1. Introduction
In agricultural field experiments, the size of the plot is selected in order to achieve a prescribed degree of precision for measurement of the character of primary interest. We then measure the character under study on the whole of the experimental unit i.e., plot. Because of the nature of the character of primary interest like yield, the plot size required is often larger than that needed to measure other characters. In order to save expense and time the measurements of additional characters of interest can be made by sampling a fraction of the whole plot. For example, for plant height, the measurements can be made only from say 10 of the 200 plants in the plot, for tiller number, count only 1 m$^2$ of the 15 m$^2$ plot, for leaf area, measure from only 20 of the approximately 2000 leaves in the plot. For such cases like plant height, leaf area etc. it may not be always feasible or desirable to get the plot wise measurements. Here we resort to sampling in each plot and obtain the measurements on a certain number of sampling units in each plot and subject the data for statistical analysis.

For plot sampling, each experimental plot is a population. Population value, which is the same as the plot value, is estimated from a few plants selected from each plot. The procedure for selecting the plants to be measured and used for estimating the plot value is called the plot sampling technique. To develop a plot sampling technique for the measurement of a character in a given trial, the researcher must clearly specify the sampling unit, the sample size and the sampling design.

1.1 Sampling Unit
The sampling unit is the unit on which actual measurement is made. The important features of an appropriate sampling unit are ease of identifications, ease of measurement, high precision and low cost. It should provide an estimate, or a sample value, that is as close as possible to the value that would have been obtained had all plants in the plot been measured - the plot value. The difference between the sample value and the plot value constitutes the sampling error. Thus a good sampling technique is one that gives small sampling error.

1.2 Sample Size
The number of sampling units taken from the population is sample size. In a replicated field trial where each plot is a population, sample size could be the number of plants per plot used for measuring plant height, or the number of leaves per plot used for measuring leaf area, or the number of hills per plot used for counting tillers. The required sample size for a particular experiment is governed by the sampling variance and the degree of precision desired for the character of interest.
In practice, the size of the sampling variance for most plant characters is generally not known. The desired level of precision can, however, be prescribed by the researcher based on experimental objective and previous experience, in terms of the margin of error, either of the plot mean or of the treatment mean. For example, the researcher may prescribe that the sample estimate should not deviate from the true value by more than 5% or 10%.

**Margin of Error of the Plot Mean**: The sample size for a simple random sampling design that can satisfy a prescribed margin of error of the plot mean is computed as:

\[
n = \frac{(Z_\alpha^2)(v_s)}{(d^2)(\bar{X}^2)}
\]

where \(n\) is the required sample size, \(Z_\alpha\) is the value of the standardized normal variate corresponding to the level of significance \(\alpha\), \(v_s\) is the sampling variance, \(\bar{X}\) is the mean value, and \(d\) is the margin of error expressed as a fraction of the plot mean.

**Margin of Error of the Treatment Mean**: The information of primary interest to the researcher is usually the treatment means or actually the difference of means, rather than the plot mean. Thus, the desired degree of precision is usually specified in terms of the margin of error of the treatment mean rather than of the plot mean. In such a case, sample size is computed as:

\[
n = \frac{(Z_\alpha^2)(v_s)}{r(D^2)(\bar{X}^2) - (Z_\alpha^2)(v_p)}
\]

where \(n\) is the required sample size, \(r\) is the number of replications, \(Z_\alpha\) and \(v_s\) are as defined earlier, \(v_p\) is the variance between plots of the same treatment (i.e., experimental error), and \(D\) is the prescribed margin of error expressed as a fraction of the treatment mean. In this case, additional information on the size of the experimental error \((v_p)\) is needed to compute sample size.

### 1.3 Sampling Design

A sampling design specifies the manner in which the \(n\) sampling units are to be selected from the whole plot. There are five commonly used sampling designs in replicated field trials: simple random sampling, multistage random sampling, stratified random sampling, stratified multistage random sampling and sub-sampling with an auxiliary variable.

