

## Augmented Block Design (ABD): the choice design for large scale farmer participatory on-farm trials

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**Abstract.** Farmer participatory trials are usually kept simple with few treatments and farmers, but this needs not be the case if higher levels of adoption and impact are desired. This paper addresses a design useful for large-scale trials with treatments far from few and with as many farmers as are available. The procedure relies heavily on the ability to construct blocks of seemingly similar farms, sites or farmers. Augmented block designs involve the expansion of blocks with already assigned treatments to accommodate additional ones that are not usually replicated. The design is illustrated with examples and mathematical models for analysis.

### Introduction

Basic considerations in the design of experiments are covered extensively in texts (for example Cochran and Cox, 1957; Cox, 1958; Federer, 1955; Fisher, 1958,1966; Hicks, 1973; John, 1971). However experimental procedures for on-farm farmer participatory trials are not well documented. Indeed, there has been a long-standing view that on farm trials does not conform to conventional trial designs and can therefore not be analysed conventionally. This view is not exactly true as on farm trials have been designed and analysed successfully under various scenario (Korie and Okechukwu, 2000; Mutsaers and Walker, 1991; Mutsaers *et al.*, 1997).

In planning acceptable and statistically valid farmer participatory trials, there is need for balance between small and large numbers of treatments. A very large number of treatments may impose considerable strain on the number of farmers or sites to be used. However, farm or farmer heterogeneity will need to be watched carefully and incorporated in the design (Nokoe, 2000). In the end, the primary goal will be to ensure wide coverage of application of treatments or conditions and consequently enhanced probability of adoption and impact.

Classical designs may not be applicable wholesale under on-farm scenario but the basic

principles of experimentation – replication, randomisation, and coverage – must be maintained. However, it is feasible to design trials with some treatments replicated and others non-replicated because of a large number of treatments, low budget, inadequate personnel, widely dispersed locations and restricted or unequal block sizes, it is possible. This article addresses the augmented block design and how it can be used for large-scale on-farm farmer involved trials.

**Augmented Block Design (ABD).** ABDs involve the enlargement of blocks of a design (with treatments already assigned) to accommodate new treatments which appear usually once in the entire experiment. The design allows for a wide range of technologies to be tested without necessarily straining resources or stifling farmers' interest [e.g. 1000 lines on farm?]. Basic strategies in blocking apply.

**Block Designs.** In block designs treatments are randomly and independently assigned in blocks (of experimental units or subjects). A completely randomised design has in principle only one block. Complete block designs (RCBD) have all treatments present in all blocks. Incomplete block designs may be fully balanced (treatment pairs with same frequency), partially balanced or unbalanced. In the on-farm scenario, blocks could be of varying sizes (Figure 1) and also need not be contiguous (Figure 2).

**Blocking strategies.** Units receiving the experimental treatments constitute the blocks. Thus under on farm scenario, blocks may be any of the following:

- (i) Each farmer: several sites in farmer field (site is the block)
- (ii) Groups of farmers, set of sites (groups or sets are the blocks).

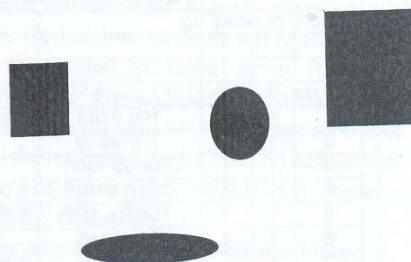


Fig. 1. Varying block sizes is common for on-farm trials.

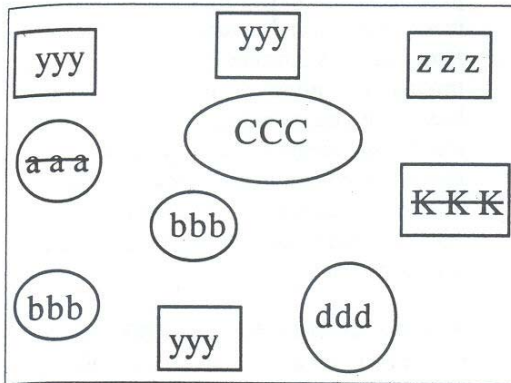


Fig. 2. Non-contiguous blocks- units of the same shape with same code constitute blocks.

These groups of farmers or sites constituting blocks need not be contiguous. The blocks would have been constituted on the basis of objectively-verifiable criteria using various statistical (multivariate classificatory procedures - cluster, principal component analysis, and correspondence analysis) or non-mathematical methods.

Classification variables normally include agronomic, socio-economic, and demographic variables among others. These blocks must be relevant to the objectives of the study; they must represent the target population and should therefore be appropriately delineated. It is necessary to caution that stringent mathematical manipulation must not override common sense, as classification methods do not necessarily yield the same results.

