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**ON THE POSSIBILITY OF APPLICATION OF INCOMPLETE BLOCK DESIGNS IN  
DUS TRIALS WITH GROUPS OF GENOTYPES**

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# ON THE POSSIBILITY OF APPLICATION OF INCOMPLETE BLOCK DESIGNS IN DUS TRIALS WITH GROUPS OF GENOTYPES

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## Summary

The possibility of application of 1-resolvable incomplete designs in DUS trials is discussed in the case when genotypes are subdivided into several groups. In typical situation in DUS testing only complete blocks are used even if the number of genotypes is relatively high. Incomplete blocks have proved their high efficiency in testing genotypes for value for cultivation and use (VCU trials) so it was expected that they could be also useful in DUS trials. In the case when varieties are subdivided into several groups some constraint on randomization must be imposed.

## 1. Introduction

The only two experimental designs used in ordinary DUS trials are completely randomized design and randomized complete block design. On experimental basis incomplete blocks were used in some DUS trials in Denmark (Kristensen, 1999) and in Poland (Pilarczyk, 1999). On the other hand in so called VCU trials incomplete block designs are widely used. Such incomplete experimental designs as square, rectangular and cubic lattice were introduced to practice in years 1940s. These designs exist only for some number of varieties and in all these designs the blocks were of the same size dependent on the number of varieties being compared. When non-lattice number of varieties had to be compared the only solution was to add some additional (dummy) varieties or to withdraw some other to receive suitable number of varieties. In 1980s much wider class of resolvable block designs was introduced to practice in many countries of Europe. These designs exist practically for every number of varieties, but in some cases blocks of different sizes must be used [Patterson at al. 1978]. In practice blocks that differ for one plot are used. Before being used in a field designs must be randomized. In resolvable block designs randomization consists of three steps. Randomization of replicates (superblocks), randomization of incomplete blocks within superblocks and randomization of varieties within incomplete blocks. In some situations additional constrains on placement of varieties is imposed. For example when varieties belonging to different competition groups are compared [David and Kempton, 1996]. When varieties of different height are compared it is sometimes better to constrain randomization and use a special approach proposed by David et. al. [1996]. In that approach varieties are grouped into three groups, very high, medium high and short. After using mentioned approach none of very high varieties will be put on adjacent plot to short variety. The main aim of restricted randomization was to decrease the inter-plot neighbouring influences. A little different situation appears in DUS testing. Researchers often form groups of varieties and want them to be placed on neighbouring plots as it facilitates making immediate comparisons of similar varieties growing close to each other.

## 2. Designs for nested structure of treatments

### 2.1 Design for “independent” groups of treatments

Sometimes treatments are grouped according to natural or artificial criterion. If for example there is 24 varieties to be compared and they form two groups (G1 and G2) of 12 varieties so if we are not interested in comparisons of treatments assigned to different groups, we can apply disconnected incomplete block design with blocks of 12 plots. If we assume for simplicity that only two replicates are used and plots are formed in two rows, the design can have a form (after randomization):

Block 3 (group G2)												Block 1 (group G1)											
18	20	15	16	19	22	21	14	13	17	24	12	6	2	8	1	5	7	9	3	11	10	4	12
Block 4 (group G1)												Block 2 (group G2)											
7	8	11	4	10	1	5	9	6	3	12	2	19	15	24	20	23	14	21	18	17	13	16	22

Fig. 1

Field scheme of disconnected trial with two groups of varieties (first group – numbers from 1 to 12 and second one – numbers from 13 to 24)

If necessary the guard plots can be used to separate blocks. The randomization in such design consists of two steps:

- random allocation of blocks (groups) within replicates;
- random allocation of varieties within blocks.

The design is disconnected and as the result of it the comparisons of treatments belonging to different groups are impossible on the intra-block basis as they are completely confounded with block effects but such comparisons are possible on the inter-block basis, Kempton et al. [1997]). In mentioned book it is also shown how much the variance of variety comparisons can be higher in inter-block analysis in comparison to intra-block analysis. But if we are not interested in such comparisons we can use such design as within groups comparisons are made with full efficiency. We can look for this design as for two group designs of 12 treatments. The comparisons are limited to within-group treatments and only common thing for both groups is mean square for error having summed degrees of freedom from both component designs. It is particularly important when groups are small and mean squares for error have low degrees of freedom. The extending of the idea for more than two groups is straightforward. When one or several of groups consist of numerous genotypes incomplete block design can be used for such groups while for smaller groups randomized complete block are more appropriate. An example of this kind design is given in a book by Kempton and Fox [1957]. Also the discussion about the sizes of variances of variety comparisons is presented in mentioned book.

## 2.2 Designs for limitation of between group influences

When separation of varieties belonging to different groups is senseless (or impossible) or if we are interested also in comparisons between varieties belonging to different groups and if there are high neighbouring influences expected between varieties belonging to different groups we can use one of designs constructed in such a way that varieties belonging to extreme groups (the elements of such groups can cause the highest neighbouring influences when placed in adjacent plots) never met on neighbouring plots belonging or not belonging to the same incomplete block. Groups of varieties are then called the interference groups. How to plan such experiments with use resolvable blocks and with additional constraints imposed on randomization we can find in David et al. [1996]. Plans of such designs can be generated by especially prepared programs such as ALPHA+ (Williams and Talbot, 1993) or CycDesigN (Whitaker et al., 1999). An example of such two-replicate design when there are three interference groups, the first one consisting of varieties 1,2,3 and 4, the second one consisting of varieties 5,6,..., 20 and the third one of 21,22,23 and 24 is given in figure 2. As you can see neither two varieties (one belonging to the first group and the second belonging to the third group) occur on adjacent plots. The efficiency of such design is usually a bit smaller than typical  $\alpha$ -design with the same block sizes but with no additional constraints in randomization. The efficiency factor of the design presented below is 0.650. The effectiveness of such design in limitation of inter-plot treatment influences depends heavily on proper identification of interference groups. Wrong identification of such groups can lead to a larger interference than with a standard design without variety grouping.

Block 1				Block 1				Block 3				Block 4				Block 5				Block 6			
1	16	17	19	6	8	21	10	22	20	3	15	4	7	23	18	24	13	5	12	14	9	11	2

  

Block 7				Block 8				Block 9				Block 10				Block 11				Block 12			
15	1	11	8	24	10	4	20	18	2	16	22	12	6	9	19	3	14	23	5	17	21	13	7

Fig. 2

Field scheme of trial with three interference groups (first group – varieties 1,...,4, second group – varieties 5, 6,...,20 and third one – varieties 21,...,24).

The analysis of variance of the results of an experiment conducted in such design can be restricted to simpler intra-block analysis but as the coefficient of efficiency of this design is only 0.650 what means that 35% of information on variety comparisons is placed between blocks, so better solution is to apply the analysis with recovery of inter-block information.

**Literature**

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