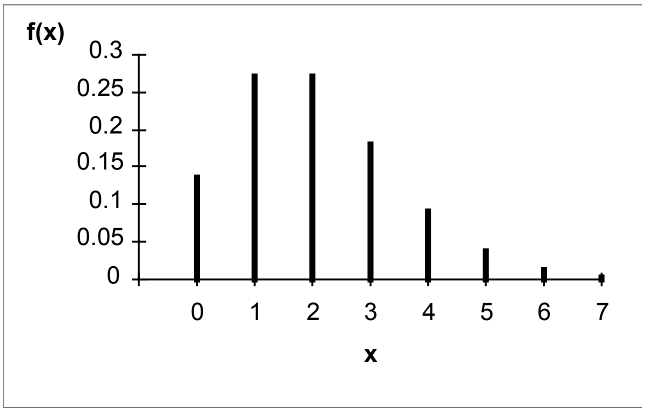

Figure 2

Poisson probability function if λ=2.

5. THE MOST IMPORTANT CONTINUOUS PROBABILITY DISTRIBUTIONS

The difference between the discrete and the continuous random variable is: while the discrete random variable can assume only specific values (usually integers) and involves counting, the continuous random variable may assume any value in one or more intervals. Since there is an infinite number of values in any interval, it is inappropriate to express the probability of the random variable as a specific value, but in terms of the probability that a continuous random variable lies within a specific interval.

In the continuous case, the counterpart of the probability function f(x) is the probability density function, also denoted by f(x). For a continuous random variable, the probability density function provides the probability of the variable of an interval (e.g. $a \leq x < b$) by calculating the area under the graph of f(x) between a and b.

5.1. Normal distribution

The most important continuous distribution is called the normal or Gaussian distribution. (e.g., measured data). The density function of the normal distribution is:

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}$$

where e is the base of natural logarithm, μ is the expected value and σ^2 is the variance of the normal distribution. The graph of f(x) is a bell shaped curve (Figure 3). The μ and the σ are characterising parameters of the normal distribution.

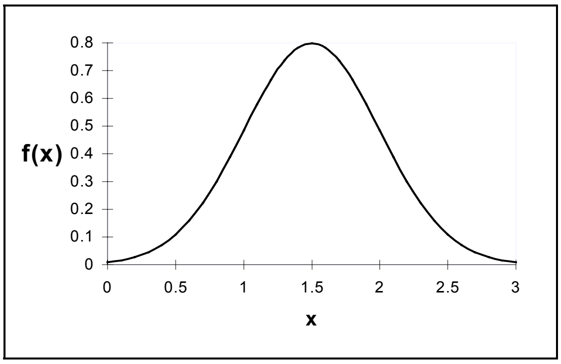

Figure 3

Density function of the normal distribution N(μ=1.5; σ=0.5)

The spread of the curve depends on σ. It is really a probability density function since

$$\int_{-\infty}^{\infty} \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}} dx = 1$$

The probability that x lies between two specified values a and b can be calculated as follows:

$$P(a \le x \le b) = \int_{a}^{b} \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}} dx .$$

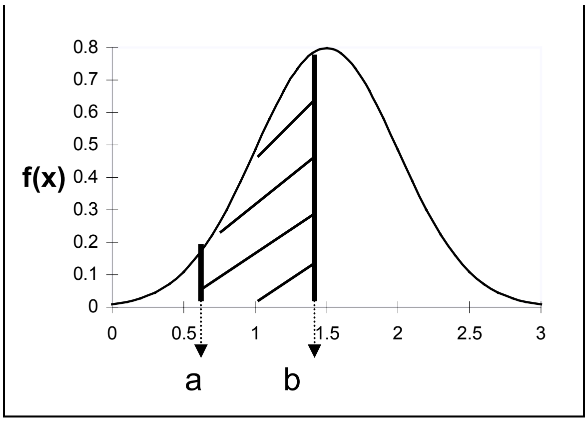

Figure 4

Probability interpretation with normal density curve

A special type of normal distribution is the standard normal distribution in which two parameters are μ=0 and σ=1. The curve of the standard normal distribution is centred at zero. The probability that u (probability variable) lies between -1 and +1 equals 68.26%, between -2 and +2 equals 95.44% and between -3 and +3 equals 99.72%. Which can be obtained from Table I. in Appendix.

Any other normal distribution can be transformed into the standard normal distribution using the following transformation:

$$u = \frac{x - \mu}{\sigma} .$$

5.2. The Student's t-distribution

From independent standard normal random variables new variables would be constructed, which could follow special continuous distributions.

The variable t will be constructed from N+1 standard normal independent random variable of x_1, x_2, ...x_N and y as follows:

$$t = \frac{y\sqrt{N}}{\sqrt{x_1^2 + x_2^2 + ... + x_N^2}} ,$$

this gives a random variable with an expected value of zero and a variance depending on the degree of freedom of N, the number of the elements in the denominator. Appendix Table II. contains the critical values of the t-distribution).

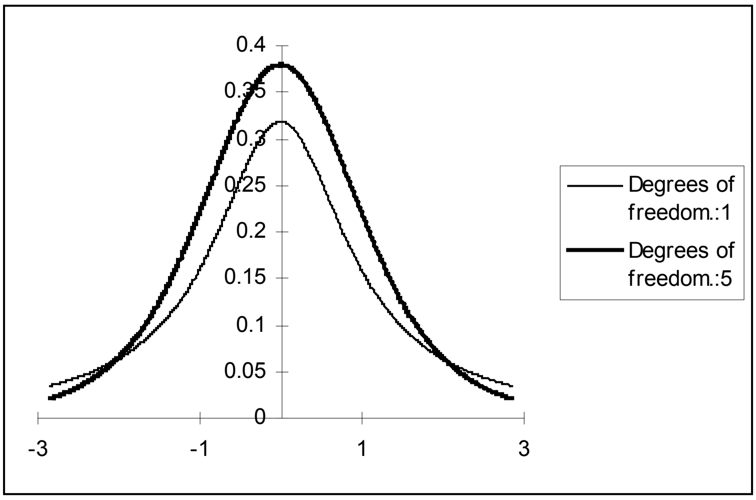

Figure 5
Comparative shapes of the density function of different degrees of freedom of t-distribution

The t-test is based on the t-distribution, by which important practical problems would be solved (see page 19). E.g. whether two samples could originate from the same normally distributed seed lot.

5.3. The χ^2 (chi-squared) distribution

For N standard normal independent random variables expressed as $x_1, x_2, ..., x_N$, a new variable (χ^2) can be constructed INCORPORER as follows:

$$\chi^2 = x_1^2 + x_2^2 + ... + x_N^2$$

with degree of freedom = N . The chi-squared density function range is the set of non-negative numbers, the actual shape of which depends on the number of components (The different values of χ^2 critical values can be found in Appendix Table III.) .

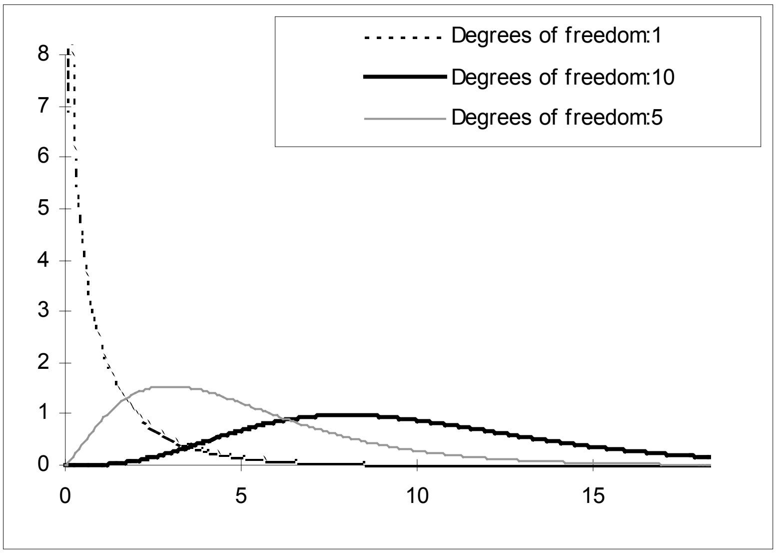

Figure 6

Density function of χ^2 distribution with different degrees of freedom

The χ^2-test is based on the chi-squared distribution (see page 20). This test could be applied to several problems in seed testing, e.g. computation of critical H-values to the heterogeneity H-test.

5.4. The F distribution

For N standard normal independent random variables expressed as X_1, X_2, ...,X_N and M standard normal independent random variables Y_1, Y_2, ...,Y_M, a new variable F can be constructed as follows:

$$F = \frac{\frac{1}{N}(x_1^2 + x_2^2 + \ldots + x_N^2)}{\frac{1}{M}(y_1^2 + y_2^2 + \ldots + y_M^2)},$$

with degrees of freedom N and M. The F (named after Fisher) density function range can be described by the set of non-negative numbers, the actual shape of which depends on the number of components, these critical value of the F can be found in Table IV and in most of other statistical reference books.

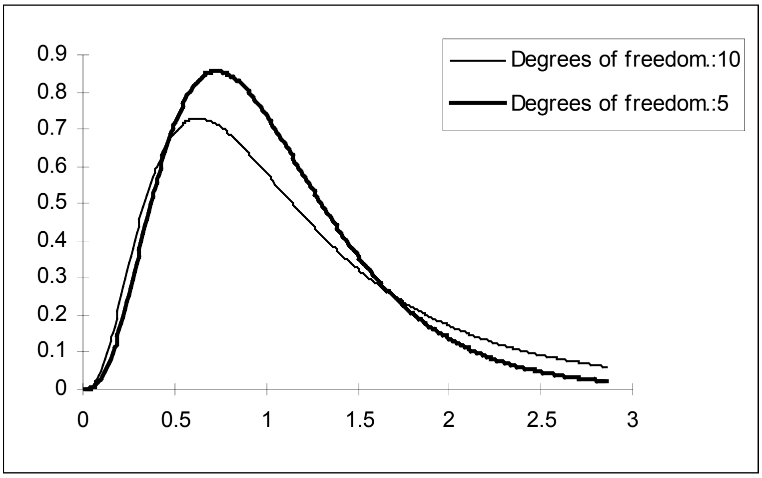

Figure 7

Density function of F-distribution with different degrees of freedom

6. STATISTICAL TESTS

It is often necessary to test hypotheses on population parameters. A statistical hypothesis is an assumption made about some parameter. Such assumptions could be completely verified if the entire population could be examined. However, in most cases, only estimates of the parameters obtained from random samples are available, thus, the assumptions must be tested using such estimates. These tests are called significance tests or hypothesis tests.

The assumption that there are no differences in the parameters is called the null hypothesis and is generally denoted by H_o, while alternatives to the null hypothesis are called alternative hypotheses and is generally denoted by H_1.

If statistical tests are restricted to those involving the normal or the Student's t-distributions, all estimates of the parameters may be assumed to be normally distributed. Such parameters can be standardized using the null hypothesis H_o as:

$$z = \frac{\text{estimate} - \text{null hypothesis parameter}}{\sqrt{\text{variance of the estimate}}},$$

and then z follows either the normal distribution N(0,1) or the t-distribution.

The occurrence of the value z in the tail of the distribution can occur from two different reasons. Either a rare event has occurred or the original null hypothesis was wrong. In statistical testing we conclude that the second of these possibilities is correct, with the added proviso that the probability of our conclusion being wrong is equal to the probability of the rare event mentioned in the first possibility above. This probability fixes the extent of the tail of the distribution by fixing the critical z_c values. If z is outside the critical value it gives a significant result, whereas, the z value inside this critical value gives a non-significant result.

A significant result means that the null hypothesis should be rejected and the alternative hypothesis, be accepted, while a non-significant result means the null hypothesis should not be rejected.

Note: A non-significant result does not mean that the null hypothesis should be rejected. It means only that the counter-evidence is not obtained.

The interval between the critical z_c values is called the confidence interval, the size of which depends on the determined (desired) significance level. At higher significance levels, (e.g., 5%), the confidence interval is smaller than at lower (1%) levels, thus the decision for rejection of the null hypothesis is more rigorous at the higher significance level.

The limits of the confidence interval can be determined by two critical values of z. In this case it is called a two-tailed test (or two-sided test). If only one critical z_c-value is determined as the limit, then it is called a one-tailed test (or one-sided test).The difference between these tests is shown in Figure 8

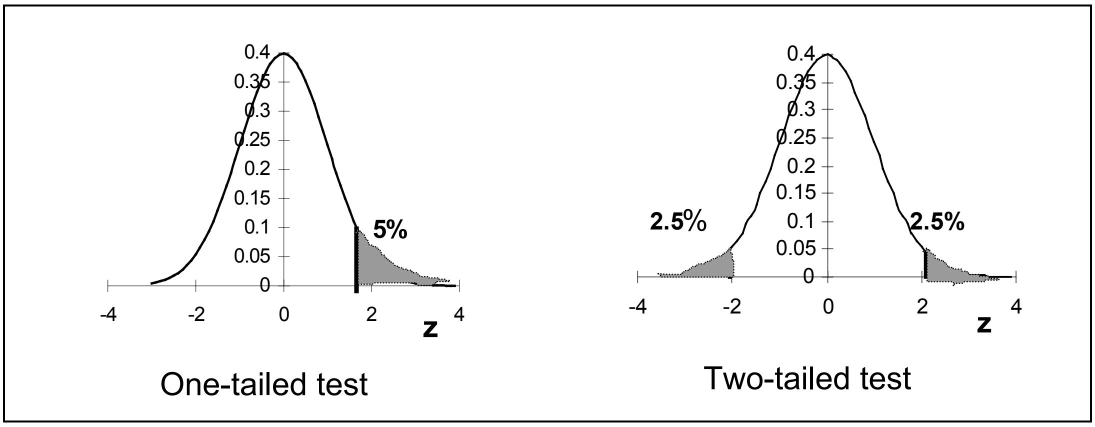

Figure 8.

There are two different cases in seed quality control in which tests of significance should be used.

1. When quality parameters of a seed lot must be determined for labelling purposes.
2. When the labelled parameters are to be controlled by a second test.

In the second case, there are two questions which might need to be answered:

- Is the second test result compatible with the first measurement?
- Does the repeated test give a significantly inferior result than the first test (labelled value)?

In order to check the compatibility of the two test results it is necessary to apply a two-sided significance test.

To control whether the second test gives a significantly inferior result, a one-sided test must be used.

In practice, the difference between the two test results is usually checked. Thus the random variable is the difference (d) between the two measured values:

x_1 = the first estimate (or a given value)

x_2 = the second estimate (control value)

$$\mathbf{d = x_2 - x_1}\ .$$

The null hypothesis is that the expected value of **d** is zero.

$$\mathbf{H_o: E(d) = 0.}$$

After determining the significance level, the critical value $\mathbf{d_c}$ can be computed, e.g., at the 5% significance level, the critical values are:

$\mathbf{d_c} = \mathbf{d_{2.5\%}}$ and $\mathbf{d_{-c}} = \mathbf{d_{-2.5\%}}$ for two sided test,

and $\mathbf{d_c} = \mathbf{d_{5\%}}$ for one sided test.

The critical $\mathbf{d_c}$ values can be found in the tolerance tables.

When **d** is greater than $\mathbf{d_c}$ in the tolerance table based on two-sided test, the two test results should be regarded as incompatible.

When **d** is greater than the $\mathbf{d_c}$ value using a tolerance table based on a one sided test, then the second test result is significantly lower than the first one, i.e., the labelled value cannot be accepted as a true quality characteristic of the controlled seed lot.

7. SPECIAL SIGNIFICANCE TESTS: t- , χ^2 – and F-test

It is often necessary to decide whether the sample could have originated from a normal distribution with the mean μ. Generally the variance is not known. Thus, an estimate s^2 for σ^2 must be calculated from the sample:

$$s^2 = \frac{\sum (x - \bar{x})^2}{N - 1}.$$

By calculating the $t = \frac{\bar{x} - E(X)}{s}\sqrt{N}$

variable which follows the Student' t - distribution. A decision concerning the origin of the sample in question can be made on the basis of a significance test using a t-table (Appendix Table II). Critical t-values depend on the chosen significance level and N-1 degrees of freedom.

In order to check whether two samples would have originated from the same seed lot (normal distribution), the t-test would be used, too.

$$t = \sqrt{\frac{N_1 N_2 (N_1 + N_2 - 2)}{N_1 + N_2}} \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{(N_1 - 1)s_1^2 + (N_2 - 1)s_2^2}},$$

where $\bar{x}_1$ = mean of the first sample

$\bar{x}_2$ = mean of the second sample

s_1^2 = variance of the first sample

s_2^2 = variance of the second sample

N_1 = size of the first sample

N_2 = size of the second sample

For deciding whether a sample could have originated from a normal distribution with variance V(x), another test must be applied, in which case the knowledge of the mean value is not necessary. The construction of a variable

$$\chi^2 = \frac{(N-1)s^2}{V(x)}$$

with (N-1) degree of freedom follows the chi-square distribution. The critical χ^2 – values can be found in Appendix Table III using the desired significance level and (N-1) degrees of freedom.