In a **simple random sampling design**, there is only one type of sampling unit and, hence, the sample size \((n)\) refers to the total number of sampling units to be selected from each plot consisting of \(N\) units. The selection of the \(n\) sampling units is done in such a way that each of the \(N\) units in the plot is given the same chance of being selected in plot sampling, two of the most commonly used random procedures for selecting \(n\) sampling units per plot are the random-number technique and the random-pair technique.

The **random-number technique** is most useful when the plot can be divided into \(N\) distinct sampling units, such as \(N\) single-plant sampling units or \(N\) single-hill sampling units. The procedure is firstly, divide the \(N\) distinctly differentiable sampling units; randomly select \(n\) distinctly different numbers, each within the range of 1 to \(N\), following a randomization
Sampling in Field Experiments

scheme; and finally, use the sample obtained by taking all the sampling units whose assigned numbers correspond to the random numbers selected.

The random-pair technique is applicable whether or not the plot can be divided uniquely into N sampling units. It is a more widely used technique. Two cases are covered under this technique. Case I is one with clear division of N sampling units per units. First, determine the width (W) and length (L) of the plot in terms of the sampling unit specified, such that \( W \times L = N \). Select n random pairs of numbers, with the first number of each pair ranging from 1 to W and the second number ranging from 1 to L. Use the point of intersection of each random pair of numbers to represent each selected sampling unit.

Case II is one without clear division of N sampling units per plot. Under this the step involved are as follows: Specify the width (W) and length (L) of the plot using the same measurement unit as that of the sampling unit. Select n random pairs of numbers, following the random number procedure, with the first number of the pair lying between 1 and W and the second number lying between 1 and L. Use the point of intersection of each of the random pairs of numbers to represent the starting point of each selected sampling unit.

In contrast to the simple random sampling design, where only one type of sampling unit is involved, the multistage random sampling design is characterized by a series of sampling stages. Each stage has its own unique sampling unit. This design is suited for cases where the sampling unit is not the same as the measurement unit. For example, in a rice field experiment, the unit of measurement for panicle length is a panicle and that for leaf area is a leaf. The use of either the panicle or the leaf as the sampling unit, however, would require the counting and listing of all panicles or all leaves in the plot which is time-consuming task that would definitely not be practical. The selection of the sample is done separately and independently at each stage of sampling, starting with the first stage sampling, then the second stage sampling, and so on, in the proper sequence. At each sampling stage, the random selection procedure follows that of the simple random sampling design.

The stratified random sampling design is useful where there is large variation between sampling units and where important sources of variability follow a consistent pattern. In such cases, the precision of the sample estimate can be improved by grouping the sampling units into different strata in such a way that variability between sampling units within a stratum is smaller than that between sampling units from different strata. The efficiency of the stratified random sampling design relative to the simple random sampling design will be high only if an appropriate stratification technique is used. Some examples of stratification criterion used in agricultural experiments are as follows:

(i) Soil Fertility Pattern. In an insecticide trial where block is based primarily on the direction of insect migration, known patterns of soil fertility cause substantial variability among plants in the same plot. In such a case, a stratified random sampling design may be used so that each plot is first divided into several strata based on the known fertility patterns and sample plants are then randomly selected from each stratum.
(ii) **Stress Level.** In a variety screening trial for tolerance for soil salinity, areas within the same plot may be stratified according to the salinity level before sample plants are randomly selected from each stratum.

(iii) **Within-Plant Variance.** In a rice hill, panicles from the taller tillers are generally larger than those from the shorter ones. Hence, in measuring such yield components as panicle length or number of grains per panicles, panicles within a hill are stratified according to the relative height of the tillers before sample panicles are randomly selected from each position (or stratum).

When the stratification technique is combined with the multistage sampling technique, the resulting design is known as **stratified multistage random sampling.** In it, multistage sampling is applied first and then stratification is used on one or more of the identified sampling stages. Consider the case where a rice researcher wishes to measure the average number of grains per panicle through the use of a two-stage sampling design with individual hills in the plot as the primary sampling unit and individual panicles in a hill as the secondary sampling unit. It is realized that the number of grains per panicle varies greatly between the different panicles of the same hill. A logical alternative is to apply the stratification technique by dividing the panicles in each selected hill (i.e., primary sampling unit) into k strata, based on their relative position in the hill, before a simple random sample of m panicles from each stratum is taken separately and independently for the k strata. In this case, the sampling technique is based on a two-stage sampling design with stratification applied on the secondary unit. Of course, instead of the secondary unit (panicles) the researcher could have stratified the primary unit (i.e., single-hill) based on any source of variation pertinent to his experiment. In that case, the sampling technique would have been a two-stage sampling design with stratification of the primary unit. Or, the researcher could have applied both stratification criteria, one on the hills and another on the panicles, and the resulting sampling design would have been a two-stage sampling with stratification of both the primary and secondary units.