**Treatment allocation in ABD.** In allocating treatments, we separate treatments to be replicated from those that are not to be replicated. The latter

may be referred to as the new lines, while the replicated treatments are equivalent to 'checks' or 'controls' in agronomy and breeding trials. The non-replicated treatments are the augmented 'ones'. An illustration of a simple ABD is given in Table 1, in which the blocks are the farms with different sizes. Block 1 (Farm 1) has 10 sites or units to which are assigned 3 replicated treatments (a, b, c) and 7 non-replicated ones (n1-n7). The basic design is RCBD with 3 treatments and 20 augmented ones.

A second example is given in Figure 3. In this example, there are 2 checks (replicated treatments) and 55 *different* unknown and non-replicated lines in *each* of the 9 blocks. The total number of entries is thus 497 (i.e.  $55 \times 9 + 2$ ).

**Statistical models for conventional analysis of ABD.**

Four models are proposed. They all have the same functional form but differ in the assumptions on the nature of effects (random or fixed) and on the methodology for fitting. Additional coding is required for the latter models. An example is given in Figure 4. In the expressions, m is the overall mean while b represents the effect of block.

Table 1. Illustration of a simple augmented block design

Farm1	Farm2	Farm3	Farm4	Farm5
a, b, c	a, b, c	a, b, c	a, b, c	a, b, c
n1-7	n8-9	n10-15	n16-19	n20
10	5	9	7	4

Note: 1. Complete block design for treatments a, b, c. 2. Treatments n1-n20 appear only once in a block. 3. Last row gives the block sizes (i.e. No. of treatments that are accommodated).

Evaluation of local land races for resistance to					
Date planted 18/3/2000					
Date of inoculation 27/07/2000					
Date harvested 09/12/2000					
Weight of peels 5g					
Peg no	R	Blk	clone	Wt	No
1	1	1	TDr 2383	0.60	3
2	1	1	TDr 99 -3		
3	1	1	TDr 95 -300		
4	1	1	TDr Yb 105	0.06	1
5	1	1	TDr Pe 102	0.08	2
6	1	1	TDr 3546		
7	1	1	TDr 179	0.74	3
8	1	1	TDr 1823	0.09	1

- 2 checks
- 55 unknown in each block
- 9 blocks
- Total  $55 \times 9 + 2 = 497$  entries

Fig. 3. An Example of a simple Augmented Block Design

Pegno	R	Blk	clone	Wt	Numcode	fixedclone	Nonnumcode
58	1	1	TDr 2042	0.40	1	999	L
36	1	1	TDc 94 - 1	0.00	1	999	L
63	1	1	TDc 95 - 152	0.80	1	999	L
10	1	1	TDc 95 - 66	0.28	1	999	L
24	1	1	TDr Bp 111	0.17	1	999	L
57	1	1	TDr Yb 111	1.12	1	999	L
46	1	1	TDr 1640	0.76	1	999	L
34	1	1	TDr 1757	0.49	1	999	L
7	1	1	TDr 179	0.74	1	999	L
8	1	1	TDr 1823	0.09	1	999	L
59	1	1	TDr 2224	0.48	1	999	L
18	1	1	TDr 2269	0.04	1	999	L
1	1	1	TDr 2383	0.60	1	999	L
33	1	1	TDr 2510	0.37	1	999	L
6	1	1	TDr 3546	0.00	1	999	L
21	1	1	TDr 3595	0.46	1	999	L
44	1	1	TDr 3661	0.00	1	999	L
13	1	1	TDr 3663	0.15	1	999	L
51	1	1	TDr 93 - 1	0.09	1	999	L
29	1	1	TDr 93 - 46	0.30	0		check
43	1	1	TDr 93 - 46	0.06	1	999	L
19	1	1	TDr 93 - 49	2.30	1	999	L
41	1	1	TDr 93 - 67	0.00	1	999	L
38	1	1	TDr 95 - 189	0.66	1	999	L
3	1	1	TDr 95 -300	0.00	1	999	L
48	1	1	TDr 99 - 21	0.44	0		check
14	1	1	TDr 99 - 21	0.69	1	999	L
32	1	1	TDr 99 - 7	0.00	1	999	L
2	1	1	TDr 99 -3	0.00	1	999	L
61	1	1	TDr Ag 103	1.87	1	999	L
11	1	1	TDr AG 109	0.01	1	999	L

Fig. 4. Sample coding of data for analysis

**Model 1**

$$Y_{ijk} = \mu + \beta_i + \tau_j + \epsilon_{k(ij)} \quad (1)$$

for  $j=1, \dots, k$ ; where  $k$  is the number of known or replicated lines. The term  $\tau_j$  is the  $j^{\text{th}}$  (replicated) treatment effect while  $e$  is the residual term to be minimised. Note that the non-replicated lines are not incorporated in the model.