The F-test can be used for deciding whether two samples could have originated from normal distributions with no significant difference between their variances by constructing the variance ratio:

$$F = \frac{s_1^2}{s_2^2},$$

following the F - distribution.
To compare the variances by the F-distribution it is unnecessary to know the means of the two populations. The numerical F-values are found in the F-table (Appendix Table IV). Since the tabulated F-values are not less than 1, the larger s^2 must be divided by the smaller one. The chosen significance level in that table is 5%, thus the question is whether or not the two variances could be considered as the same. If the calculated F-value is greater than the critical value of F, then the two variances are considered significantly different. Only in 5% of all cases would be F-value be greater than F_{crit} when the variances do not differ significantly.

8. SAMPLING PROCEDURES

8.1. Sampling of fixed size

The quality characteristics of a seed lot should be determined on the basis of samples taken from it. Since the measured data from the sample can be expected to vary randomly, the quality characteristics of the sample cannot be identified with those of the whole lot. If the probability distribution of the sample data is known, then it is possible to make an estimate of the lot characteristics (E.g. when characteristics of a lot have to be checked against a fixed, predetermined level of quality).

The purity and the germination data are known to follow the binomial distribution and the other seed count data follow the Poisson distribution. (Leggatt 1935). The prescribed sample sizes as well as the tolerances in the Rules were computed on the basis of the corresponding distributions.

In the quality control of seed lots two types of error occur:

Error of the first kind (type 1) = rejecting a good lot.

Error of the second kind (type 2)= accepting a bad lot.

The probability of error concerning these two types:

α = probability of type 1 error = producer's risk,

ß = probability of type 2 error = consumer's risk.

A decision about the lot quality on the basis of sample data is essentially a significance test., i.e., a decision concerning a lot quality characteristic or truth-in-labelling decision about a seed lot. Neither the sample size nor the significance level are determined by the user, but are prescribed by the international Rules. **Although an increase in sample size improves the reliability of the decision, the increase is not**

proportional. Furthermore, all deviations from the official prescriptions disturb the comparison.

Most of the prescribed samples are of a fixed size, meaning that the entire sample must be examined before a decision is made.

For the quality control it is important to determine the following requirements:

p_1 = AQL - acceptable quality level

p_2 = LQ - unacceptable quality level (limiting quality).

On the basis of these predetermined parameters the operating characteristic curve (OC-curve) can be drawn (Figure 9). It shows the acceptance probability as a function of the real p level of quality in the lot: AP(p).

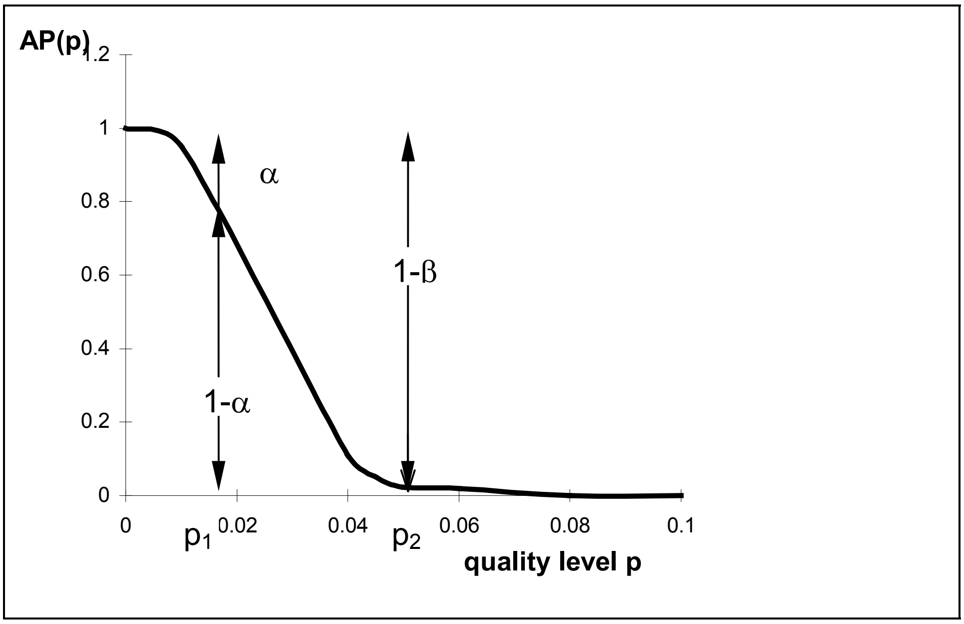

Figure 9

Operating characteristic curve

Each quality control system should be characterised by its OC-curve.

8.2. Sequential sampling

When the quality requirements are predetermined and the task of the quality control is to check for the fulfilment of these, then the sequential sampling method could be applied. It means that the decision concerning acceptance or rejection could be made stepwise. Hereby the whole sample size is not predetermined, but depends on the decision in each former step. The basis of this sampling method is the probability ratio test ; (Wald 1947).

On the basis of the quality requirements the following probabilities could be computed:

$P_1(m,k)$ = the probability that k defects are in the sample, m if $p = p_1$ (acceptable).

$P_2(m,k)$ = the probability that k defects are in the sample, if $p = p_2$ (non acceptable).

The probability ratio test examines the ratio: $\frac{P_2(m,k)}{P_1(m,k)}$

Compering it with the ratios read from the OC-curve:

If $\frac{P_2(m,k)}{P_1(m,k)} \leq \frac{\beta}{1-\alpha}$ acceptance.

If $\frac{P_2(m,k)}{P_1(m,k)} \geq \frac{1-\beta}{\alpha}$ rejection.

If $\frac{\beta}{1-\alpha} < \frac{P_2(m,k)}{P_1(m,k)} < \frac{1-\beta}{\alpha}$ continuation.

On the basis of the predetermined parameters p_1 and p_2, the

A_m acceptance number and the

R_m rejection number can be computed, too.

By using these numbers a table can be compiled for practical application (see example on table below).

Similarly a sequential sampling scheme can be drawn by which the decision in each step could be made. If the point of the test result falls below the lower line, the lot can be accepted as complying with label or with a given requirement. If the point of the test result falls above the upper line, the lot can be rejected as in non-compliance. If the point falls between the two parallel lines, the examination must be continued without a decision. Since this so-called open sequential sampling plan can take too much time, it is possible to compile a truncated or a triangular sequential sampling plan restricted to a predetermined smaller number of steps. The comparison of these sequential sampling plans are shown in Figure 10.

The sequential sampling method can be used only for compliance with predetermined requirements and is not suitable for the estimation of lot quality characteristics.

Example

Sequential sampling plans for quality control of seeds

quality levels chosen p_1=0.01, p_2=0.04, risks chosen α=β=0.05

No.of products tested	open test	$E(p_1)$=160 $E(p_2)$=102	truncated test	m_{max}=400	triangular test	m_{max}=400
m	accep-tance number **A_m**	rejection number **R_m**	accep-tance number **A_m**	rejection number **R_m**	accep-tance number **A_m**	rejection number **R_m**
50	0	3	0	3	0	3
100	1	4	1	4	1	4
150	2	5	2	5	2	5
200	3	6	3	6	3	6
250	4	7	4	7	5	7
300	5	8	5	8	6	7
350	6	9	6	9		
400	7	10	8	9		

In this example examine 50 more seeds at each step if no decision is reached.

At the „open test" it would be happened that no decision could be made after examining the prescribed number of seeds for fixed sample size.

In case of very good or very bad lots, decision could be made on the basis of smaller sample size. At the „truncated" as well as the „triangular" sequential test decision will be made on the basis of smaller sample size on the same probability level. This is the advantage of the sequential sampling method.

8.3. COMPARISON OF SEQUENTIAL SAMPLING SCHEMES

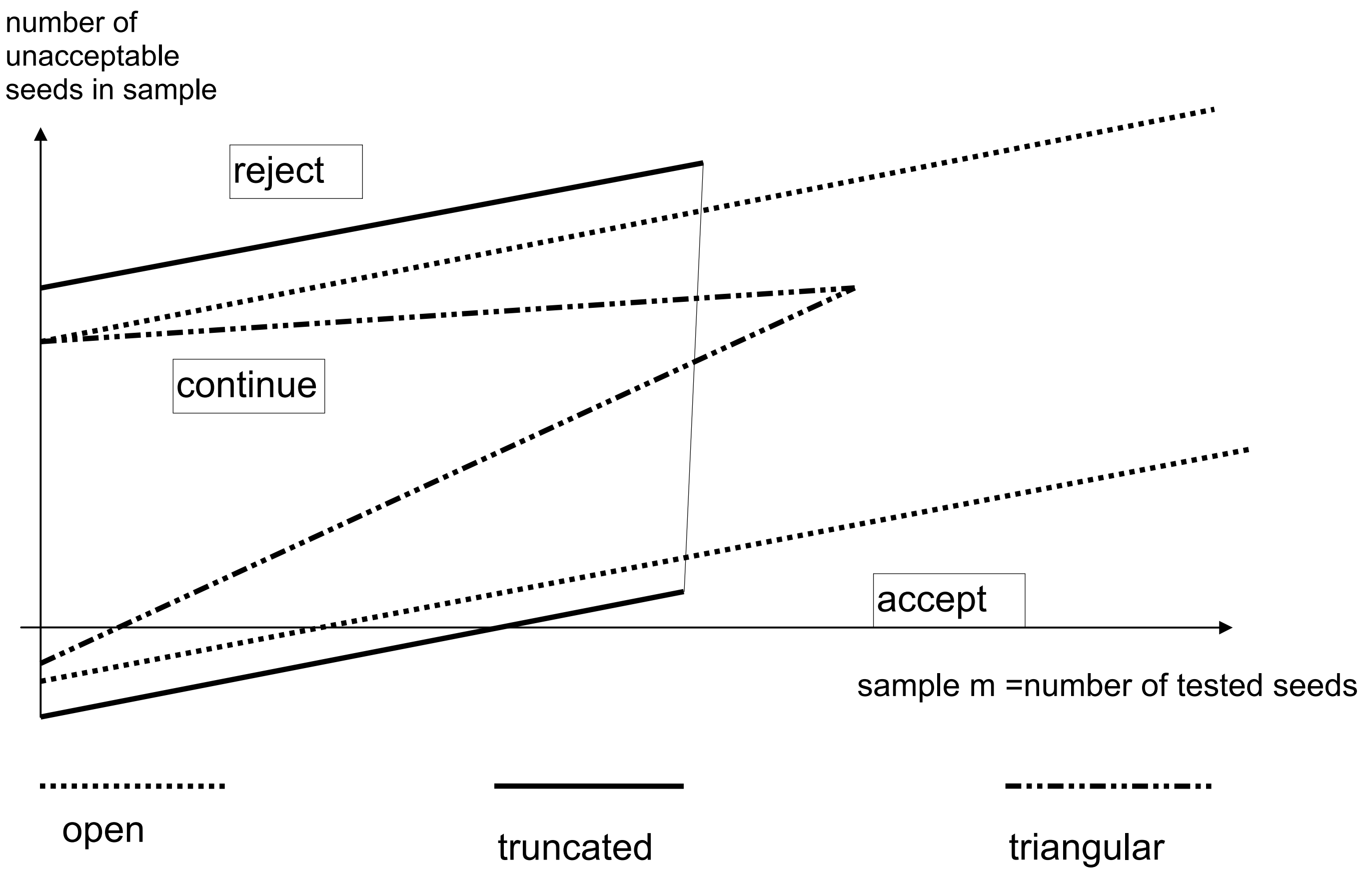

Figure 10

9. DEVELOPMENT OF APPLICATION OF STATISTICAL METHODS IN SEED TESTING

C.W. Leggatt proved on the basis of statistical computations that the purity and the germination data follow the binomial distribution and that foreign seed content (other seed counts) follows the Poisson distribution. His results in the 1930s were derived not only from theoretical computations but also from practical data evaluation. He proposed tolerances for purity, germination and foreign seed testing and, further studies are based on his pioneer work.

The second statistical problem to which Leggatt found a solution, was the heterogeneity of a seed lot. He suggested the relative variability as a measurement of heterogeneity in 1933, derived from the ratio of the observed standard deviation to the theoretical standard deviation (i.e., standard deviation from random sampling). This measurement became the basis of all later heterogeneity tests.

The third statistical method proposed by Leggatt was the sequential sampling procedure for the seed testing in 1949, some years after the first publication of this new procedure by A. Wald.

The ISTA Statistics Committee was established in 1956 in order to develop statistical methods for application to seed testing.

Statistics Committee member, S.R. Miles, developed tolerances for purity, germination and other seed count tests at several significance levels. He has written the Handbook of Tolerances which contained tolerances for seed testing, including both one-sided and two-sided tests. The current tolerances in the ISTA Rules have drawn from tolerances in Miles' Handbook.

Miles suggested two heterogeneity tests. He developed the H-test as a continuation of Leggatt's "relative variability". His test was based on the ratio of the observed variance to the theoretical variance (i.e., random sampling variance). In order to have an expected value of zero for H, if the lot is homogeneous, he constructed the H-value as measurement of heterogeneity:

$$H = \frac{V}{W} - 1 \ ,$$

where **V** is the observed variance and **W** is the theoretical variance.
The H-values should be used to characterise the heterogeneity of seed lot.

J.G. Tattersfield and A. Bould further developed Miles' H heterogeneity test for easier application in the 1970s.

A.Bould computed the critical H-values on the basis of the chi-squared distribution. The ISTA Rules contain these critical H-values for making decisions in seed lot quality control.

The other heterogeneity test suggested by Miles was the "short heterogeneity test", based on the range test, which was rejected by ISTA in 196O. However, a new version of this short heterogeneity test was developed by the Statistics Committee in the 1980s as the R-value heterogeneity test and was accepted in the Rules in 1993.

The Statistics Committee suggested a compatibility test for large compound lots in order to avoid heterogeneity of lots which exceed the maximum lot size limits. This test was accepted as a provisional rule in 1993.

10. PRACTICAL APPLICATION OF STATISTICAL METHODS IN SEED TESTING

10.1. Proper use of tolerance tables

Tolerance tables are used in testing for significance. The "Handbook of Tolerances and of Measures of Precision for Seed Testing" by Miles (1963) was used to establish the tolerances for ISTA Rules. (Tolerances for purity, germination and other seed count) Special explanations are necessary for ISTA Rules concerning the proper use of tolerances. This Handbook on Statistics will attempt to explain the use of tolerances in the ISTA Rules and show some application of the tables in Miles' Handbook of tolerances.

A description of the use of tolerance tables is given under the heading of each table along with examples.

Each table has a certain significance level. It means the probability of error of the first kind. This is the risk of refusing a good lot. A higher significance level gives a more rigorous requirement than a lower one, because it gives a smaller tolerable difference between the two compared values.

For the proper use of a given table it is important to know whether the tolerances are based on one-sided (one-way) or two-sided (two-way) tests. A one-sided test is made to decide if an estimate is significantly lower than a "specification". It may also be made to decide if a "second" estimate is significantly lower than a "first" estimate. A two-sided test is made to decide if one value is significantly different (i.e. either better or worse) from another one, or conversely whether two estimates are compatible.

It should be noted that the denominations „one-way” and „two-way” tests were written by Miles in his 1963 Handbook and similarly in the ISTA Rules. However the authors of this handbook prefer the designations „one-sided” and „two-sided” which are more statistically adequate and more general nowadays .

10.1.1. **Purity tolerances in Table 3.1.**

These tolerances are suitable for comparing purity results on duplicate samples from the same submitted sample analysed by the same laboratory. These can be used for any component of the purity test (pure seeds, inert matter, etc.). Tolerances in this table are based on a two-sided test at the 5% significance level.

This table is used by computing the average of the two test results (columns 1 or 2). The appropriate tolerance is found in one of columns 3 and 4 for half working samples and in one of columns 5 and 6 for whole working samples, depending on whether the seed type is chaffy or non-chaffy.

Examples

1. Purity tests on 2 half working samples from the same submitted sample of *Poa annua* were made in the same laboratory.

The first result: 97.0 %

The second result: 98.6 %

Average: 97.8 %

Difference: 1.6 %

Tolerated diff. 1.54% for chaffy seeds.

Decision: the two results are **not compatible**.

2. Purity tests on two whole working samples from the same submitted sample of *Daucus carota* made in the same laboratory

The first result: 96.30%

The second result: 97.24%

Average: 96.77%

Difference: 0.94%

Tolerated diff. 1.3% for non-chaffy seeds.

Decision: the two results are **compatible**.