The main features of a design for **subsampling with an auxiliary variable** are:

- In addition to the character of interest, say X, another character, say Z, which is closely associated with and is easier to measure than X, is chosen.

- Character Z is measured both on the main sampling unit and on the subunit, whereas variable X is measured only on the subunit. The subunit is smaller than the main sampling unit and is embedded in the main sampling unit.

This design is usually used when the character of interest, say X, is so variable that the large size of sampling unit or the large sample size required to achieve a reasonable degree of precision or both, would be impractical. To improve the precision in the measurement of X, without unduly increasing either the sample size or the size of sampling unit, the subsampling with an auxiliary variable design can be used. Improvement is achieved by measuring Z from a unit larger than the unit where X is measured. Since Z and X are closely related and their relationship is known, it is as if X is measured from the large unit. Care should be taken that measurement of Z must be with minimum cost.
2. Supplementary Techniques
So far, we have discussed sampling techniques for individual plots, each of which is treated independently and without reference to other plots in the same experiment. However, in a replicated field trial where the sampling technique is to be applied to each and all plots in the trial, a question usually raised is whether the same set of random sample can be repeated in all plots or whether different random processes are needed for different plots. And, when data of a plant character are measured more than once over time, the question is whether the measurements should be made on the same samples at all stages of observation or should randomization be applied.

The two techniques aimed at answering these questions are block sampling and sampling for repeated measurements.

2.1 Block Sampling
It is a technique in which all plots of the same block (i.e. replication) are subjected to the same randomization scheme (i.e. using the same sample location in the plot) and different sampling schemes are applied separately and independently for different blocks.

The block sampling technique has the following desirable features:

- Randomization is minimized. With block sampling randomization is done only r times instead of rt times as it is when randomization is done separately for each and all plots.

- Data collection is facilitated. With block sampling, all plots in the same block have the pattern of sample locations so that an observer (data collector) can easily move from plot to plot within a block without the need to reorient himself to a new pattern of sample locations.

- Uniformity between plots of the same block is enhanced because there is no added variation due to changes in sample location from plot to plot.

- Data collection by block is encouraged. For example, if data collection is to be done by several persons, each can be conveniently assigned to a particular block which facilitates the speed and uniformity of data collection. Even if there is only one observer for the whole experiment, he can complete the task one block at a time, taking advantage of the similar sample locations of plots in the same block and minimizing one source of variation among plots, namely, the time span in data collection.

2.2 Sampling for Repeated Measurements.
Plant characters are commonly measured at different growth stages of the crop. For example, tiller number in rice may be measured at 30, 60, 90 and 120 days after transplanting or at the tillering, flowering and harvesting stages. If such measurements are made on the same plants at all stages of observation, the resulting data may be biased because plants that are subjected to frequent handling may behave differently from others. In irrigated wetland rice, for example, frequent trampling around plants or frequent handling of plants not only affects the plant characters being measured but also affects the plants’ final yields. On the other hand, the use of an entirely different set of sample plants at different growth stages could introduce variation due to differences between sample
plants. The partial replacement procedure provides for a satisfactory compromise between the two conflicting situations. With partial replacement, only a portion \( p \) of the sample plants used in one growth stage is retained for measurement in the succeeding stage. The other portion of \( (1-p) \) sample plants is randomly obtained from the remaining plants in the plot. The size of \( p \) depends on the size of the estimated undesirable effect of repeated measurements of the sample plants in a particular experiment. The smaller this effect, the larger \( p \) should be. For example, in the measurement of plant height and tiller number in transplanted rice, \( p \) is usually about 0.75. That is, about 75% of the sample plants measured at given growth stage is retained for measurement in the succeeding stage and the remaining 25% is obtained at random from the other plants in the plot.