Model 1 is ordinary ANOVA of check or  $k$ -treatments in a block design. Estimate of standard error from this model is used to construct LSD(s) or equivalents for comparing treatments in the same, and across blocks. The standard error for comparing treatments in the same block is given as  $\sqrt{2 \cdot EMS}$ , while for treatments across blocks the standard error to use is  $\sqrt{2[EMS+(BMS-EMS)/k]}$ .

**Model 2**

$$Y_{ijk} = \mu + \beta_i + \gamma_j + \epsilon_{k(ij)} \quad (2)$$

$j=1, \dots, k+p$

where  $p$  is the number of non replicated lines, and  $k$

is the number of known or replicated lines. The term  $\gamma$  covers all the treatments (replicated and not).

We compute the Least Squares Means (in SAS) or adjusted means (GENSTAT) and associated standard errors for comparisons.

**Model 3**

$$Y_{ijk} = \mu + \beta_i + \phi_v + \delta_{c(v)} + \text{residual} \quad (3)$$

We fit as nested ANOVA. The term  $\phi_v$  simply tests the contrast 't treatments versus others', while analysis are further done on these sets of treatments nested in the global treatment group  $[\delta_{c(v)}]$ . To achieve this, we add an additional code to our data. The  $\phi_v$  column in the data set will assign a code or name to all the replicated (say, CHECK) and another to all the non-replicated ones (say, LINES). The term  $d$  covers all the treatments.

All effects up to Model 3 are assumed fixed.

**Model 4**

$$Y_{ijk} = \mu + \lambda_z + \beta_i + \kappa \cdot \gamma_j + \text{residual} \quad (4)$$

Model 4 is the preferred model for augmented designs. The modelling and fitting procedures enable effective recovery of both inter-block and inter-treatment information and are based on the mixed model algorithm (Wolfinger *et al.*, 1997). The model is partitioned into fixed and random effects.

The fixed part includes one factor, being  $l_k$  which provides estimates of the  $k+1$  levels (i.e.  $k$  replicated lines + all the new ones treated as one level);  $b_i$  and  $g_j$  are assigned as random ( $g$  is as defined in Model 2).

We provide a further coding ( $k$ ) to the data by assigning numeric values of 1 to the non-replicated lines, and zero to the replicated (designed or check treatments). Multiplying  $g_j$  by the numeric  $k$  leads to the exclusion of the  $k$  replicated lines from random part of the model.

### An extension and illustration

**Cluster ABDs.** ABDs can be done in clusters and data jointly analysed if need be. An example of a large scale-cassava trial in Kenya is illustrated. The strategy involved a stakeholder meeting of farmers, agricultural extension officers, government representatives and researchers in the network. Farmers were classified according to agreed criteria. Farmers were very much aware of the importance of the study and were too eager to have cassava back into their agricultural systems (after the devastation by pests of local varieties). They were therefore keen to evaluate as many clones as possible.

Additional characteristics of the trials are as follows:

- Location: Three sites in northwest Kenya [Siaya,

- One cluster of the trial
- 3-4 checks in IBD
- 20 non replicated lines
- Farmers know clones on farms in cluster; visits encouraged

Mumias, Teso districts] and four in southern region [Rachuonyo(2), Kuria and Migori districts]

- Trials initiated at start of the short rains of 2000.
- At each site, four farms were selected and assigned a certain number of clones in addition to agreed checks. Thus each set of four farms constituted an ABD cluster.
- The basic design for known or replicated lines was IBD (incomplete block design) – Using GENDEX as described in Nguyen (1993). Non-replicated clones were then assigned according to the sizes of the farms (i.e. blocks in cluster).
- Farmers were aware of clones in other farms in the cluster; and were encouraged to visit these farms to assess other clones' performance.
- In each cluster the arrangements of non-replicated lines were not necessarily the same as in other clusters.
- It is also necessary to note that Local (Waite), for example, is a check in one cluster but not in the others (See Figures 5 and 6)

Cluster ABDs enable complete analysis to be done at the district (site), and regional levels. Only slight modifications in the models for analysis are required. Here, blocks are nested in Clusters, while cluster itself is a term in the model. Thus, we only add the effect Cluster, and replace Block with Block within Cluster. Cluster and Block within Cluster are treated as random effects.