10.1.2. Purity tolerances in Tables 3.2. and 3.3.

Tolerances in Table 3.2. can be applied for purity tests on two different submitted samples from the same lot when a second test is made in the same or a different laboratory. These tolerances can be used for any component of a purity test for deciding whether the result of a second test is lower than the first test. The average of the two test results will be compared in columns 1 or 2. The appropriate tolerance is found in columns 3 or 4 depending on whether the seeds are chaffy or non-chaffy.
These tolerances are based on a one-sided test at the 1% significance level, meaning that the control of a seed lot for commercialisation does not require such strictness or rigor as a test conducted for truth-in-labelling determinations. Thus, the aim, in this case is to decrease the risk of refusing good lots.

Tolerances in Table 3.3 are suitable for purity tests on two different submitted samples from the same lot when the first has been used to label a particular seed lot and the second test is made in the same or a different laboratory. These are suitable to decide whether the second estimate is compatible with the label. They can be used for any component of a purity test. The average of the two test results should be found in columns 1 or 2. The appropriate tolerance is found in columns 3 or 4, depending on whether the seeds are chaffy or non-chaffy. These tolerances are based on the two-sided test at a 1% significance level. This table is suitable to compare test results in referee-tests or tests made by different analysts in order to verify the reliability of their work.

Examples

1. Purity tests on two different submitted samples from the same lot of *Dactylis glomerata* made in two different laboratories. The first estimate is the labelled value provided by the seller. The second test is made in the official seed testing

laboratory in order to check on the validity of the labelled value. Table 3.2. should be used.

The first result:	95.0%	
The second result:	93.4%	
Average:	94.2%	
Difference:	1.6%	
Tolerated diff.	2.3%	for chaffy seeds
Decision:	the labelled value can be **accepted**.	

2. Purity tests on two different submitted samples from the same lot of *Medicago sativa* seeds made in the same laboratory for truth-in-labelling purposes. Table 3.3. should be used.

The first result:	97.5%	
The second result:	98.9%	
Average:	98.2%	
Difference:	1.4%	
Tolerated diff.	1.3%	for non-chaffy seeds.
Decision:	the two test results **cannot be accepted** as compatible.	

10.1.3. **Tolerances for other seeds by number in Tables 4.1. and 4.2.**

Tolerances for the determination of other seeds by number when tests are made on the same or a different submitted sample in the same or a different laboratory (Table 4.1) are suitable to decide if a second estimate is compatible with a labelled analysis. Both samples have to be of approximately the same weight. The table is used by selecting the level equal to the average of the two test results in column 1 to find the maximum tolerated difference in column 2. These tolerances are based on a two-sided test at the 5% significance level .

Tolerances for the determination of other seeds by number when tests are made on different submitted samples, the second being made in the same or in a different laboratory (Table 4.2.), are suitable to decide whether the second test result is significantly differ from the labelled value. Both samples are to be of approximately the same weight. The table is used by selecting the average of the two test results in column 1 and the maximum tolerated difference is found in column 2. The tolerances are based on a one-sided test at the 5% significance level.

The use of these tolerances is necessary in all cases in which the result of the control test is poorer than the labelled value. If the result of the control test is better than the labelled value, the guaranteed parameter should be accepted without the need to make a significance test.

The ISTA Rules do not contain tolerance tables for comparing an estimated value of other seed content with a specification. It is possible to use Table 4.2. for such purposes.

It should be understood that tolerances cannot be computed for the presence of prohibited species.

Examples

1. Two samples of the prescribed weight were tested for the determination of other seeds by number on different submitted samples from the same lot in different laboratories. The aim of the examination is to decide, whether the second test results are compatible with the labelled value. Table 4.1. should be used.

The first result:	11 seeds of a particular species
The second result:	26 seeds of the same species
Average:	18.5
Difference:	15
Tolerated diff.	13
Decision:	the two results **cannot be accepted** as compatible.

2. Two samples of the prescribed weight were tested for the determination of other seeds by number on different submitted samples from the same lot. The first estimate was made by the seller and the second test was conducted by an

official seed testing station. The aim of the examination was to check the validity of the labelled value. Table 4.2. should be used.

The first result:	6 seeds of a particular species
The second result:	12 seeds of the same species
Average:	9
Difference:	6
Tolerated diff.	8.
Decision:	the second estimate is not significantly greater than the first, therefore **the labelled value can be accepted**.

3. Two samples of the same weight were examined for the determination of other seeds by number on different submitted samples from the same lot. The first estimate was made by the seller and the second test by the buyer for truth-in-labelling. Table 4.2. should be used.

The first result:	0 seed of a particular species
The second result:	7 seeds of the same species
Average:	3.5
Difference:	7
Tolerated diff.	5.
Decision:	the difference exceeds the tolerance and the second estimate is significantly greater than the first. Thus the **labelled value cannot be accepted**.

4. If, in the previous example the sample for the first estimate contained 7 seeds of a particular species, but the other sample for the verification contained no seeds of the same species. This means that the second result is better than the first, therefore it is not necessary to make a significance test. There is no question about whether, the lot has better quality characteristics than the labelled values. Thus the labelled value could be accepted.

10.1.4. **Germination tolerances in Tables 5.1., 5.2. and 5.3.**

The maximum tolerated range among four 100-seed replicates of a germination test is found in Table 5.1. of the ISTA Rules. This table contains the maximum tolerated differences between the highest and lowest values of the replicates at the 2.5% significance level based on a two-sided test. The table is used by selecting the level equal to the average of the four replicates in column 1 or 2, to find the maximum tolerated range in column 3. The use of this table is suitable for checking homogeneity within a sample. If the calculated range among the four 100-seed replicates in one germination test exceeds the maximum tolerated range, the whole germination procedure should be repeated.

Tolerances in Table 5.2. for germination tests on the same or a different submitted sample from the same lot when the tests are made in the same or a different laboratory on 400 seeds can be used to decide whether results of second test are compatible with the labelled value. These tolerances can be used for percentages of normal seedlings, abnormal seedlings, dead seeds, hard seeds or any combinations of these. The table is applied by selecting the level equal to the average percentage of the two test results (rounded off to the nearest whole number) in columns 1 or 2 of the table. The test results are compatible if the difference between the second estimate and the labelled rate does not exceed the tolerance given in column 3. The tolerances are based on a two-sided test at the 2.5% significance level.

Tolerances in Table 5.3. for germination tests on two different submitted samples from the same lot on 400 seeds in the same or a different laboratory can be applied to decide whether the results of the second test are below the labelled value. The table gives tolerances for percentages of normal seedlings, abnormal seedlings, dead seeds, hard seeds, or any combination of these. This table is used by selecting the average (nearest whole number) of the two test results in column 1 or 2 and the maximum tolerated difference is found in column 3. These tolerances are based on a one-sided test at the 5% significance level. This table is suitable to check the validity of the labelled germination percentage value provided by the seller of the seed lot.

Examples

1. Germination test on four 100-seed sub-samples of *Hordeum vulgare* were made in the same laboratory. The resulting percentage are:

First sub-sample:	82%	
Second sub-sample:	90%	
Third sub-sample:	89%	
Fourth sub-sample:	95%	
Average percentage:	89%	
Maximum difference:	13%	
Tolerated diff.	12%	in Table 5.1.
Decision:	the germination test should be **repeated**.	
Results of the repeated test:		
First sub-sample:	86%	
Second sub-sample:	84%	
Third sub-sample:	92%	
Fourth sub-sample:	84%	
Average of 4 sub-samples:	87%	
Max. diff.	6%	
Tolerated diff.	13%	in Table 5.1.
Average of the two tests:	88%	
Range of two tests:.	2%	
Tolerated diff. of two test results:	5%	in Table 5,2,
Decision:	the two test results are **compatible** on the basis of 8 sub-samples. The test result, based on two tests: 88% can be **accepted**.	

2. Germination tests were made in two different laboratories on two 400-seed samples from different submitted samples from the same lot. The aim of the examination is to decide whether the second estimate is compatible with the first.

The first result: 95%

The second result:	89%	
Average:	92%	
Difference:	6%	
Tolerated diff.	4%	in Table 5.2.
Decision:	the two test results are **not compatible**.	

3. Two germination tests were made in two different laboratories each on 400 seeds from different submitted samples from the same lot. The aim of the examination is to check the validity of the labelled germination value.

The first result:	87%	declared by the seller
The second result	80%	obtained by the customer
Average:	84%	
Difference:	7%	
Tolerated diff.	7%	in Table 5.3.
Decision:	The labelled value **can be accepted**.	

4. Two germination tests were made in two different laboratories on 400 seeds each from different submitted samples taken from the same lot. The aim of the examination is to check the validity of the labelled germination value.

The first result	80%	declared by the seller
The second result	88%	obtained by the customer
Decision:	Since the second result was better than the first. The calculation is unnecessary The labelled germination value **can be accepted**.	

10.1.5. **Germination tolerances for weighted replicates in Table 13.1.**

Table 13.1 in the ISTA Rules contains the maximum tolerated ranges between weighed replicates for germination test. This test is restricted to the small seeded tree species recommended in the Annex to Chapter 13. For these species germination test should be made on a weight of material containing approximately 400 seeds and divided into four equal parts. The normal seedlings in each "replicate" will be counted. The table is used by entering it at a point equal to the sum of the numbers of seeds germinated in the four replicates, the maximum tolerated range will be found in column 2.

Example

Germination test was made on four weighed replicates of *Eucalyptus astringens* seeds. The numbers of germinated seeds found in the replicates (containing approximately 100 seeds) were :

In the first replicate	80	
In the second replicate	60	
In the third replicate	50	
In the fourth replicate	70	
Maximum difference	30	
Sum of seeds germinated in the four replicates	260	
Tolerated difference	34	from Table 13.1.
Decision:	the maximum difference among the four replicates does not exceed the tolerated difference, therefore, the result of germination tests for weighed replicates **can be accepted**.	

The test result is the average of the four replicates: 65% in this case.

10.1.6. Tetrazolium test tolerances in Table 5.1, 6.1,6.2

The main purpose of the tetrazolium test (TEZ) is to distinguish viable and non-viable seeds .

Whether a seed is rated viable or non-viable is derived directly from the importance of the different seed tissues responsible for the emergence and development of a normal seedling, which is species specific. Viable seeds are those that show the potential to produce normal seedlings. Such seeds stain completely, or if only partly stained, the staining patterns indicate that the essential structures are viable. Non-viable seeds are those that do not meet these requirements and in addition include seeds which reveal uncharacteristic coloring and/or flaccid essential structures. Seeds with obviously abnormal development of the embryo or other essential structures shall be regarded as non-viable whether stained or not. Rudimentary embryos of coniferous seeds are non-viable.

Viability, as measured by the tetrazolium test, is a distinct and unique quality characteristic of a resting seed. Viability is clearly independent of realisation in a germination test. However, there will be no significant difference between viability and germination percentages only in the case where a seed:

- is not dormant nor hard-seeded or has been properly pre-treated for breaking dormancy and hard-seededness,
- is not infected or has been properly disinfected,
- has not been sprayed in the field nor dressed during processing or fumigated during storage with harmful chemicals,
- has not sprouted,
- has not been deteriorated during germination tests of normal or extended duration,
- has been germinated under optimal conditions.

Tolerances

The result of a viability test can be relied upon only if the difference between the highest and the lowest replicate is within accepted tolerances. To check the reliability of a test result, the average percentage of the replicates is calculated and compared with Table 5.1 of the Annexe to Chapter 17. The result is considered reliable, if the difference between the highest and the lowest replicate does not exceed the tolerance indicated.

To decide if two tests, which were performed independently in the same laboratory are compatible, Table 6.1 of the Annexe to Chapter 15 is used. When the two tests were performed in different laboratories, Table 6.2 of the Annexe to Chapter 15 is used. For both situations the average percentage viability of the two tests is calculated. The tests are compatible if the difference between the two results does not exceed the tolerance indicated for the calculated average in the respective Table.

Examples

1. Two tetrazolium tests were made in two different laboratories on 400 seeds each from different submitted samples taken from the same lot. The aim of the examination is to check the viability of the seedlot.

The first result (from Lab1)	89% declared by the seller
The second result (from Lab2)	77% obtained by the customer
The calculated avarage	83%
The difference of the two tests	13%
The tolerated difference	12% from **table 6.2**

Decision: The labelled viability value **can not be accepted.**

2. TEZ viability test on four 100-seed sub-samples were made in the same laboratory. The resulting percentage are:

First sub-sample:	84%	
Second sub-sample:	90%	
Third sub-sample:	89%	
Fourth sub-sample:	93%	
Average percentage:	89%	
Maximum difference:	9%	
Tolerated difference	12%	in **Table 5.1**.

Decision: the viability test can be accepted and reported as 89%.

10.2. Heterogeneity tests

A lot submitted for quality control should be homogeneous. This means that there is no significant variation among different parts of the seed lot. A lot can be characterised by one sample value only in this case. The Rules require that sampling be refused if the lot is so heterogeneous that differences between containers or primary samples are visible to the sampler. For doubtful cases, heterogeneity tests may be used (Appendix D in the Rules 1996). The heterogeneity testing enables the detection of heterogeneity which makes the seed lot technically unacceptable.

Heterogeneity of a seed lot can be due to an irregular, though fairly continuous distribution in seed purity, other seed count, or germination characteristics through successive containers of the lot. Such cases are referred to as in-range heterogeneity.

Heterogeneity can also be due to a non-continuous distribution of seed characteristics exceeding reasonable tolerated limits, e.g., in the case of outliers (containers with extremely differing seed quality) or the combining of two or more lots of quite different seed quality without effective blending. Such cases are referred to as off-range heterogeneity.

The H-value heterogeneity test is appropriate for detecting in-range heterogeneity but may indicate the presence of off-range heterogeneity as well. The R-value heterogeneity test is more suitable for checking off-range heterogeneity.

The H-value heterogeneity test was based on the ratio of the observed variance V of independent container-samples to the theoretical variance W computed on the basis of the suitable probability distribution. This test was first suggested by Miles in 1962 for calculating the measure of heterogeneity as follows.

$$H = \frac{V}{W} - 1$$

This method was slightly changed in 2001 due to the work of Michael Kruse based on different calculation and practical investigations.

10.2.1.The H-value test

Definitions of terms and symbols

The testing of predominantly in-range heterogeneity of an attribute adopted as indicator involves a comparison between the observed variance and the acceptable variance of that attribute. The container-samples of a seed lot are samples drawn independently of each other from different containers. The examinations of container-samples for the indicating attribute must also be mutually independent. Since there is only one source of information for each container, heterogeneity within containers is not directly involved. The acceptable variance is calculated by multiplying the theoretical variance caused by random variation with a factor f for additional variation, taking into account the level of heterogeneity which is achievable in good seed production practice. The theoretical variance can be calculated from the respective probability distributions, which is the binomial distribution in the case of purity and germination, and the Poisson distribution in the case of the other seed count.

N_o number of containers in the lot

N number of independent container-samples

n number of seeds tested from each container-sample (1000 for purity, 100 for germination and 10 000 for other seed count, see Rules 3.3.)

X test result of the adopted attribute in a container-sample symbol for sum of all values

f factor for multiplying the theoretical variance to obtain the acceptable variance (see Table D.1.)

$$\overline{X} = \frac{\sum X}{N}$$

mean of all X-values determined for the lot in respect of the adopted attribute

$$W = \frac{\overline{X} \cdot (100 - \overline{X})}{n} \cdot f$$

acceptable variance of independent container-samples in respect of purity or germination percentages

$W = \overline{X} \cdot f$ — acceptable variance of independent container-samples in respect of number of other seeds

$$V = \frac{N\sum X^2 - \left(\sum X\right)^2}{N(N-1)}$$

observed variance of independent container-samples based on all X-values in respect of the adopted attribute

H-value: $H = \frac{V}{W} - f$

Negative H-values are reported as zero

Table D.1. Factors for additional variation in seed lots to be used for calculating W and finally the H-value

Attributes	Non-chaffy seeds	Chaffy seeds
Purity	1.1	1.2
Other seed count	1.4	2.2
Germination	1.1	1.2

Remarks

- For purity and germination calculate to two decimal places if N is less than 10 and to three decimal places if N is 10 or more.
- For the number of other seeds, calculate to one decimal place if N is less than 10, and two decimal places if N is 10 or more.
- For definition of non-chaffy and chaffy seeds see Annex 3.6.A.3 of the ISTA Rules. The chaffiness of various genera is listed in Table 3.2.1.A in the Annex of the ISTA Rules.

Sampling the lot

The number of independent container-samples shall be not less than presented in Table D.2.

Table D.2. Sampling intensity and critical H-values
Number of independent container-samples to be drawn as depending on the number of containers in the lot and critical H-values for seed lot heterogeneity at a significance level of 1% probability.