3. Analysis
The various steps involved in the analysis of sampled data are described here considering a block design setting. Suppose an experiment is conducted with ‘t’ treatments replicated ‘r’ times and let there be ‘n’ observations made in each plot. We assume the following linear additive model for the block design.

\[
Y_{ijk} = \mu + \tau_i + \beta_j + e_{ij} + \eta_{ijk}
\]

where \( Y_{ijk} \) is the observation on the \( k^{th} \) sample for the \( i^{th} \) treatment in the \( j^{th} \) replicate (\( i = 1,2,\ldots,t ; j = 1,2,\ldots,r ; k = 1,2,\ldots,n \)), \( \mu \) is the general mean effect, \( \tau_i \) is the effect of \( i^{th} \) treatment, \( \beta_j \) is the effect of \( j^{th} \) replication, \( e_{ij} \) is the plot error distributed as \( N(0, \sigma_e^2) \), \( \eta_{ijk} \) is the sampling error distributed as \( N(0, \sigma_s^2) \).

The analysis of variance will be of the form given below:

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>SS</th>
<th>MS</th>
<th>E(MS)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>(r-1)</td>
<td>SST</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Treatments</td>
<td>(t-1)</td>
<td>SSR</td>
<td>( \sigma_s^2 + n\sigma_e^2 + \frac{m}{t-1} \sum (\tau_i - \tau.)^2 )</td>
<td></td>
</tr>
<tr>
<td>Treatment x Replication</td>
<td>(t-1)(r-1)</td>
<td>SSRT</td>
<td>( \sigma_s^2 )</td>
<td></td>
</tr>
<tr>
<td>(Plot error)</td>
<td></td>
<td></td>
<td>( \sigma_s^2 + n\sigma_e^2 )</td>
<td></td>
</tr>
<tr>
<td>Sampling Error</td>
<td>rt(n-1)</td>
<td>SSE</td>
<td>( s_2^2 )</td>
<td></td>
</tr>
<tr>
<td>(Samples within plots)</td>
<td></td>
<td></td>
<td>( \sigma_s^2 )</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>rt(n-1)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The sampling error is estimated as \( \hat{\sigma}_s^2 = s_2^2 \).

The plot error is estimated as \( \hat{\sigma}_e^2 = \frac{s_1^2 - s_2^2}{n} \).

When \( \hat{\sigma}_e^2 \) is negative, it is taken as zero.

The variance of the \( i^{th} \) treatment mean (\( \bar{Y}_{.,i} \)) based on \( r \)-replications and \( s \)-samples per plot

\[
= \frac{\sigma_s^2 + n\sigma_e^2}{rn}
\]
The estimated variance of \( (\bar{Y}_{i..}) \) = \( \frac{(\hat{\sigma}_s^2 + n\hat{\sigma}_c^2)}{rm} \)

Taking the number of sampling units in a plot to be large (infinite), the estimated variance of a treatment mean when there is complete recording (i.e., the entire plot is harvested) = \( \frac{\hat{\sigma}_c^2}{r} \)

The efficiency of sampling as compared to complete recording

\[
\frac{\hat{\sigma}_c^2/r}{(\sigma_s^2 + n\sigma_c^2)/m}
\]

The standard error of a treatment mean (\( \bar{Y}_{i..} \)) with ‘n’ samples per plot and with ‘r’ replications is

\[
\left[ \frac{\hat{\sigma}_s^2 + \hat{\sigma}_c^2}{m} \right]^{1/2}
\]

The percentage standard error or coefficient of variation is

\[
p = \frac{\left[ \frac{\hat{\sigma}_s^2 + \hat{\sigma}_c^2}{m} \right]^{1/2}}{\bar{Y}_{i..}} \times 100
\]

Thus

\[
n = \frac{\hat{\sigma}_s^2}{r} \left[ \frac{1}{p^2(\bar{Y}_{i..})^2} - \frac{\hat{\sigma}_c^2}{(100)^2} \right]
\]

For any given \( r \) and \( p \), there will be \( t \) values for \( s \) corresponding to the \( t \) treatment means. The maximum \( s \) will ensure the estimation of any treatment mean with a standard error not exceeding \( p \) percent.