**Mother-baby trials.** Related to Cluster ABDs are mother-baby-trials. These involve combination of

Site	S/location	Farmname	Clone
Kehancha	Nyaitara	M. Mogibai	MM96/1871
Kehancha	Nyaitara	M. Mogibai	MM96/4884
Kehancha	Nyaitara	M. Mogibai	MM96/1871
Kehancha	Nyaitara	M. Mogibai	SS4
Kehancha	Nyaitara	M. Mogibai	MIGERA
Kehancha	Nyaitara	M. Mogibai	LOCAL(WAITE)
Kehancha	Taranganya	J. Chacha	MM96/7151
Kehancha	Taranganya	J. Chacha	SS4
Kehancha	Taranganya	J. Chacha	MM96/7688
Kehancha	Taranganya	J. Chacha	LOCAL(WAITE)
Kehancha	Taranganya	J. Chacha	MM96/5280
Kehancha	Taranganya	J. Chacha	MM96/4884
Kehancha	Taranganya	J. Chacha	MM96/1871
Kehancha	Taranganya	J. Chacha	MIGERA
Kehancha			
Kehancha			
Kehancha			
Kehancha			
Kehancha			
Kehancha			
Kehancha			
Kehancha			
Kehancha	Nyaitara	M. Mogibai	MIGERA
Kehancha	Nyaitara	M. Mogibai	MM96/4884
Kehancha	Nyaitara	M. Mogibai	MM96/1871
Kehancha	Nyaitara	M. Mogibai	SS4
Kehancha	Nyaitara	M. Mogibai	LOCAL(WAITE)
Kehancha	Nyaitara	M. Mogibai	TME14
Kehancha	Nyaitara	M. Mogibai	MM96/5280
Kehancha	Nyaitara	M. Mogibai	MM96/3888

Fig. 5. Cluster Augmented Block Design– Cassava trial

Mabera	Ngisiru	J. Masubo	SS4
Mabera	Ngisiru	J. Masubo	
Mabera	Ngisiru	J. Masubo	MM96/9352
Mabera	Ngisiru	J. Masubo	MM96/4466
Mabera	Ngisiru	J. Masubo	MM96/5280
Mabera	Ngisiru	J. Masubo	MIGERA
Mabera	Ngisiru	J. Masubo	MH95/0183
Mabera	Mabera	S. Rioba	MM96/5280
Mabera	Mabera	S. Rioba	MIGERA
Mabera	Mabera	S. Rioba	
Mabera	Mabera	S. Rioba	MM96/7151
Mabera	Mabera	S. Rioba	SS4
Mabera	Mabera	S. Rioba	MM96/7688
Mabera	Mabera	S. Rioba	MM96/4684
Mabera	Mabera	P. Mabere	Unknown2
Mabera	Mabera	P. Mabere	MM96/1871
Mabera	Mabera	P. Mabere	MM96/5280
Mabera	Mabera	P. Mabere	MIGERA
Mabera	Mabera	P. Mabere	MM96/4052
Mabera	Mabera	P. Mabere	SS4
Mabera	Mabera	P. Mabere	
Mabera	Mabera	P. Mabere	MM96/3868
Mabera	Ngisiru	C. Mang'iti	LOCAL(WAITE)
Mabera	Ngisiru	C. Mang'iti	MIGERA
Mabera	Ngisiru	C. Mang'iti	MM96/9308
Mabera	Ngisiru	C. Mang'iti	MM96/5280
Mabera	Ngisiru	C. Mang'iti	MM96/1871
Mabera	Ngisiru	C. Mang'iti	MM96/4684
Mabera	Ngisiru	C. Mang'iti	TME14

- Note that arrangements of non-replicated lines are not necessary the same as in other clusters
- Note also that Local (Waite) is no longer a check in this cluster

Fig. 6. Cluster Augmented Block Design— Second cluster for Kenya Cassava Study

'on-station' and 'ABD or IBD on farms' (Figure 7). The 'on-station' trial could actually be on a farmer's field but with all the treatments, while designs for the baby trials could be ABDs with replicated and non-replicated treatments.

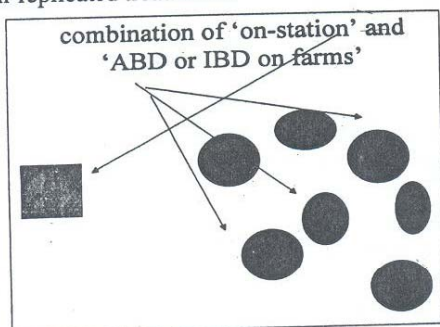


Fig. 7. illustrating Mother(square)- baby trials (circles)

## Conclusions

On farm, farmer participatory trials need not suffer from restriction on number of treatments. Effective blocking is principal criterion for achieving good coverage and enhanced impact. The basic trial design will depend on the nature of the block structure and sizes. While design concepts are not at variant from classical and commonly known ones, effective analysis of ABD requires the use of MIXED modelling procedure. The procedure enables recovery of both inter and intra block variation.

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