Number of containers in the lot (No)	Number of independent container-samples (N)	Critical H-value for purity and germination attributes		Critical H-value for other seed count attributes	
		non-chaffy seeds	chaffy seeds	non-chaffy seeds	chaffy seeds
5	5	2.55	2.78	3.25	5.10
6	6	2.22	2.42	2.83	4.44
7	7	1.98	2.17	2.52	3.98
8	8	1.80	1.97	2.30	3.61
9	9	1.66	1.81	2.11	3.32
10	10	1.55	1.69	1.97	3.10
11-15	11	1.45	1.58	1.85	2.90
16-25	15	1.19	1.31	1.51	2.40
26-35	17	1.10	1.20	1.40	2.20
36-49	18	1.07	1.16	1.36	2.13
50 or more	20	0.99	1.09	1.26	2.00

Use of Table D.2 and reporting results

Table D.2 shows the critical H-values which would be exceeded in only 1% of tests from seed lots with an acceptable distribution of the attribute adopted as indicator. If the calculated H-value exceeds the critical H-value belonging to the sample number N, the attribute and the chaffiness in Table D.2, then the lot is considered to show significant heterogeneity in the in-range, or possibly also the off-range sense. If, however, the calculated H-value is less than or equal to the tabulated critical H-value, then the lot is considered to show no heterogeneity in the in-range, or possibly off-range sense with respect to the attribute being tested.

The results of the H-value test shall be reported as follows:

$\overline{X}$, N, No, calculated H-value and the statement that “This H-value does/does not indicate significant heterogeneity”.

If $\overline{X}$ is outside of the following limits, the H-value shall not be calculated or reported:

purity components: above 99.8% or below 0.2%

germination above: 99.0% or below 1.0%

number of specified seeds: below two per sample.

10.2.2. The R-value Test

The object of this test is to detect off-range heterogeneity of the seed lot using the attribute adopted as an indicator. The test for off-range heterogeneity involves comparing the maximum difference found between samples of similar size drawn from the lot with a tolerated range. This tolerated range is based on the acceptable standard deviation, which is achievable in good seed production practice.

Each independent container-sample is taken from a different container, so that heterogeneity within containers is not directly involved. Information about heterogeneity within containers is contained, however, in the acceptable standard deviation which is in fact incorporated into the tabulation of tolerated ranges. The acceptable standard deviation was calculated by the standard deviation due to random variation according to the binomial distribution in the case of purity and germination, and to the Poisson distribution in the case of the other seed count, multiplied by the square root of the factor f given in Table D.1, respectively. The spread between containers is characterised by the calculated range to be compared with the corresponding tolerated range.

Definitions of terms and symbols

N_o number of containers in the lot

N number of independent container-samples

n number of seeds tested from each container-sample (1000 for purity, 100 for germination and 10 000 for other seed count, see 3.3.)

X test result of the adopted attribute in a container-sample

Σ symbol for sum of all values

$\overline{X} = \frac{\sum X}{N}$ mean of all X-values determined for the lot in respect of the adopted attribute

$R = X_{max} - X_{min}$	the range found as maximum difference between independent container samples of the lot in respect of the adopted attribute

Remark: For precision of X for the R-value test see 3.1. 'Remarks' to the H-value test.

Sampling the lot

Sampling for the R-value test is the same as for the H-value test (see 3.2.), the same samples must be used.

Testing procedure

The same testing procedures of purity, germination and the other seed count are used for the R-value test as are used for the H-value test (see 3.3.). For calculations, the same set of data must be used.

Use of tables and reporting of results

Seed lot off-range heterogeneity is tested by using the appropriate table for tolerated, i.e. critical range.

Table **D.3** for components of pure seed analyses,

Table **D.4** for germination determinations and

Table **D.5** for numbers of other seeds.

Find the value $\overline{X}$ in the 'Average' columns of the appropriate table. When entering the table, round averages following the usual procedure; read off the tolerated range which would be exceeded in only 1% of tests from seed lots with an acceptable distribution of the attribute

in Column 5-9 for cases when N = 5 to 9,

in Column 10-19 for cases when N = 10 to 19, or

in Column 20 when N = 20.

If the calculated R-value exceeds this tolerated range, then the lot is considered to show significant heterogeneity in the off-range sense. If, however, the calculated R-value is less than or equal to the tabulated tolerated range, then the lot is considered to show no heterogeneity in the off-range sense with respect to the attribute being tested.

The results of the R-value test must be reported as follows:

$\overline{X}$, N, N_o, calculated R-value and the statement that "This R-value does/does not indicate significant heterogeneity".

When using the tables, round averages to the next tabulated value (if in the middle, then downwards).

Interpretation of results

Whenever either of the two tests, the H-value test or the R-value test, indicates significant heterogeneity, then the lot must be declared heterogeneous. When, however, neither of the two tests indicates significant heterogeneity, then the lot must be adopted as non-heterogeneous, having a non-significant level of heterogeneity.

The R-value heterogeneity test was originally a new version of the Miles' "short heterogeneity test". It was suggested by the Statistics Committee and accepted by ISTA in 1993 and modified by the Congress in 2001.

Examples

1. A seed lot containing 40 bags of non-chaffy seeds was tested for germination heterogeneity. According to the specified sampling intensity N=18 bags were sampled and the appropriate attribute (germination) independently tested on 100-seed samples simultaneously. The average of the 18 values was $\overline{X}$ = 80. The theoretical variance was W = 16·f. The observed variance was V = 40. From Table D.1. we can find f=1.1 in case of germination of non-chaffy seeds.

The computed H-value: H = (40:17.6) –1.1 = 1.17. Since this value **exceeds** 1.07, the critical H-value in Table D.2., the lot must be declared **heterogeneous** even if the R-value test did not indicate significant heterogeneity.

2. A seed lot containing 50 bags of chaffy seeds was tested for number of other seeds heterogeneity. The sampling intensity was N=20 and other seed count was chosen for calculating heterogeneity. The average of 20 values was $\overline{X}$= 32. The theoretical variance is W = 32·f according to the Poisson distribution. The observed variance was V = 82. From Table D.1. we can find

f=2.2 in case of number of other seeds of a chaffy seedlot. The computed H-value:

H = (82:70.4) – 2.2 = -1.035. This H-value reported as H=0 and **does not exceed** 2.00, the critical H-value in Table D.2 meaning that the H-test **does not indicate significant heterogeneity**. Nevertheless the computed R-value was R = 58 because of an outlier value in one of the samples. Since 58 exceeds 54 the critical R-value in Table D.5.B, the R-test indicates significant heterogeneity. Therefore the lot must be declared **heterogeneous**.

3. A seed lot containing 25 bags of chaffy seeds was tested for purity heterogeneity. The sampling intensity was N=15 and purity was chosen for calculating heterogeneity. The obtained purity % are as follows X: 98.50 98.60 98.70 98.80 98.60 98.70 98.60 98.80 98.70 98.80 98.70 98.70 95.00 98.60 98.80

The average of 15 values was $\overline{X}$ = 98.44. The number of seeds in one sample n=1000 the theoretical variance is W=0.18· according to the Poisson distribution and f=1.2 (from Table D.1). The observed variance was V =0.91.. The computed H-value:

$H = \frac{V}{W} - f$ = 3.76. This H-value reported as H=3.76 which is **exceed** 1.31, the critical H-value in Table D.2. That means the H-test **indicate significant heterogeneity**. The computed R-value was R = 3.8 because of an outlier value 95.00. Since 3.8 exceeds 2.2 the critical R-value in Table D.3.B, the R-test also indicates significant heterogeneity. Therefore the lot must be declared **heterogeneous**.

It is possible to choose any seed characteristic for use in detecting heterogeneity. It is not necessary to test all the three main characteristics. Thus, the choice of seed property for use in calculating heterogeneity depends on practical viewpoints.

10.3. Compatibility test

Heterogeneity tests are suitable for use in detecting heterogeneity but can not eliminate it. A new test has been suggested by the Statistics Committee in order to avoid heterogeneity of compound lots since much lot heterogeneity may originate by combining seed lots of very different quality. Since there is no restriction concerning the mixing of seed lots, the blending of lots of widely different quality characteristics often occurs in the seed trade. Since the mixing procedures may not be perfect and since the lots may be combined without blending, the risk of subsequent heterogeneity is increased.

The new compatibility test is based on reverse of the R-value heterogeneity test. The main questions of the compatibility test are as follows:

- Can the quality characteristics of all the N component lots be considered as elements of the same approximately normally-distributed population?
- If the N components do not all belong to the same population could these be split into clusters or sub-populations?

If the three most important quality characteristics, purity, germination and other seed content, are determined separately, the null hypothesis of the first question is:

Ho: $E(x_1) = E(x_2) = ... = E(x_N)$.

This means that the expected values of the observed data for the seed characteristic in question are equal. Similarly, it should be assumed that the variances are also equal:

$V(x_1) = V(x_2) = ... = V(x_N)$.

When a particular quality characteristic can be assumed to belong to the same population, then the small lots to be combined can be considered as sub-populations of the possible compound lot. Thus the heterogeneity of the future lot can be examined by the R-test.

The main question of the compatibility test as a "converse heterogeneity test" is:
What is the maximum tolerated difference between each of the quality characteristics which does not make the compound lot heterogeneous?

For practical use the critical R values have been tabulated at the 1% significance level for all three quality parameters (Tables B1, B2 and B3 in Appendix B of the 1999 Rules). These tables allow decisions about the compatibility of the N small lots to be combined.

If $R = x_{max} - x_{min}$ does not exceed the tolerated R value found in the adequate table in column N, then the N lots can be mixed. If R exceeds the tolerated R value then combining is not permitted.

For checking compatibility it is necessary to test <u>the three quality characteristics</u> (germination, purity and other seed content). The decision for combining is only possible if compatibility for all properties can be proved. In cases when the compatibility of all the N lots can not be demonstrated, a <u>grouping method</u> could be applied in order to find a stepwise way to optimize lot groups. The test procedure begins with ordering the component lots into the sequence of one selected seed property (e.g., germination). Then the first lot should be taken in the order to add the second, third, etc., as long as the R-test does not indicate significant heterogeneity in any property. Thus, an acceptable homogeneous group of seed lots is obtained. All possible "next groups" begin with the component lot after the foregoing group (i.e., compound lot) has been finished.

The compatibility test has been accepted by the ISTA as a "Provisional Rule" for the issue of ISTA seed lot certificates on Herbage and Amenity seed lots exceeding the maximum lot size in Table 2 being transported loose in bulk containers. The description of the test as well as the proper use of the tolerance tables containing the critical R-values for all the three main seed properties can be found in Appendix B in the 1996 Rules. The tables are used by entering the straight average in "The average of all lots" column. The maximum tolerated value of R can be found in column N for the number of lots involved. Decisions can be made on the basis of whether or not the computed R-value exceeds the tolerated critical R-value.

Examples

1. Number of component lots $N = 4$

   Average of purity results $\bar{x} = 96\%$

   Range of results $R = x_{max} - x_{min} = 1.5\%$

   Tolerated range in **Table B1**. $R = 1.7\%$

Since R does not exceed the tolerated range, the **lots are compatible** from the aspect of purity percentages.

   Average of germination results $\bar{x} = 90\%$

   Range of results $R = x_{max} - x_{min} = 5\%$

   Tolerated range in **Table B2**. $R = 7\%$

Since R does not exceed the tolerated range, the **lots are compatible** from the aspect of germination percentages.

   Average of other seed counts $\bar{x} = 8$

   Range of results $R = x_{max} - x_{min} = 16$

   Tolerated range in **Table B3**. $R = 12$

Since R exceeds the tolerated range, the **4 lots are not compatible** with respect to other seed counts. Therefore the 4 lots **cannot be combined** to form a compound lot.

In using the tables it is not necessary to repeat all tests on quality characteristics when the important data exists as labelled values of the component lots.

2. Number of component lots: $N=4$

   Purity results: 96.8%; 95.7%; 96.3%; 95.2%

   Average of purity results $\bar{x} = 96\%$

   Range of results $R= 1.6\%$

   Tolerated range in **Table B1** $R= 1.7\%$

The lots **are compatible** from the aspect of purity..

Germination results:	93%; 89%; 91%; 87%
Average of germination results	$\bar{x}$ = 90%
Range of results	R= 6%
Tolerated range in **Table B2**	R= 7%

The lots **are compatible** from the aspect of germination.

Other seed counts results:	4; 10; 6; 12
Average of other seed counts	$\bar{x}$ = 8
Range of results	R= 8
Tolerated range in **Table B3**	R= 12

The lots **are compatible** from the aspect of other seed counts. Therefore the 4 lots **can be unified**.

11. GLOSSARY

Accepted number of other seeds in a sample

the maximum tolerated value for other seed count in the prescribed sample or sub-sample

Acceptable quality level (AQL)

a small ratio of defects which is still acceptable

Acceptance probability (AP)

the probability as function of the real ratio of defects (see OC-curve)

Alternative hypothesis (H_1)

opposing hypothesis against the null-hypothesis

Arithmetic mean ($\overline{X}$)

straight mean i.e., sum of the N values divided by N

Attribute

qualitative property (e.g., percent germination)

Average

synonym of arithmetic mean

Binomial distribution

discrete distribution with parameters n and p

Bulk lot

large seed lot in heap (or in large storage bin)

Chi-squared distribution

a type of continuous distribution based on the sum of N squared standard normal distributed random variables

Compound lot

seed lot formed by combining two or more component lots

Confidence interval

interval which contains the true value of the attribute in question with high probability (e.g.95% or 99%)

Consumer's risk

probability of the acceptance of a bad lot (type 2 error)

Continuous distribution

probability distribution of a continuous random variable

Continuous random variable

random variable which can take any value in a continuous finite or infinite interval

Control test

examination to check the validity of a given (labelled) value

Critical value

a given value for decision making in a control test

Degrees of freedom

number of independent comparisons in the test procedure

Density function

a function which gives the probability of occurrence of a continuous random variable in any interval by the area over the interval in question

Discrete distribution

probability distribution of a discrete random variable

Discrete random variable

random variable which can take only a finite number or countable infinite number of values

Distribution function

cumulative distribution of a probability distribution

Error of first kind

type 1 error i.e., a good lot has been refused

Error of second kind

type 2 error i.e., a bad lot has been accepted

Estimate

value of a lot parameter determined on the basis of a sample taken out from the lot

Expected value

the mean value of a population; an estimation of the expected value can be made by the mean value of sample data

F-distribution

a type of continuous distribution based on the ratio of two chi-squared distributed random variables

F-test

significance test based on the F-distribution, it is suitable to check on variances of two normal distributed populations, whether these differ significantly from each other

Gaussian distribution

normal distribution for continuous variables

Heterogeneity test (H)

test to detect in-range heterogeneity based on the chi-square test

Heterogeneity test (R)

test to detect off-range heterogeneity based on the range-test

Limiting quality level (LQ)

ratio of defects which is not acceptable

Median value

central value in an ordered series of values

Modal value (mode)

value which occurs at the highest frequency

Normal distribution (Gaussian distribution)

a type of continuous probability distribution with bell-shaped density function

One-sided test (one-way test)

test for decision whether the second test gives a poorer result than the first

Operating characteristic curve (OC-curve)

curve of the acceptance probability function

Outlier

extreme value in a data series

Parameter

quality characteristic of a population

Poisson distribution

a type of discrete distribution with parameter λ (as expected value and variance)

Primary sample

the first sample to be taken out from the lot

Primary sampling intensity

number of primary samples prescribed by the Rules

Producer's risk

probability of the rejection of a good lot (type 1 error)

Prohibited species

seed species which are not permitted in the lot (e.g. noxious weed seed)

Random

chosen entirely by chance, with no personal influence

Range

difference between the maximum and minimum values in a data series

Reject number of other seeds in a sample

a number large enough to lead to the decision that a lot has more other seeds of the species in question than stated by a specification or a first estimate

Restricted species

non-prohibited species for which a maximum number of seeds in the sample or in kg is specified

Sample size (fixed)

prescribed magnitude of sample; it can be determined by weight (for purity) or by number of seed to be tested (for germination)

Sequential sampling method

test procedure in which decision on acceptance or rejection can be made stepwise on the basis of sub-samples

Standard deviation

a measure of dispersion, it is the positive square root of variance

Standard normal distribution

special type of the normal distribution if μ=0 and σ=1

Submitted sample (laboratory sample)

sample of specified size taken out from the composite sample of primary samples to be sent to laboratory for testing

t-distribution

continuous distribution constructed by N+1 independent standard normal random variables

t-test

significance test based on the t-distribution

Tolerance

the greatest non-significant difference between two values; these can be two estimates or a specification and an estimate

Two-sided test (two-way test)

test for decision whether or not two values are compatible

Working sample

sample of prescribed size taken from the submitted sample in order to examine any attribute of seed