The sum of squares due to different components of ANOVA can be obtained as follows:

Form a two way table between replications and treatments, each cell figure being the total over all samples from a plot.

\[
\text{Grand Total (G.T.)} = \sum_i \sum_j \sum_k y_{ijk}, \quad \text{Correction factor (C.F.)} = \frac{(G.T.)^2}{rtm}
\]

\[
\text{Total S.S.} = \sum_i \sum_j \left( \sum_k y_{ijk} \right)^2 / n - \text{C.F.}
\]

\[
T_i = \text{\textit{i}th treatment total} = \sum_j \sum_k y_{ijk}
\]

\[
R_j = \text{\textit{j}th replication total} = \sum_i \sum_k y_{ijk}
\]

\[
\text{Treatment S.S.} = \sum_i \frac{T_i^2}{m} - \text{C.F.}, \quad \text{Replication S.S.} = \sum_j \frac{R_j^2}{tn} - \text{C.F}
\]
Replication x Treatment S.S. = Total S.S. - Replication S.S - Treatment S.S.

Total S.S. of the entire data = \sum \sum \sum y_{ijk}^2 - C.F.

S.S. due to sampling error = Total S.S. of the entire data - Replication S.S. - Treatment S.S. - Replication x Treatment S.S.

**Exercise:** To study the effect of differences in the number of plants per hill on the growth of Maize crop, a randomized block design was laid out at the Agricultural College Farm, Poona. The treatments tried were A - one plant per hill, B - two plants per hill, C - three plants per hill, D - four plants per hill.

The net plot size used in the layout was 26’ × 20’ and the spacing between hills was 2’ × 2’. The table below gives the data on the length (in inches) of 5 cobs randomly selected from each plot:

<table>
<thead>
<tr>
<th>Replication</th>
<th>Cob number</th>
<th>Treatments</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>I</td>
<td>1</td>
<td>9.3</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>8.8</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>9.0</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>8.8</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>8.6</td>
</tr>
<tr>
<td>II</td>
<td>1</td>
<td>10.2</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>9.0</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>9.4</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>9.6</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>9.8</td>
</tr>
<tr>
<td>III</td>
<td>1</td>
<td>9.9</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>10.4</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>11.0</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>10.8</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>10.0</td>
</tr>
<tr>
<td>IV</td>
<td>1</td>
<td>10.6</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>9.2</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>9.9</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>10.4</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>9.9</td>
</tr>
</tbody>
</table>
Sampling in Field Experiments

<table>
<thead>
<tr>
<th>V</th>
<th>1</th>
<th>10.4</th>
<th>11.0</th>
<th>9.9</th>
<th>7.7</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2</td>
<td>9.0</td>
<td>10.4</td>
<td>9.0</td>
<td>7.0</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>9.7</td>
<td>9.0</td>
<td>8.9</td>
<td>7.0</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>9.3</td>
<td>10.2</td>
<td>8.9</td>
<td>6.7</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>9.6</td>
<td>9.6</td>
<td>9.4</td>
<td>7.2</td>
</tr>
</tbody>
</table>

(a) Analyze the data and find the standard error of treatment means.
(b) Estimate the plot and sampling components of error variance and use these estimates to find out the relative efficiency of sampling.
(c) Prepare a table giving the minimum number of sampling units per plot necessary to estimate the treatment means with 4 and 5 percent standard error when the number of replications are 5 and 6.

Calculations

**Step 1:** Form the following two way table between replications and treatments, each cell figure being the total of cob lengths in five samples from a plot.

<table>
<thead>
<tr>
<th>Replication</th>
<th>Treatments</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>I</td>
<td>44.5</td>
<td>46.6</td>
</tr>
<tr>
<td>II</td>
<td>48.0</td>
<td>49.7</td>
</tr>
<tr>
<td>III</td>
<td>52.1</td>
<td>44.9</td>
</tr>
<tr>
<td>IV</td>
<td>50.0</td>
<td>45.0</td>
</tr>
<tr>
<td>V</td>
<td>48.0</td>
<td>50.2</td>
</tr>
<tr>
<td>Total</td>
<td>242.6</td>
<td>236.4</td>
</tr>
</tbody>
</table>

**Step 2:** Calculation of sum of squares and Analysis of variance.

The various sum of squares can be obtained using the formulae given above and the ANOVA table can be obtained.

<table>
<thead>
<tr>
<th>Source</th>
<th>D.F.</th>
<th>S.S.</th>
<th>M.S.</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>4</td>
<td>4.91</td>
<td>1.23</td>
<td>0.59</td>
</tr>
<tr>
<td>Treatment</td>
<td>3</td>
<td>112.09</td>
<td>37.36</td>
<td>18.05**</td>
</tr>
<tr>
<td>Replication x Treatment</td>
<td>12</td>
<td>24.88</td>
<td>2.07</td>
<td>6.68*</td>
</tr>
<tr>
<td>(plot error)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Samples within plots</td>
<td>80</td>
<td>24.91</td>
<td>0.31</td>
<td></td>
</tr>
<tr>
<td>(Sampling error )</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>99</td>
<td>166.79</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

** denotes significant at 1 percent level and * significant at 5 percent level.
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The mean square \( (s_1^2) \) is first tested against \( s_2^2 \) if - (i) \( s_1^2 \) is significant, then treatments are tested against \( s_1^2 \) and if - (ii) \( s_1^2 \) is not significant, the treatments are tested against the pooled mean square of \( s_1^2 \) and \( s_2^2 \). In the present case \( s_1^2 \) is significant, so we test the treatments against \( s_1^2 \).

**Step 3:** Standard Error of the difference between two treatment means

\[
S.E_d = \sqrt{\frac{s_1^2}{m}} = \sqrt{\frac{2 \times 2.07}{5 \times 5}} = 0.4069 \text{ inches.}
\]

**Step 4:** Efficiency

\[
\hat{\sigma}_e^2 = \frac{s_1^2 - s_2^2}{n} = \frac{2.07 - 0.31}{5} = 0.3520
\]

\[
\hat{\sigma}_s^2 = s_2^2 = 0.31
\]

The estimated variance of

\[
\overline{Y_{i.}} = \frac{\hat{\sigma}_s^2}{m} + \frac{\hat{\sigma}_e^2}{r} = \frac{2.070}{25} = 0.0828
\]

Estimated variance in case of complete recording \( \frac{\sigma^2}{r} = \frac{0.352}{5} = 0.0704 \).

Efficiency of sampling as compared to complete recording

\[
\frac{\sigma^2}{r} = \frac{(\hat{\sigma}_s^2 + n\hat{\sigma}_e^2) / mn}{0.85}
\]

**Step 5:** Estimation of sampling units per plot

\[
s = \frac{\hat{\sigma}_e^2}{r} \left\{ \frac{1}{p^2 (\overline{Y_{i.}})^2} - \frac{\hat{\sigma}_e^2}{(100)^2} \right\}
\]

Thus the number of sampling units required to measure the treatment means with 4 and 5 per cent standard error when the number of replication are 5 and 6 is worked out and is presented below.

<table>
<thead>
<tr>
<th>Treatments</th>
<th>Treatment means</th>
<th>( p = 4 )</th>
<th>( r = 5 )</th>
<th>( r = 6 )</th>
<th>( p = 5 )</th>
<th>( r = 5 )</th>
<th>( r = 6 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>9.704</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>9.456</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>3</td>
<td>8.116</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>7.084</td>
<td>5</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>
Step 6: Conclusion
(a) The treatments are found to be highly significant.
(b) Efficiency of sampling as compared to complete recording is 85 per cent.
(c) The number of sampling units necessary to estimate treatment means with

   (i) 4 per cent standard error
       when number of replications is 5 is 5,
       when number of replications is 6 is 3.

   (ii) 5 per cent standard error
       when number of replications is 5 is 2,
       when number of replications is 6 is 1.

References and Suggested Reading