Zero species

restricted species for which the first estimate shows zero seed

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13. APPENDIX I

STATISTICAL TABLES

Density function of the standard normal distribution $\varphi(u)$

TABLE I

u	0.00	0.01	0.02	0.03	0.04	0.05	0.06	0.07	0.08	0.09
0	0.39894	0.39892	0.39886	0.39876	0.39862	0.39844	0.39822	0.39797	0.39767	0.39733
0.1	0.39695	0.39654	0.39608	0.39559	0.39505	0.39448	0.39387	0.39322	0.39253	0.39181
0.2	0.39104	0.39024	0.3894	0.38853	0.38762	0.38667	0.38568	0.38466	0.38361	0.38251
0.3	0.38139	0.38023	0.37903	0.3778	0.37654	0.37524	0.37391	0.37255	0.37115	0.36973
0.4	0.36827	0.36678	0.36526	0.36371	0.36213	0.36053	0.35889	0.35723	0.35553	0.35381
0.5	0.35207	0.35029	0.34849	0.34667	0.34482	0.34294	0.34105	0.33912	0.33718	0.33521
0.6	0.33322	0.33121	0.32918	0.32713	0.32506	0.32297	0.32086	0.31874	0.31659	0.31443
0.7	0.31225	0.31006	0.30785	0.30563	0.30339	0.30114	0.29887	0.29659	0.29431	0.292
0.8	0.28969	0.28737	0.28504	0.28269	0.28034	0.27798	0.27562	0.27324	0.27086	0.26848
0.9	0.26609	0.26369	0.26129	0.25888	0.25647	0.25406	0.25164	0.24923	0.24681	0.24439
1	0.24197	0.23955	0.23713	0.23471	0.2323	0.22988	0.22747	0.22506	0.22265	0.22025
1.1	0.21785	0.21546	0.21307	0.21069	0.20831	0.20594	0.20357	0.20121	0.19886	0.19652
1.2	0.19419	0.19186	0.18954	0.18724	0.18494	0.18265	0.18037	0.1781	0.17585	0.1736
1.3	0.17137	0.16915	0.16694	0.16474	0.16256	0.16038	0.15822	0.15608	0.15395	0.15183
1.4	0.14973	0.14764	0.14556	0.1435	0.14146	0.13943	0.13742	0.13542	0.13344	0.13147
1.5	0.12952	0.12758	0.12566	0.12376	0.12188	0.12001	0.11816	0.11632	0.1145	0.1127
1.6	0.11092	0.10915	0.10741	0.10567	0.10396	0.10226	0.10059	0.09893	0.09728	0.09566
1.7	0.09405	0.09246	0.09089	0.08933	0.0878	0.08628	0.08478	0.08329	0.08183	0.08038
1.8	0.07895	0.07754	0.07614	0.07477	0.07341	0.07206	0.07074	0.06943	0.06814	0.06687
1.9	0.06562	0.06438	0.06316	0.06195	0.06077	0.05959	0.05844	0.0573	0.05618	0.05508
2	0.05399	0.05292	0.05186	0.05082	0.0498	0.04879	0.0478	0.04682	0.04586	0.04491
2.1	0.04398	0.04307	0.04217	0.04128	0.04041	0.03955	0.03871	0.03788	0.03706	0.03626
2.2	0.03547	0.0347	0.03394	0.03319	0.03246	0.03174	0.03103	0.03034	0.02965	0.02898
2.3	0.02833	0.02768	0.02705	0.02643	0.02582	0.02522	0.02463	0.02406	0.02349	0.02294
2.4	0.02239	0.02186	0.02134	0.02083	0.02033	0.01984	0.01936	0.01888	0.01842	0.01797
2.5	0.01753	0.01709	0.01667	0.01625	0.01585	0.01545	0.01506	0.01468	0.01431	0.01394
2.6	0.01358	0.01323	0.01289	0.01256	0.01223	0.01191	0.0116	0.0113	0.011	0.01071
2.7	0.01042	0.01014	0.00987	0.00961	0.00935	0.00909	0.00885	0.00861	0.00837	0.00814
2.8	0.00792	0.0077	0.00748	0.00727	0.00707	0.00687	0.00668	0.00649	0.00631	0.00613
2.9	0.00595	0.00578	0.00562	0.00545	0.0053	0.00514	0.00499	0.00485	0.0047	0.00457
3	0.00443	0.0043	0.00417	0.00405	0.00393	0.00381	0.0037	0.00358	0.00348	0.00337

$$\varphi(-u) = \varphi(u)$$

Critical values of t- distribution $P(t< t_p)=p$ **TABLE II**

	p									
DF	**0.60**	**0.70**	**0.75**	**0.80**	**0.85**	**0.90**	**0.95**	**0.975**	**0.99**	**0.995**
1	0.325	0.727	1.000	1.376	1.963	3.078	6.314	12.706	31.821	63.657
2	0.289	0.617	0.816	1.061	1.386	1.886	2.920	4.303	6.965	9.925
3	0.277	0.584	0.765	0.978	1.250	1.638	2.353	3.182	4.541	5.841
4	0.271	0.569	0.741	0.941	1.190	1.533	2.132	2.776	3.747	4.604
5	0.267	0.559	0.727	0.920	1.156	1.476	2.015	2.571	3.365	4.032
6	0.265	0.553	0.718	0.906	1.134	1.440	1.943	2.447	3.143	3.707
7	0.263	0.549	0.711	0.896	1.119	1.415	1.895	2.365	2.998	3.499
8	0.262	0.546	0.706	0.889	1.108	1.397	1.860	2.306	2.896	3.355
9	0.261	0.543	0.703	0.883	1.100	1.383	1.833	2.262	2.821	3.250
10	0.260	0.542	0.700	0.879	1.093	1.372	1.812	2.228	2.764	3.169
11	0.260	0.540	0.697	0.876	1.088	1.363	1.796	2.201	2.718	3.106
12	0.259	0.539	0.695	0.873	1.083	1.356	1.782	2.179	2.681	3.055
13	0.259	0.538	0.694	0.870	1.079	1.350	1.771	2.160	2.650	3.012
14	0.258	0.537	0.692	0.868	1.076	1.345	1.761	2.145	2.624	2.977
15	0.258	0.536	0.691	0.866	1.074	1.341	1.753	2.131	2.602	2.947
16	0.258	0.535	0.690	0.865	1.071	1.337	1.746	2.120	2.583	2.921
17	0.257	0.534	0.688	0.863	1.069	1.333	1.740	2.110	2.567	2.898
18	0.257	0.534	0.688	0.862	1.067	1.330	1.734	2.101	2.552	2.878
19	0.257	0.533	0.688	0.861	1.066	1.328	1.729	2.093	2.539	2.861
20	0.257	0.533	0.687	0.860	1.064	1.325	1.725	2.086	2.528	2.845
21	0.257	0.532	0.686	0.859	1.063	1.323	1.721	2.080	2.518	2.831
22	0.256	0.532	0.685	0.858	1.061	1.321	1.717	2.074	2.508	2.819
23	0.256	0.532	0.685	0.858	1.060	1.319	1.714	2.069	2.500	2.807
24	0.256	0.531	0.685	0.857	1.059	1.318	1.711	2.064	2.492	2.797
25	0.256	0.531	0.684	0.856	1.058	1.316	1.708	2.060	2.485	2.787
30	0.256	0.530	0.683	0.854	1.055	1.310	1.697	2.042	2.457	2.750
40	0.255	0.529	0.681	0.851	1.050	1.303	1.684	2.021	2.423	2.704
60	0.254	0.527	0.679	0.848	1.046	1.296	1.671	2.000	2.390	2.660
120	0.254	0.526	0.677	0.845	1.041	1.289	1.658	1.980	2.358	2.617
>120	0.253	0.524	0.674	0.842	1.036	1.282	1.645	1.960	2.326	2.576

Critical value of chi-square distribution **TABLE III**

$P(\chi^2 < \chi_p^2) = p$

	p										
DF	**0.005**	**0.01**	**0.025**	**0.05**	**0.1**	**0.25**	**0.5**	**0.75**	**0.9**	**0.95**	**0.975**
1	0	0.0002	0.001	0.0039	0.0158	0.1015	0.4549	1.3233	2.7055	3.8415	5.0239
2	0.01	0.0201	0.0506	0.1026	0.2107	0.5754	1.3863	2.7726	4.6052	5.9915	7.3778
3	0.0717	0.1148	0.2158	0.3518	0.5844	1.2125	2.366	4.1083	6.2514	7.8147	9.3484
4	0.207	0.2971	0.4844	0.7107	1.0636	1.9226	3.3567	5.3853	7.7794	9.4877	11.1433
5	0.4117	0.5543	0.8312	1.1455	1.6103	2.6746	4.3515	6.6257	9.2364	11.071	12.8325
6	0.6757	0.8721	1.2373	1.6354	2.2041	3.4546	5.3481	7.8408	10.645	12.592	14.4494
7	0.9893	1.239	1.6899	2.1673	2.8331	4.2549	6.3458	9.0371	12.017	14.067	16.0128
8	1.3444	1.6465	2.1797	2.7326	3.4895	5.0706	7.3441	10.219	13.362	15.507	17.5345
9	1.7349	2.0879	2.7004	3.3251	4.1682	5.8988	8.3428	11.389	14.684	16.919	19.0228
10	2.1559	2.5582	3.247	3.9403	4.8652	6.7372	9.3418	12.549	15.987	18.307	20.4832
11	2.6032	3.0535	3.8157	4.5748	5.5778	7.5841	10.341	13.701	17.275	19.675	21.92
12	3.0738	3.5706	4.4038	5.226	6.3038	8.4384	11.34	14.845	18.549	21.026	23.3367
13	3.565	4.1069	5.0088	5.8919	7.0415	9.2991	12.34	15.984	19.812	22.362	24.7356
14	4.0747	4.6604	5.6287	6.5706	7.7895	10.165	13.339	17.117	21.064	23.685	26.1189
15	4.6009	5.2293	6.2621	7.2609	8.5468	11.037	14.339	18.245	22.307	24.996	27.4884
16	5.1422	5.8122	6.9077	7.9616	9.3122	11.912	15.339	19.369	23.542	26.296	28.8454
17	5.6972	6.4078	7.5642	8.6718	10.085	12.792	16.338	20.489	24.769	27.587	30.191
18	6.2648	7.0149	8.2307	9.3905	10.865	13.675	17.338	21.605	25.989	28.869	31.5264
19	6.844	7.6327	8.9065	10.117	11.651	14.562	18.338	22.718	27.204	30.144	32.8523
20	7.4338	8.2604	9.5908	10.851	12.443	15.452	19.337	23.828	28.412	31.41	34.1696
21	8.0337	8.8972	10.283	11.591	13.24	16.344	20.337	24.935	29.615	32.671	35.4789
22	8.6427	9.5425	10.982	12.338	14.042	17.24	21.337	26.039	30.813	33.924	36.7807
23	9.2604	10.196	11.689	13.091	14.848	18.137	22.337	27.141	32.007	35.173	38.0756
24	9.8862	10.856	12.401	13.848	15.659	19.037	23.337	28.241	33.196	36.415	39.3641
25	10.52	11.524	13.12	14.611	16.473	19.939	24.337	29.339	34.382	37.653	40.6465
26	11.16	12.198	13.844	15.379	17.292	20.843	25.337	30.435	35.563	38.885	41.9232
27	11.808	12.879	14.573	16.151	18.114	21.749	26.336	31.528	36.741	40.113	43.1945
28	12.461	13.565	15.308	16.928	18.939	22.657	27.336	32.621	37.916	41.337	44.4608
29	13.121	14.257	16.047	17.708	19.768	23.567	28.336	33.711	39.088	42.557	45.7223
30	13.787	14.954	16.791	18.493	20.599	24.478	29.336	34.8	40.256	43.773	46.9792
40	20.707	22.164	24.433	26.509	29.051	33.66	39.335	45.616	51.805	55.759	59.3417
50	27.991	29.707	32.357	34.764	37.689	42.942	49.335	56.334	63.167	67.505	71.4202
60	35.535	37.485	40.482	43.188	46.459	52.294	59.335	66.982	74.397	79.082	83.2977
70	43.275	45.442	48.758	51.739	55.329	61.698	69.335	77.577	85.527	90.531	95.0232
80	51.172	53.54	57.153	60.392	64.278	71.145	79.334	88.13	96.578	101.88	106.629
90	59.196	61.754	65.647	69.126	73.291	80.625	89.334	98.65	107.57	113.15	118.136
100	67.328	70.065	74.222	77.93	82.358	90.133	99.334	109.14	118.5	124.34	129.561

Critical value of F distribution p=0.95 **TABLE IV**

DF_1 / DF_2	1	2	3	4	5	6	7	8	9	10	12	15	20	24	30	40	60	120	∞
1	161.45	199.50	215.71	224.58	230.16	233.99	236.77	238.88	240.54	241.88	243.91	245.95	248.01	249.05	250.10	251.14	252.20	253.25	254.30
2	18.51	19.00	19.16	19.25	19.30	19.33	19.35	19.37	19.38	19.40	19.41	19.43	19.45	19.45	19.46	19.47	19.48	19.49	19.50
3	10.13	9.55	9.28	9.12	9.01	8.94	8.89	8.85	8.81	8.79	8.74	8.70	8.66	8.64	8.62	8.59	8.57	8.55	8.53
4	7.71	6.94	6.59	6.39	6.26	6.16	6.09	6.04	6.00	5.96	5.91	5.86	5.80	5.77	5.75	5.72	5.69	5.66	5.63
5	6.61	5.79	5.41	5.19	5.05	4.95	4.88	4.82	4.77	4.74	4.68	4.62	4.56	4.53	4.50	4.46	4.43	4.40	4.36
6	5.99	5.14	4.76	4.53	4.39	4.28	4.21	4.15	4.10	4.06	4.00	3.94	3.87	3.84	3.81	3.77	3.74	3.70	3.67
7	5.59	4.74	4.35	4.12	3.97	3.87	3.79	3.73	3.68	3.64	3.57	3.51	3.44	3.41	3.38	3.34	3.30	3.27	3.23
8	5.32	4.46	4.07	3.84	3.69	3.58	3.50	3.44	3.39	3.35	3.28	3.22	3.15	3.12	3.08	3.04	3.01	2.97	2.93
9	5.12	4.26	3.86	3.63	3.48	3.37	3.29	3.23	3.18	3.14	3.07	3.01	2.94	2.90	2.86	2.83	2.79	2.75	2.71
10	4.96	4.10	3.71	3.48	3.33	3.22	3.14	3.07	3.02	2.98	2.91	2.85	2.77	2.74	2.70	2.66	2.62	2.58	2.54
12	4.75	3.89	3.49	3.26	3.11	3.00	2.91	2.85	2.80	2.75	2.69	2.62	2.54	2.51	2.47	2.43	2.38	2.34	2.3
15	4.54	3.68	3.29	3.06	2.90	2.79	2.71	2.64	2.59	2.54	2.48	2.40	2.33	2.29	2.25	2.20	2.16	2.11	2.07
20	4.35	3.49	3.10	2.87	2.71	2.60	2.51	2.45	2.39	2.35	2.28	2.20	2.12	2.08	2.04	1.99	1.95	1.90	1.84
24	4.26	3.40	3.01	2.78	2.62	2.51	2.42	2.36	2.30	2.25	2.18	2.11	2.03	1.98	1.94	1.89	1.84	1.79	1.73
30	4.17	3.32	2.92	2.69	2.53	2.42	2.33	2.27	2.21	2.16	2.09	2.01	1.93	1.89	1.84	1.79	1.74	1.68	1.62
40	4.08	3.23	2.84	2.61	2.45	2.34	2.25	2.18	2.12	2.08	2.00	1.92	1.84	1.79	1.74	1.69	1.64	1.58	1.51
60	4.00	3.15	2.76	2.53	2.37	2.25	2.17	2.10	2.04	1.99	1.92	1.84	1.75	1.70	1.65	1.59	1.53	1.47	1.39
120	3.92	3.07	2.68	2.45	2.29	2.18	2.09	2.02	1.96	1.91	1.83	1.75	1.66	1.61	1.55	1.50	1.43	1.35	1.25
∞	3.84	3.00	2.60	2.37	2.21	2.10	2.01	1.94	1.88	1.83	1.75	1.67	1.57	1.52	1.46	1.39	1.32	1.22	1.00

14. APENDIX II

TOLERANCE TABLES

Table 3.1. Tolerances for purity tests on the same submitted sample in the same laboratory (two-way test at 5% significance level)

This table gives tolerances for comparing purity results on duplicate samples from the same submitted sample analyzed in the same laboratory. It can be used for any component of a purity test. The table is used by entering it at the average of the two test results (columns 1 or 2). The appropriate tolerance is found in one of columns 3 to 6, determined as to whether the seeds are chaffy or non-chaffy and half or whole working samples have been analyzed.

The tolerances in columns 5 and 6 are extracted from Miles (1963), Table P11, columns C and F respectively, and rounded to one decimal place. Those for half working samples, columns 3 and 4, are calculated from Table P11, columns C and F in Miles (1963) by multiplication with the square root of two.

Average of the two test results		Tolerances for differences between			
		Half working samples		Whole working samples	
		Non-chaffy seeds	Chaffy seeds	Non-chaffy seeds	Chaffy seeds
1	2	3	4	5	6
99.95-100.00	0.00- 0.04	0.20	0.23	0.1	0.2
99.90- 99.94	0.05- 0.09	0.33	0.34	0.2	0.2
99.85- 99.89	0.10- 0.14	0.40	0.42	0.3	0.3
99.80- 99.84	0.15- 0.19	0.47	0.49	0.3	0.4
99.75- 99.79	0.20- 0.24	0.51	0.55	0.4	0.4
99.70- 99.74	0.25- 0.29	0.55	0.59	0.4	0.4
99.65- 99.69	0.30- 0.34	0.61	0.65	0.4	0.5
99.60- 99.64	0.35- 0.39	0.65	0.69	0.5	0.5
99.55- 99.59	0.40- 0.44	0.68	0.74	0.5	0.5
99.50- 99.54	0.45- 0.49	0.72	0.76	0.5	0.5
99.40- 99.49	0.50- 0.59	0.76	0.82	0.5	0.6
99.30- 99.39	0.60- 0.69	0.83	0.89	0.6	0.6
99.20- 99.29	0.70- 0.79	0.89	0.95	0.6	0.7
99.10- 99.19	0.80- 0.89	0.95	1.00	0.7	0.7
99.00- 99.09	0.90- 0.99	1.00	1.06	0.7	0.8
98.75- 98.99	1.00- 1.24	1.07	1.15	0.8	0.8
98.50- 98.74	1.25- 1.49	1.19	1.26	0.8	0.9
98.25- 98.49	1.50- 1.74	1.29	1.37	0.9	1.0
98.00- 98.24	1.75- 1.99	1.37	1.47	1.0	1.0
97.75- 97.99	2.00- 2.24	1.44	1.54	1.0	1.1
97.50- 97.74	2.25- 2.49	1.53	1.63	1.1	1.2
97.25- 97.49	2.50- 2.74	1.60	1.70	1.1	1.2
97.00- 97.24	2.75- 2.99	1.67	1.78	1.2	1.3
96.50- 96.99	3.00- 3.49	1.77	1.88	1.3	1.3
96.00- 96.49	3.50- 3.99	1.88	1.99	1.3	1.4
95.50- 95.99	4.00- 4.49	1.99	2.12	1.4	1.5
95.00- 95.49	4.50- 4.99	2.09	2.22	1.5	1.6
94.00- 94.99	5.00- 5.99	2.25	2.38	1.6	1.7
93.00- 93.99	6.00- 6.99	2.43	2.56	1.7	1.8
92.00- 92.99	7.00- 7.99	2.59	2.73	1.8	1.9
91.00- 91.99	8.00- 8.99	2.74	2.90	1.9	2.1
90.00- 90.99	9.00- 9.99	2.88	3.04	2.0	2.2
88.00- 89.99	10.00-11.99	3.08	3.25	2.2	2.3
86.00- 87.99	12.00-13.99	3.31	3.49	2.3	2.5
84.00- 85.99	14.00-15.99	3.52	3.71	2.5	2.6
82.00- 83.99	16.00-17.99	3.69	3.90	2.6	2.8
80.00- 81.99	18.00-19.99	3.86	4.07	2.7	2.9
78.00- 79.99	20.00-21.99	4.00	4.23	2.8	3.0
76.00- 77.99	22.00-23.99	4.14	4.37	2.9	3.1
74.00- 75.99	24.00-25.99	4.26	4.50	3.0	3.2
72.00- 73.99	26.00-27.99	4.37	4.61	3.1	3.3
70.00- 71.99	28.00-29.99	4.47	4.71	3.2	3.3
65.00- 69.99	30.00-34.99	4.61	4.86	3.3	3.4
60.00- 64.99	35.00-39.99	4.77	5.02	3.4	3.6
50.0- 59.99	40.00-49.99	4.89	5.16	3.5	3.7

Table 3.2. Tolerances for purity tests on two different submitted samples from the same lot when a second test is made in the same or a different laboratory (one-way test at 1% significance level)

This table gives the tolerances for purity results made on two different submitted samples each drawn from the same lot and analyzed in the same or a different laboratory. It can be used for any component of a purity test when the result of the second test is poorer than that of the first test. The table is used by entering it at the average of the two test results (columns 1 or 2). The appropriate tolerance is found in columns 3 or 4, determined as to whether the seeds are chaffy or non-chaffy. The tolerances in columns 3 and 4 are extracted from columns D and G respectively of Table P1 in Miles (1963).

Average of the two test results		Tolerance	
50-100%	Less than 50%	Non chaffy seeds	Chaffy seeds
1	2	3	4
99.95-100.00	0.00- 0.04	0.2	0.2
99.90- 99.94	0.05- 0.09	0.3	0.3
99.85- 99.89	0.10- 0.14	0.3	0.4
99.80- 99.84	0.15- 0.19	0.4	0.5
99.75- 99.79	0.20- 0.24	0.4	0.5
99.70- 99.74	0.25- 0.29	0.5	0.6
99.65- 99.69	0.30- 0.34	0.5	0.6
99.60- 99.64	0.35- 0.39	0.6	0.7
99.55- 99.59	0.40- 0.44	0.6	0.7
99.50- 99.54	0.45- 0.49	0.6	0.7
99.40- 99.49	0.50- 0.59	0.7	0,8
99.30- 99.39	0.60- 0.69	0.7	0.9
99.20- 99.29	0.70- 0.79	0.8	0.9
99.10- 99.19	0.80- 0.89	0.8	1.0
99.00- 99.09	0.90- 0.99	0.9	1.0
98.75- 98.99	1.00- 1.24	0.9	1.1
98.50- 98.74	1.25- 1.49	1.0	1.2
98.25- 98.49	1.50- 1.74	1.1	1.3
98.00- 98.24	1.75- 1.99	1.2	1.4
97.75- 97.99	2.00- 2.24	1.3	1.5
97.50- 97.74	2.25- 2.49	1.3	1.6
97.25- 97.49	2.50- 2.74	1.4	1.6
97.00- 97.24	2.75- 2.99	1.5	1.7
96.50- 96.99	3.00- 3.49	1.5	1.8
96.00- 96.49	3.50- 3.99	1.6	1.9
95.50- 95.99	4.00- 4.49	1.7	2.0
95.00- 95.49	4.50- 4.99	1.8	2.2
94.00- 94.99	5.00- 5.99	2.0	2.3
93.00- 93.99	6.00- 6.99	2.1	2.5
92.00- 92.99	7.00- 7.99	2.2	2.6
91.00- 91.99	8.00- 8.99	2.4	2.8
90.00- 90.99	9.00- 9.99	2.5	2.9
88.00- 89.99	10.00-11.99	2.7	3.1
86.00- 87.99	12.00-13.99	2.9	3.4
84.00- 85.99	14.00-15.99	3.0	3.6
82.00- 83.99	16.00-17.99	3.2	3.7
80.00- 81.99	18.00-19.99	3.3	3.9
78.00- 79.99	20.00-21.99	3.5	4.1
76.00- 77.99	22.00-23.99	3.6	4.2
74.00- 75.99	24.00-25.99	3.7	4.3
72.00- 73.99	26.00-27.99	3.8	4.4
70.00- 71.99	28.00-29.99	3.8	4.5
65.00- 69.99	30.00-34.99	4.0	4.7
60.00- 64.99	35.00-39.99	4.1	4.8
50.00- 59.99	40.00-49.99	4.2	5.0

Table 3.3. Tolerances for purity tests on two different submitted samples from the same seed lot when a second test is made in the same or a different laboratory (two-way test at 1% significance level).

This table gives the tolerances for purity results made on two different submitted samples each drawn from the same lot and analyzed in the same or a different laboratory. It can be used for any component of a purity test to decide whether two

estimates are compatible. The table is used by entering it at the average of the two test results (columns 1 or 2). The appropriate tolerance is found in columns 3 or 4, determined by whether the seeds are chaffy or non-chaffy.
The tolerances in columns 3 and 4 are extracted from columns D and G, respectively, of Table P7 in Miles (1963).

Average of the two test results		Tolerance	
50-100%	Less than 50%	Non chaffy seeds	Chaffy seeds
1	2	3	4
99.95-100.00	0.00- 0.04	0.2	0.2
~~99.90- 99.94~~	~~0.05- 0.09~~	~~0.3~~	~~0.4~~
99.85- 99.89	0.10- 0.14	0.4	0.5
99.80- 99.84	0.15- 0.19	0.4	0.5
99.75- 99.79	0.20- 0.24	0.5	0.6
99.70- 99.74	0.25- 0.29	0.5	0.6
99.65- 99.69	0.30- 0.34	0.6	0.7
99.60- 99.64	0.35- 0.39	0.6	0.7
99.55- 99.59	0.40- 0.44	0.6	0.8
99.50- 99.54	0.45- 0.49	0.7	0.8
99.40- 99.49	0.50- 0.59	0.7	0.9
99.30- 99.39	0.60- 0.69	0.8	1.0
99.20- 99.29	0.70- 0.79	0.8	1.0
99.10- 99.19	0.80- 0.89	0.9	1.1
99.00- 99.09	0.90- 0.99	0.9	1.1
98.75- 98.99	1.00- 1.24	1.0	1.2
98.50- 98.74	1.25- 1.49	1.1	1.3
98.25- 98.49	1.50- 1.74	1.2	1.5
98.00- 98.24	1.75- 1.99	1.3	1.6
97.75- 97.99	2.00- 2.24	1.4	1.7
97.50- 97.74	2.25- 2.49	1.5	1.7
97.25- 97.49	2.50- 2.74	1.5	1.8
97.00- 97.24	2.75- 2.99	1.6	1.9
96.50- 96.99	3.00- 3.49	1.7	2.0
96.00- 96.49	3.50- 3.99	1.8	2.1
95.50- 95.99	4.00- 4.49	1.9	2.3
95.00- 95.49	4.50- 4.99	2.0	2.4
94.00- 94.99	5.00- 5.99	2.1	2.5
93.00- 93.99	6.00- 6.99	2.3	2.7
92.00- 92.99	7.00- 7.99	2.5	2.9
91.00- 91.99	8.00- 8.99	2.6	3.1
90.00- 90.99	9.00- 9.99	2.8	3.2
88.00- 89.99	10.00-11.99	2.9	3.5
86.00- 87.99	12.00-13.99	3.2	3.7
84.00- 85.99	14.00-15.99	3.4	3.9
82.00- 83.99	16.00-17.99	3.5	4.1
80.00- 81.99	18.00-19.99	3.7	4.3
78.00- 79.99	20.00-21.99	3.8	4.5
76.00- 77.99	22.00-23.99	3.9	4.6
74.00- 75.99	24.00-25.99	4.1	4.8
72.00- 73.99	26.00-27.99	4.2	4.9
70.00- 71.99	28.00-29.99	4.3	5.0
65.00- 69.99	30.00-34.99	4.4	5.2
60.00- 64.99	35.00-39.99	4.5	5.3
50.00- 59.99	40.00-49.99	4.7	5.5

Table 4.1. Tolerances for the determination of other seeds by number when tests are made on the same or a different submitted sample in the same or a different laboratory (two-way test at 5% significance level)

This table gives the maximum difference in the numbers of other seeds, used to decide if two test results are compatible. The tests are to be made on the same or a different submitted sample in the same or a different laboratory. Both samples have to be of approximately the same weight. The table is used by entering it at the average of the two test results (column 1), and the maximum tolerated difference is found in column 2.

The tolerances are extracted from Table F1b (foreign seeds) in Miles (1963).

Average of the two test results 1	Tolerance 2	Average of the two test results 1	Tolerance 2	Average of the two test results 1	Tolerance 2
3	5	76-81	25	253-264	45
4	6	82-88	26	265-276	46
5-6	7	89-95	27	277-288	47
7-8	8	96-102	28	289-300	48
9-10	9	103-110	29	301-313	49
11-13	10	111-117	30	314-326	50
14-15	11	118-125	31	327-339	51
16-18	12	126-133	32	340-353	52
19-22	13	134-142	33	354-366	53
23-25	14	143-151	34	367-380	54
26-29	15	152-160	35	381-394	55
30-33	16	161-169	36	395-409	56
34-37	17	170-178	37	410-424	57
38-42	18	179-188	38	425-439	58
43-47	19	189-198	39	440-454	59
48-52	20	199-209	40	455-469	60
53-57	21	210-219	41	470-485	61
58-63	22	220-230	42	486-501	62
64-69	23	231-241	43	502-518	63
70-75	24	242-252	44	519-534	64

Table 4.2. Tolerances for the determination of other seeds by number when tests are made on different submitted samples, the second being made in the same or in a different laboratory (one-way test at 5% significance level)

This table gives the tolerances for counts of number of other seeds, made on two different submitted samples each drawn from the same lot and analyzed in the same or a different laboratory. Both samples are to be of approximately the same weight. The table can be used when the result of the second test is poorer than that of the first test. The table is used by entering it at the average of the two test results (column 1), and the maximum tolerated difference is found in column 2.

The tolerances appeared in Report of the Rules Committee, International Seed Testing Association. Revision of International Rules for Seed Testing. Proceedings of the International Seed Testing Association 27, 291-304, 1962.

Average of the two test results 1	Tolerance of the two test results 2	Average 1	Tolerance of the two test results 2	Average 1	Tolerance of the two test results 2	Average 1	Tolerance of the two test results 2
3-4	5	66-72	20	211-223	35	439-456	50
5-6	6	73-79	21	224-235	36	457-474	51
7-8	7	80-87	22	236-249	37	475-493	52
9-11	8	88-95	23	250-262	38	494-513	53
12-14	9	96-104	24	263-276	39	514-532	54
15-17	10	105-113	25	277-290	40	533-552	55
18-21	11	114-122	26	291-305	41		
22-25	12	123-131	27	306-320	42		
26-30	13	132-141	28	321-336	43		
31-34	14	142-152	29	337-351	44		
35-40	15	153-162	30	352-367	45		
41-45	16	163-173	31	368-386	46		
46-52	17	174-186	32	387-403	47		
53-58	18	187-198	33	404-420	48		
59-65	19	199-210	34	421-438	49		

Table 5.1. Maximum tolerated range between four replicates of 100 seeds in one germination test (two-way test at 2.5% significance level)

This table indicates the maximum range (i.e. difference between highest and lowest) in germination percentage tolerable between replicates, allowing for random sampling variation only at 0.025 probability. To find the maximum tolerated range in any case calculate the average percentage, to the nearest whole number, of the four replicates: if necessary, form 100-seed replicates by combining the sub-replicates of 50 or 25 seeds which were closest together in the germinator. Locate the average in column 1 or 2 of the table and read off the maximum tolerated range opposite in column 3.

The tolerances are extracted from Table G1, column D, in Miles (1963).

Average percentage germination		Maximum range	Average percentage germination		Maximum range
1	2	3	1	2	3
99	2	5	87 to 88	13 to 14	13
98	3	6	84 to 86	15 to 17	14
97	4	7	81 to 83	18 to 20	15
96	5	8	78 to 80	21 to 23	16
95	6	9	73 to 77	24 to 28	17
93 to 94	7 to 8	10	67 to 72	29 to 34	18
91 to 92	9 to 10	11	56 to 66	35 to 45	19
89 to 90	11 to 12	12	51 to 55	46 to 50	20

Table 5.2. Tolerances for germination tests on the same or a different submitted sample when tests are made in the same or a different laboratory on 400 seeds (two-way test at 2.5% significance level)

This table gives the tolerances for percentages of normal seedlings, abnormal seedlings, dead seeds, hard seeds, or any combination of these when tests are made on the same or a different submitted sample in the same or a different laboratory. To determine if the two tests are compatible calculate the average percentage of the two test results to the nearest whole number and locate this in columns 1 or 2 of the table. The tests are compatible if the difference between the percentage of the two tests does not exceed the tolerance given in column 3.
The tolerances are extracted from Table G2, column L, in Miles (1963).

Average percentage germination	Maximum	range	Maximum germination	Average percentage	range
1	2	3	1	2	3
98 to 99	2 to 3	2	77 to 84	17 to 24	6
95 to 97	4 to 6	3	60 to 76	25 to 41	7
91 to 94	7 to 10	4	51 to 59	42 to 50	8
85 to 90	11 to 16	5			

Table 5.3. Tolerances for germination tests on two different submitted samples in the same or a different laboratory on 400 seeds (one-way test at 5% significance level)

This table gives the tolerances for percentages of normal seedlings, abnormal seedlings, dead seeds, hard seeds, or any combination of these when the tests are made in the same or different laboratories on samples drawn from the same lot. The table can be used when the results of the second test is poorer than that of the first test. The table is used by entering it at the average (nearest whole number) of the two test results in columns 1 and 2, and the maximum tolerated difference is found in column 3.
The tolerances are extracted from Table G3, column C, in Miles (1963).

Average percentages		Tolerance	Average percentages		Tolerance	
More than 50%	50% or less		More than 50%	50% or less		
1	2	3	1	2	3	
99	2	2	82 to 86	15 to 19	7	
97 to 98		3 to 4	3	76 to 81	20 to 25	8
94 to 96		5 to 7	4	70 to 75	26 to 31	9
91 to 93		8 to 10	5	60 to 69	32 to 41	10
87 to 90		11 to 14	6	51 to 59	42 to 50	11

Table 6.1.
Tolerances for tetrazolium viability tests on the same or a different submitted sample when tests are made in the same laboratory each on 400 seeds (two-way test at 2.5 % significance level)

The tolerances take into account the experimental error within a laboratory as described in the TEZ Committee Report 2000 and are not extracted from Miles (1963).

Average percentage viability		Maximum range	Average percentage viability		Maximum range
1	2	3	1	2	3
98 to 99	2 to 3	2	83 to 88	13 to 18	6
96 to 97	4 to 5	3	75 to 82	19 to 26	7
93 to 95	6 to 8	4	58 to 74	27 to 43	8
89 to 92	9 to 12	5	51 to 57	44 to 50	9

Table 6.2.
Tolerances for tetrazolium viability tests on two different submitted samples in different laboratories each on 400 seeds (one-way test at 5 % significance level)

The tolerances take into account the experimental error between the laboratories as described in the TEZ Committee Report 2000 and are not extracted from Miles (1963).

Average percentage viability		Maximum range	Average percentage viability		Maximum range
1	2	3	1	2	3
99	2	4	86 to 88	13 to 15	11
98	3	5	82 to 85	16 to 19	12
97	4	6	78 to 81	20 to 23	13
95 to 96	5 to 6	7	73 to 77	24 to 28	14
93 to 94	7 to 8	8	65 to 72	29 to 36	15
91 to 92	9 to 10	9	51 to 64	37 to 50	16
89 to 90	11 to 12	10			

Table 13.1. Maximum tolerated range between replicates

This table based on the Poisson distribution indicates the maximum range (i.e. maximum difference between the highest and the lowest) in germination data tolerable between weighed replicates, allowing for random variation at 0.05 probability. To find the maximum tolerated range in any case calculate the sum of the numbers of seeds germinated in the four replicates. Locate the sum in column 1 of the table and read off the maximum tolerated range in column 2.

Number of seeds germinated in the total weight of seeds tested	Maximum range	Number of seeds germinated in the total weight of seeds tested	Maximum range
1	2	1	2
0-6	4	161-174	27
7-10	6	175-188	28
11-14	8	189-202	29
15-18	9	203-216	30
19-22	11	217-230	31
23-26	12	231-244	32
27-30	13	245-256	33
31-38	14	257-270	34
39-50	15	271-288	35
51-56	16	289-302	36
57-62	17	303-321	37
63-70	18	322-338	38
71-82	19	339-358	39
83-90	20	359-378	40
91-102	21	379-402	41
103-112	22	403-420	42
113-122	23	421-438	43
123-134	24	439-460	44
135-146	25	>460	45
147-160	26		

Table B.1. **Tolerances for purity percentages deviation of component lots at 1% significance level (N = number of lots being blended)**

Average of all lots		N=2	N=3	N=4	N=5	N=6	N=7	N=8	N=9	N=10
99.9	0.1	0.2	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3
99.8	0.2	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.5	0.5
99.7	0.3	0.4	0.5	0.5	0.5	0.5	0.5	0.5	0.6	0.6
99.6	0.4	0.5	0.5	0.6	0.6	0.6	0.6	0.6	0.6	0.7
99.5	0.5	0.5	0.6	0.6	0.6	0.7	0.7	0.7	0.7	0.7
99.4	0.6	0.6	0.6	0.7	0.7	0.7	0.8	0.8	0.8	0.8
99.3	0.7	0.6	0.7	0.7	0.8	0.8	0.8	0.8	0.8	0.9
99.2	0.8	0.6	0.7	0.8	0.8	0.8	0.9	0.9	0.9	0.9
99.1	0.9	0.7	0.8	0.8	0.9	0.9	0.9	0.9	1.0	1.0
99.0	1.0	0.7	0.8	0.9	0.9	0.9	1.0	1.0	1.0	1.0
98.5-98.9	1.1- 1.5	0.9	1.0	1.1	1.1	1.2	1.2	1.2	1.2	1.3
98.0-98.4	1.6- 2.0	1.0	1.2	1.2	1.3	1.3	1.4	1.4	1.4	1.4
97.5-97.9	2.1- 2.5	1.1	1.3	1.4	1.4	1.5	1.5	1.6	1.6	1.6
97.0-97.4	2.6- 3.0	1.2	1.4	1.5	1.6	1.6	1.7	1.7	1.7	1.8
96.5-96.9	3.1- 3.5	1.3	1.5	1.6	1.7	1.7	1.8	1.8	1.8	1.9
96.0-96.4	3.6- 4.0	1.4	1.6	1.7	1.8	1.9	1.9	2.0	2.0	2.0
95.5-95.9	4.1- 4.5	1.5	1.7	1.8	1.9	2.0	2.0	2.1	2.1	2.1
95.0-95.4	4.6- 5.0	1.6	1.8	1.9	2.0	2.1	2.1	2.2	2.2	2.2
94.5-94.9	5.1- 5.5	1.7	1.9	2.0	2.1	2.2	2.2	2.3	2.3	2.4
94.0-94.4	5.6- 6.0	1.7	2.0	2.1	2.2	2.3	2.3	2.4	2.4	2.5
93.5-93.9	6.1- 6.5	1.8	2.0	2.2	2.3	2.3	2.4	2.5	2.5	2.5
93.0-93.4	6.6- 7.0	1.9	2.1	2.2	2.3	2.4	2.5	2.5	2.6	2.6
92.5-92.9	7.1- 7.5	1.9	2.2	2.3	2.4	2.5	2.6	2.6	2.7	2.7
92.0-92.4	7.6- 8.0	2.0	2.2	2.4	2.5	2.6	2.6	2.7	2.8	2.8
91.5-91.9	8.1- 8.5	2.0	2.3	2.5	2.6	2.7	2.7	2.8	2.8	2.9
91.0-91.4	8.6- 9.0	2.1	2.4	2.5	2.6	2.7	2.8	2.9	2.9	3.0
90.5-90.9	9.1- 9.5	2.1	2.4	2.6	2.7	2.8	2.9	2.9	3.0	3.0
90.0-90.4	9.6-10.0	2.2	2.5	2.6	2.8	2.9	2.9	3.0	3.0	3.1
89.0-89.9	10.1-11.0	2.3	2.6	2.8	2.9	3.0	3.1	3.1	3.2	3.2
88.0-88.9	11.1-12.0	2.4	2.7	2.9	3.0	3.1	3.2	3.2	3.3	3.4
87.0-87.9	12.1-13.0	2.4	2.8	3.0	3.1	3.2	3.3	3.4	3.4	3.5
86.0-86.9	13.1-14.0	2.5	2.9	3.1	3.2	3.2	3.4	3.5	3.5	3.6
85.0-85.9	14.1-15.0	2.6	2.9	3.1	3.3	3.4	3.5	3.6	3.6	3.7
84.0-84.9	15.1-16.0	2.7	3.0	3.2	3.4	3.5	3.6	3.7	3.7	3.8
83.0-83.9	16.1-17.0	2.7	3.1	3.3	3.5	3.6	3.7	3.7	3.8	3.9
82.0-82.9	17.1-18.0	2.8	3.2	3.4	3.5	3.7	3.7	3.8	3.9	4.0
81.0-81.9	18.1-19.0	2.9	3.2	3.5	3.6	3.7	3.8	3.9	4.0	4.0
80.0-80.9	19.1-20.0	2.9	3.3	3.5	3.7	3.8	3.9	4.0	4.0	4.1
79.0-79.9	20.1-21.0	3.0	3.4	3.6	3.7	3.9	4.0	4.1	4.1	4.2
78.0-78.9	21.1-22.0	3.0	3.4	3.6	3.8	3.9	4.0	4.1	4.2	4.3
77.0-77.9	22.1-23.0	3.1	3.5	3.7	3.9	4.0	4.1	4.2	4.3	4.3
76.0-76.9	23.1-24.0	3.1	3.5	3.8	3.9	4.1	4.2	4.3	4.3	4.4
75.0-75.9	24.1-25.0	3.2	3.6	3.8	4.0	4.1	4.2	4.3	4.4	4.5
74.0-74.9	25.1-26.0	3.2	3.6	3.9	4.0	4.2	4.3	4.4	4.5	4.5
73.0-73.9	26.1-27.0	3.2	3.7	3.9	4.1	4.2	4.3	4.4	4.5	4.6
72.0-72.9	27.1-28.0	3.3	3.7	4.0	4.1	4.3	4.4	4.5	4.6	4.6
71.0-71.9	28.1-29.0	3.3	3.7	4.0	4.2	4.3	4.4	4.5	4.6	4.7
70.0-70.9	29.1-30.0	3.3	3.8	4.0	4.2	4.4	4.5	4.6	4.7	4.7
69.0-69.9	30.1-31.0	3.4	3.8	4.1	4.3	4.4	4.5	4.6	4.7	4.8
68.0-68.9	31.1-32.0	3.4	3.8	4.1	4.3	4.4	4.6	4.7	4.7	4.8
67.0-67.9	32.1-33.0	3.4	3.9	4.1	4.3	4.5	4.6	4.7	4.8	4.9
66.0-66.9	33.1-34.0	3.4	3.9	4.2	4.4	4.5	4.6	4.7	4.8	4.9
65.0-65.9	34.1-35.0	3.5	3.9	4.2	4.4	4.5	4.7	4.8	4.8	4.9
64.0-64.9	35.1-36.0	3.5	4.0	4.2	4.4	4.6	4.7	4.8	4.9	5.0
63.0-63.9	36.1-37.0	3.5	4.0	4.2	4.4	4.6	4.7	4.8	4.9	5.0
62.0-62.9	37.1-38.0	3.5	4.0	4.3	4.5	4.6	4.7	4.8	4.9	5.0
61.0-61.9	38.1-39.0	3.6	4.0	4.3	4.5	4.6	4.8	4.9	5.0	5.0
60.0-60.9	39.1-40.0	3.6	4.0	4.3	4.5	4.7	4.8	4.9	5.0	5.1
59.0-59.9	40.1-41.0	3.6	4.1	4.3	4.5	4.7	4.8	4.9	5.0	5.1
58.0-58.9	41.1-42.0	3.6	4.1	4.3	4.5	4.7	4.8	4.9	5.0	5.1
57.0-57.9	42.1-43.0	3.6	4.1	4.4	4.6	4.7	4.8	4.9	5.0	5.1
56.0-56.9	43.1-44.0	3.6	4.1	4.4	4.6	4.7	4.8	5.0	5.0	5.1
55.0-55.9	44.1-45.0	3.6	4.1	4.4	4.6	4.7	4.9	5.0	5.1	5.1
54.0-54.9	45.1-46.0	3.6	4.1	4.4	4.6	4.7	4.9	5.0	5.1	5.1
53.0-53.9	46.1-47.0	3.6	4.1	4.4	4.6	4.8	4.9	5.0	5.1	5.2
52.0-52.9	47.1-48.0	3.6	4.1	4.4	4.6	4.8	4.9	5.0	5.1	5.2
51.0-51.9	48.1-49.0	3.6	4.1	4.4	4.6	4.8	4.9	5.0	5.1	5.2
50.0-50.9	49.1-50.0	3.6	4.1	4.4	4.6	4.9	4.9	5.0	5.1	5.2

Table B.2. Tolerances for germination percentages deviation of component lots at 1% significance level (N = number of lots being blended)

Average of all lots		N=2	N=3	N=4	N=5	N=6	N=7	N=8	N=9	N=10
99	1	2	2	2	2	2	2	2	3	3
98	2	3	3	3	3	3	3	3	4	4
97	3	3	4	4	4	4	4	4	4	4
96	4	4	4	4	5	5	5	5	5	5
95	5	4	4	5	5	5	5	5	6	6
94	6	4	5	5	5	6	6	6	6	6
93	7	5	5	6	6	6	6	6	6	7
92	8	5	6	6	6	6	7	7	7	7
91	9	5	6	6	7	7	7	7	7	7
90	10	5	6	7	7	7	7	7	8	8
89	11	6	6	7	7	7	8	8	8	8
88	12	6	7	7	7	8	8	8	8	8
87	13	6	7	7	8	8	8	8	9	9
86	14	6	7	8	8	8	8	9	9	9
85	15	6	7	8	8	8	9	9	9	9
84	16	7	8	8	8	9	9	9	9	9
83	17	7	8	8	9	9	9	9	10	10
82	18	7	8	8	9	9	9	10	10	10
81	19	7	8	9	9	9	10	10	10	10
80	20	7	8	9	9	10	10	10	10	10
79	21	7	8	9	9	10	10	10	10	11
78	22	8	9	9	10	10	10	10	11	11
77	23	8	9	9	10	10	10	10	11	11
76	24	8	9	9	10	10	10	11	11	11
75	25	8	9	10	10	10	11	11	11	11
74	26	8	9	10	10	10	11	11	11	11
73	27	8	9	10	10	11	11	11	11	11
72	28	8	9	10	10	11	11	11	11	12
71	29	8	9	10	10	11	11	11	12	12
70	30	8	9	10	11	11	11	11	12	12
69	31	8	10	10	11	11	11	12	12	12
68	32	8	10	10	11	11	11	12	12	12
67	33	9	10	10	11	11	11	12	12	12
66	34	9	10	10	11	11	12	12	12	12
65	35	9	10	10	11	11	12	12	12	12
64	36	9	10	11	11	11	12	12	12	12
63	37	9	10	11	11	11	12	12	12	12
62	38	9	10	11	11	12	12	12	12	13
61	39	9	10	11	11	12	12	12	12	13
60	40	9	10	11	11	12	12	12	12	13
59	41	9	10	11	11	12	12	12	12	13
58	42	9	10	11	11	12	12	12	13	13
57	43	9	10	11	11	12	12	12	13	13
56	44	9	10	11	11	12	12	12	13	13
55	45	9	10	11	11	12	12	12	13	13
54	46	9	10	11	11	12	12	12	13	13
53	47	9	10	11	11	12	12	12	13	13
52	48	9	10	11	11	12	12	12	13	13
51	49	9	10	11	11	12	12	12	13	13
50	50	9	10	11	11	12	12	12	13	13

Table B.3. Tolerances for seed counts deviation of component lots at 1% significance level (N = number of lots being blended)

Average of all lots	N=2	N=3	N=4	N=5	N=6	N=7	N=8	N=9	N=10
1	4	4	4	5	5	5	5	5	5
2	5	6	6	7	7	7	7	7	7
3	6	7	8	8	8	8	9	9	9
4	7	8	9	9	10	10	10	10	10
5	8	9	10	10	11	11	11	11	12
6	9	10	11	11	12	12	12	12	13
7	10	11	12	12	13	13	13	13	14
8	10	12	12	13	13	14	14	14	15
9	11	12	13	14	14	15	15	15	15
10	12	13	14	15	15	15	16	16	16
11	12	14	15	15	16	16	17	17	17
12	13	14	15	16	16	17	17	18	18
13	13	15	16	17	17	18	18	18	19
14	14	15	16	17	18	18	19	19	19
15	14	16	17	18	18	19	19	20	20
16	15	16	18	18	19	20	20	20	21
17	15	17	18	19	20	20	21	21	21
18	15	17	19	20	20	21	21	22	22
19	16	18	19	20	21	21	22	22	22
20	16	18	20	21	21	22	22	23	23
21	17	19	20	21	22	22	23	23	24
22	17	19	21	22	22	23	23	24	24
23	17	20	21	22	23	23	24	24	25
24	18	20	22	23	23	24	24	25	25
25	18	21	22	23	24	24	25	25	26
26	19	21	22	23	24	25	25	26	26
27	19	21	23	24	25	25	26	26	27
28	19	22	23	24	25	26	26	27	27
29	20	22	24	25	26	26	27	27	28
30	20	23	24	25	26	27	27	28	28
31	20	23	24	26	27	27	28	28	29
32	21	23	25	26	27	28	28	29	29
33	21	24	25	26	27	28	29	29	30
34	21	24	26	27	28	28	29	30	30
35	22	24	26	27	28	29	30	30	31
36	22	25	26	28	29	29	30	30	31
37	22	25	27	28	29	30	30	31	31
38	22	25	27	28	29	30	31	31	32
39	23	26	27	29	30	30	31	32	32
40	23	26	27	29	30	31	32	32	33
41	23	26	28	29	30	31	32	33	33
42	24	27	29	30	31	32	32	33	33
43	24	27	29	30	31	32	33	33	34
44	24	27	29	31	32	32	33	34	34
45	24	28	30	31	32	33	33	34	35
46	25	28	30	31	32	33	34	34	35
47	25	28	30	32	33	33	34	35	35
48	25	29	30	32	33	34	35	35	36
49	25	29	31	32	33	34	35	36	36
50	26	29	31	33	34	35	35	36	36
51	26	29	31	33	34	35	36	36	37
52	26	30	32	33	34	35	36	37	37
53	26	30	32	33	35	36	36	37	38
54	27	30	32	34	35	36	37	37	38
55	27	31	33	34	35	36	37	38	38
56	27	31	33	34	36	37	37	38	39
57	27	31	33	35	36	37	38	38	39
58	28	31	34	35	36	37	38	39	39
59	28	32	34	35	37	37	38	39	40
60	28	32	34	36	37	38	39	39	40
61	28	32	34	36	37	38	39	40	40
62	29	32	35	36	37	38	39	40	41
63	29	33	35	37	38	39	40	40	41
64	29	33	35	37	38	39	40	41	41
65	29	33	35	37	38	39	40	41	42

Table D.1. Factors for additional variation in seed lots to be used for calculating W and finally the H-value

Attributes	Non-chaffy seeds	Chaffy seeds
Purity	1.1	1.2
Other seed count	1.4	2.2
Germination	1.1	1.2

Table D.2. Sampling intensity and critical H-values
Number of independent container-samples to be drawn as depending on the number of containers in the lot and critical H-values for seed lot heterogeneity at a significance level of 1% probability.

Number of containers in the lot (No)	Number of independent container-samples (N)	Critical H-value for purity and germination attributes		Critical H-value for other seed count attributes	
		non-chaffy seeds	chaffy seeds	non-chaffy seeds	chaffy seeds
5	5	2.55	2.78	3.25	5.10
6	6	2.22	2.42	2.83	4.44
7	7	1.98	2.17	2.52	3.98
8	8	1.80	1.97	2.30	3.61
9	9	1.66	1.81	2.11	3.32
10	10	1.55	1.69	1.97	3.10
11-15	11	1.45	1.58	1.85	2.90
16-25	15	1.19	1.31	1.51	2.40
26-35	17	1.10	1.20	1.40	2.20
36-49	18	1.07	1.16	1.36	2.13
50 or more	20	0.99	1.09	1.26	2.00

Table D.3.A. Maximum tolerated ranges for the R-value test at a significance level of 1% probability using components of purity analyses as indicating attribute in non-chaffy seeds.

Average % of the component and its complement		Tolerated range for number of independent samples (N)			Average % of the component and its complement		Tolerated range for number of independent samples (N)		
		5-9	10-19	20			5-9	10-19	20
99.9	0.1	0.5	0.5	0.6	88.0	12.0	5.0	5.6	6.1
99.8	0.2	0.7	0.8	0.8	87.0	13.0	5.1	5.8	6.3
99.7	0.3	0.8	0.9	1.0	86.0	14.0	5.3	5.9	6.5
99.6	0.4	1.0	1.1	1.2	85.0	15.0	5.4	6.1	6.7
99.5	0.5	1.1	1.2	1.3	84.0	16.0	5.6	6.3	6.9
99.4	0.6	1.2	1.3	1.4	83.0	17.0	5.7	6.4	7.0
99.3	0.7	1.3	1.4	1.6	82.0	18.0	5.9	6.6	7.2
99.2	0.8	1.4	1.5	1.7	81.0	19.0	6.0	6.7	7.4
99.1	0.9	1.4	1.6	1.8	80.0	20.0	6.1	6.8	7.5
99.0	1.0	1.5	1.7	1.9	78.0	22.0	6.3	7.1	7.8
98.5	1.5	1.9	2.1	2.3	76.0	24.0	6.5	7.3	8.0
98.0	2.0	2.1	2.4	2.6	74.0	26.0	6.7	7.5	8.2
97.5	2.5	2.4	2.7	2.9	72.0	28.0	6.9	7.7	8.4
97.0	3.0	2.6	2.9	3.2	70.0	30.0	7.0	7.8	8.6
96.5	3.5	2.8	3.1	3.4	68.0	32.0	7.1	8.0	8.7
96.0	4.0	3.0	3.4	3.7	66.0	34.0	7.2	8.1	8.9
95.5	4.5	3.2	3.5	3.9	64.0	36.0	7.3	8.2	9.0
95.0	5.0	3.3	3.7	4.1	62.0	38.0	7.4	8.3	9.1
94.0	6.0	3.6	4.1	4.5	60.0	40.0	7.5	8.4	9.2
93.0	7.0	3.9	4.4	4.8	58.0	42.0	7.5	8.4	9.2
92.0	8.0	4.1	4.6	5.1	56.0	44.0	7.6	8.5	9.3
91.0	9.0	4.4	4.9	5.4	54.0	46.0	7.6	8.5	9.3
90.0	10.0	4.6	5.1	5.6	52.0	48.0	7.6	8.6	9.4
89.0	11.0	4.8	5.4	5.9	50.0	50.0	7.6	8.6	9.4

Table D.3.B. Maximum tolerated ranges for the R-value test at a significance level of 1% probability using components of purity analyses as indicating attribute in chaffy seeds.

Average % of the component and its complement		Tolerated range for number of independent samples (N)			Average % of the component and its complement		Tolerated range for number of independent samples (N)		
		5-9	10-19	20			5-9	10-19	20
99.9	0.1	0.5	0.6	0.6	88.0	12.0	5.2	5.8	6.4
99.8	0.2	0.7	0.8	0.9	87.0	13.0	5.4	6.0	6.6
99.7	0.3	0.9	1.0	1.1	86.0	14.0	5.5	6.2	6.8
99.6	0.4	1.0	1.1	1.2	85.0	15.0	5.7	6.4	7.0
99.5	0.5	1.1	1.3	1.4	84.0	16.0	5.8	6.6	7.2
99.4	0.6	1.2	1.4	1.5	83.0	17.0	6.0	6.7	7.4
99.3	0.7	1.3	1.5	1.6	82.0	18.0	6.1	6.9	7.5
99.2	0.8	1.4	1.6	1.7	81.0	19.0	6.3	7.0	7.7
99.1	0.9	1.5	1.7	1.8	80.0	20.0	6.4	7.1	7.8
99.0	1.0	1.6	1.8	1.9	78.0	22.0	6.6	7.4	8.1
98.5	1.5	1.9	2.2	2.4	76.0	24.0	6.8	7.6	8.4
98.0	2.0	2.2	2.5	2.7	74.0	26.0	7.0	7.8	8.6
97.5	2.5	2.5	2.8	3.1	72.0	28.0	7.2	8.0	8.8
97.0	3.0	2.7	3.0	3.3	70.0	30.0	7.3	8.2	9.0
96.5	3.5	2.9	3.3	3.6	68.0	32.0	7.4	8.3	9.1
96.0	4.0	3.1	3.5	3.8	66.0	34.0	7.5	8.5	9.3
95.5	4.5	3.3	3.7	4.1	64.0	36.0	7.6	8.6	9.4
95.0	5.0	3.5	3.9	4.3	62.0	38.0	7.7	8.7	9.5
94.0	6.0	3.8	4.2	4.6	60.0	40.0	7.8	8.8	9.6
93.0	7.0	4.1	4.6	5.0	58.0	42.0	7.9	8.8	9.7
92.0	8.0	4.3	4.8	5.3	56.0	44.0	7.9	8.9	9.7
91.0	9.0	4.6	5.1	5.6	54.0	46.0	7.9	8.9	9.8
90.0	10.0	4.8	5.4	5.9	52.0	48.0	8.0	8.9	9.8
89.0	11.0	5.0	5.6	6.1	50.0	50.0	8.0	8.9	9.8

Table D.4.A. Maximum tolerated ranges for the R-value test at a significance level of 1% probability using components of germination tests as indicating attribute in non-chaffy seeds.

Average % of the component and its complement		Tolerated range for number of independent samples (N)			Average % of the component and its complement		Tolerated range for number of independent samples (N)		
		5-9	10-19	20			5-9	10-19	20
99	1	5	6	6	74	26	22	24	26
98	2	7	8	9	73	27	22	25	27
97	3	9	10	11	72	28	22	25	27
96	4	10	11	12	71	29	22	25	27
95	5	11	12	13	70	30	23	25	28
94	6	12	13	15	69	31	23	26	28
93	7	13	14	16	68	32	23	26	28
92	8	14	15	17	67	33	23	26	28
91	9	14	16	17	66	34	23	26	29
90	10	15	17	18	65	35	24	26	29
89	11	16	17	19	64	36	24	26	29
88	12	16	18	20	63	37	24	27	29
87	13	17	19	20	62	38	24	27	29
86	14	17	19	21	61	39	24	27	29
85	15	18	20	22	60	40	24	27	30
84	16	18	20	22	59	41	24	27	30
83	17	19	21	23	58	42	24	27	30
82	18	19	21	23	57	43	24	27	30
81	19	19	22	24	56	44	24	27	30
80	20	20	22	24	55	45	25	27	30
79	21	20	23	25	54	46	25	27	30
78	22	20	23	25	53	47	25	28	30
77	23	21	23	25	52	48	25	28	30
76	24	21	24	26	51	49	25	28	30
75	25	21	24	26	50	50	25	28	30

Table D.4.B. Maximum tolerated ranges for the R-value test at a significance level of 1% probability using components of germination tests as indicating attribute in chaffy seeds.

Average % of the component and its complement		Tolerated range for number of independent samples (N)			Average % of the component and its complement		Tolerated range for number of independent samples (N)		
		5-9	10-19	20			5-9	10-19	20
99	1	6	6	7	74	26	23	25	28
98	2	8	8	9	73	27	23	26	28
97	3	9	10	11	72	28	23	26	28
96	4	10	12	13	71	29	23	26	29
95	5	11	13	14	70	30	24	26	29
94	6	12	14	15	69	31	24	27	29
93	7	13	15	16	68	32	24	27	29
92	8	14	16	17	67	33	24	27	30
91	9	15	17	18	66	34	24	27	30
90	10	16	17	19	65	35	25	27	30
89	11	16	18	20	64	36	25	28	30
88	12	17	19	21	63	37	25	28	30
87	13	17	20	21	62	38	25	28	31
86	14	18	20	22	61	39	25	28	31
85	15	18	21	23	60	40	25	28	31
84	16	19	21	23	59	41	25	28	31
83	17	19	22	24	58	42	25	28	31
82	18	20	22	24	57	43	25	28	31
81	19	20	23	25	56	44	26	29	31
80	20	21	23	25	55	45	26	29	31
79	21	21	24	26	54	46	26	29	31
78	22	21	24	26	53	47	26	29	31
77	23	22	24	27	52	48	26	29	31
76	24	22	25	27	51	49	26	29	31
75	25	22	25	27	50	50	26	29	31

Table D.5.A. Maximum tolerated ranges for the R-value test at a significance level of 1% probability using components of other seed count analyses as indicating attribute in non-chaffy seeds.

Average count of other seeds	Tolerated range for number of independent samples (N)			Average count of other seeds	Tolerated range for number of independent samples (N)			Average count of other seeds	Tolerated range for number of independent samples (N)		
	5-9	10-19	20		5-9	10-19	20		5-9	10-19	20
1	6	7	7	47	38	42	46	93	53	59	65
2	8	9	10	48	38	43	47	94	53	60	65
3	10	11	12	49	39	43	47	95	54	60	66
4	11	13	14	50	39	44	48	96	54	60	66
5	13	14	15	51	39	44	48	97	54	61	66
6	14	15	17	52	40	45	49	98	54	61	67
7	15	17	18	53	40	45	49	99	55	61	67
8	16	18	19	54	40	45	50	100	55	62	67
9	17	19	21	55	41	46	50	101	55	62	68
10	18	20	22	56	41	46	51	102	55	62	68
11	19	21	23	57	42	47	51	103	56	62	68
12	19	22	24	58	42	47	51	104	56	63	69
13	20	23	25	59	42	47	52	105	56	63	69
14	21	23	26	60	43	48	52	106	57	63	69
15	22	24	26	61	43	48	53	107	57	64	70
16	22	25	27	62	43	49	53	108	57	64	70
17	23	26	28	63	44	49	54	109	57	64	70
18	24	26	29	64	44	49	54	110	58	65	71
19	24	27	30	65	44	50	54	111	58	65	71
20	25	28	30	66	45	50	55	112	58	65	71
21	25	28	31	67	45	50	55	113	58	65	72
22	26	29	32	68	45	51	56	114	59	66	72
23	27	30	33	69	46	51	56	115	59	66	72
24	27	30	33	70	46	52	56	116	59	66	73
25	28	31	34	71	46	52	57	117	59	67	73
26	28	32	35	72	47	52	57	118	60	67	73
27	29	32	35	73	47	53	58	119	60	67	73
28	29	33	36	74	47	53	58	120	60	67	74
29	30	33	37	75	48	53	58	121	60	68	74
30	30	34	37	76	48	54	59	122	61	68	74
31	31	34	38	77	48	54	59	123	61	68	75
32	31	35	38	78	49	54	60	124	61	68	75
33	32	36	39	79	49	55	60	125	61	69	75
34	32	36	39	80	49	55	60	126	62	69	76
35	33	37	40	81	49	55	61	127	62	69	76
36	33	37	41	82	50	56	61	128	62	70	76
37	34	38	41	83	50	56	61	129	62	70	76
38	34	38	42	84	50	56	62	130	63	70	77
39	34	39	42	85	51	57	62	131	63	70	77
40	35	39	43	86	51	57	62	132	63	71	77
41	35	40	43	87	51	57	63	133	63	71	78
42	36	40	44	88	52	58	63	134	64	71	78
43	36	41	44	89	52	58	64	135	64	71	78
44	37	41	45	90	52	58	64	136	64	72	78
45	37	41	45	91	52	59	64	137	64	72	79
46	37	42	46	92	53	59	65	138	64	72	79

Table D.5.B. Maximum tolerated ranges for the R-value test at a significance level of 1% probability using components of other seed count analyses as indicating attribute in chaffy seeds.

Average count of other seeds	Tolerated range for number of independent samples (N)			Average count of other seeds	Tolerated range for number of independent samples (N)			Average count of other seeds	Tolerated range for number of independent samples (N)		
	5-9	10-19	20		5-9	10-19	20		5-9	10-19	20
1	7	8	9	47	47	53	58	93	66	74	81
2	10	11	12	48	48	54	59	94	67	75	82
3	12	14	15	49	48	54	59	95	67	75	82
4	14	16	17	50	49	55	60	96	67	75	83
5	16	18	19	51	49	55	60	97	68	76	83
6	17	19	21	52	50	56	61	98	68	76	83
7	19	21	23	53	50	56	62	99	68	77	84
8	20	22	24	54	51	57	62	100	69	77	84
9	21	23	26	55	51	57	63	101	69	77	85
10	22	25	27	56	52	58	63	102	69	78	85
11	23	26	28	57	52	58	64	103	70	78	86
12	24	27	30	58	52	59	64	104	70	79	86
13	25	28	31	59	53	59	65	105	70	79	86
14	26	29	32	60	53	60	65	106	71	79	87
15	27	30	33	61	54	60	66	107	71	80	87
16	28	31	34	62	54	61	66	108	71	80	88
17	29	32	35	63	55	61	67	109	72	80	88
18	29	33	36	64	55	62	68	110	72	81	88
19	30	34	37	65	56	62	68	111	72	81	89
20	31	35	38	66	56	63	69	112	73	81	89
21	32	36	39	67	56	63	69	113	73	82	90
22	33	36	40	68	57	64	70	114	73	82	90
23	33	37	41	69	57	64	70	115	74	83	90
24	34	38	42	70	58	65	71	116	74	83	91
25	35	39	42	71	58	65	71	117	74	83	91
26	35	40	43	72	58	65	72	118	75	84	92
27	36	40	44	73	59	66	72	119	75	84	92
28	37	41	45	74	59	66	73	120	75	84	92
29	37	42	46	75	60	67	73	121	76	85	93
30	38	42	46	76	60	67	74	122	76	85	93
31	38	43	47	77	60	68	74	123	76	85	93
32	39	44	48	78	61	68	75	124	76	86	94
33	40	44	49	79	61	69	75	125	77	86	94
34	40	45	49	80	62	69	75	126	77	86	95
35	41	46	50	81	62	69	76	127	77	87	95
36	41	46	51	82	62	70	76	128	78	87	95
37	42	47	51	83	63	70	77	129	78	87	96
38	43	48	52	84	63	71	77	130	78	88	96
39	43	48	53	85	63	71	78	131	79	88	96
40	44	49	54	86	64	71	78	132	79	88	97
41	44	50	54	87	64	72	79	133	79	89	97
42	45	50	55	88	65	72	79	134	79	89	98
43	45	51	55	89	65	73	80	135	80	89	98
44	46	51	56	90	65	73	80	136	80	90	98
45	46	52	57	91	66	74	80	137	80	90	99
46	47	52	57	92	66	74	81	138	81	90	99