

**Statistical Consulting Report for**  
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**Background and Objective:**

Two groups of loblolly pine clones with different levels of water use efficiency (WUE) will be tested for drought tolerance in a greenhouse experiment. Two water treatments (control and drought) will be applied. There are 11 clones in each genetic group and 6 ramets per clone. The objective of the study is to compare genetic groups for their drought tolerance and test whether WUE is related to drought tolerance under a controlled environment.

The major hypotheses are;

- 1) The control and drought treatment means are not significantly different from each other for response variables ( $H_0: \mu_c = \mu_d$ )
- 2) Two genetic groups are not significantly different for response variables ( $H_0: \mu_1 = \mu_2$ ).

Let's say the drought treatment is factor A with 2 levels (Dry, Control) and genetic groups is factor B with two levels (High, Low). A classical randomized complete block split-plot design can be used to test the major hypotheses. Within each  $r$  blocks (replication), the  $a$  levels of the between factor A are randomized to the main units (whole or main plots). Because they are randomized to the main plots, the levels of  $a$  between A factor are called main treatments. Within each main plot, the  $b$  levels of between factor B are randomized to the  $b$  subunits (sub-plots). The levels of  $a$  within factor are called sub treatments. 11 clones within each genetic group (factor B) is another factor (C) with  $c$  levels. However, since each clone will have one ramet and clones are not the interest, they can be ignored.

Using the PLAN procedure of SAS, the following split plot design was generated.

The PLAN Procedure

Factor	Select	Levels	Order
block	3	3	Ordered
Treat (A)	2	2	Random
Group (B)	2	2	Random
Clones	11	11	Random

block	Treatment (A)	Group (B)	Clones										
			3	8	2	10	9	11	7	5	6	4	1
1	2	2	3	8	2	10	9	11	7	5	6	4	1
		1	11	6	4	8	1	9	3	10	2	5	7
	1	1	1	10	11	5	9	3	6	7	2	8	4
		2	10	7	4	11	9	3	5	6	2	1	8
2	2	2	5	10	8	9	6	1	11	4	7	3	2
		1	11	4	1	9	2	3	7	8	6	10	5
	1	1	9	7	10	2	6	3	1	8	11	4	5
		2	11	10	1	8	9	5	2	7	3	6	4
3	2	1	7	3	9	10	2	4	8	11	1	6	5
		2	10	11	3	5	2	7	8	9	1	4	6
	1	1	1	3	7	4	5	8	2	9	11	10	6
		2	6	1	9	5	10	4	11	7	3	8	2

F tests for different factors should be constructed correctly. I simulated a data set and analyzed using the MIXED procedure of SAS to show appropriate F tests for different factors as follows.

```
proc mixed method=type3;
  class Treat Group Block;
  model Trait = Treat|Group;
  random Block Treat*Block;
run;
```

Split Plot Design

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The Mixed Procedure

Model Information

Data Set	WORK.M
Dependent Variable	Trait
Covariance Structure	Variance Components
Estimation Method	Type 3
Residual Variance Method	Factor
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Containment

Class Level Information

Class	Levels	Values
Treat	2	1 2
Group	2	1 2
Block	3	1 2 3

Dimensions

Covariance Parameters	3
Columns in X	9
Columns in Z	9
Subjects	1
Max Obs Per Subject	132

Number of Observations

Number of Observations Read	132
Number of Observations Used	132
Number of Observations Not Used	0

Type 3 Analysis of Variance

Source	DF	Error Term	Error DF	F Value	Pr > F
<b>Treat</b>	1	MS (Treat*Block)	2	15.52	0.0588
<b>Group</b>	1	MS (Residual)	124	0.43	0.5146
<b>Treat*Group</b>	1	MS (Residual)	124	3.60	0.0601
<b>Block</b>	2	MS (Treat*Block)	2	4.27	0.1898
<b>Treat*Block</b>	2	MS (Residual)	124	0.21	0.8094
<b>Residual</b>	124	.	.	.	.

Covariance Parameter  
Estimates

Cov Parm	Estimate
Block	0.001195
Treat*Block	-0.00272
Residual	0.07593

#### Fit Statistics

-2 Res Log Likelihood	44.0
AIC (smaller is better)	50.0
AICC (smaller is better)	50.1
BIC (smaller is better)	47.2

#### Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
Treat	1	2	15.52	0.0588
Group	1	124	0.43	0.5146
Treat*Group	1	124	3.60	0.0601

The analysis can be expanded by producing least square means, their standard errors and t-test probability values. The Estimate statements in MIXED procedure are handy to calculate any linear combinations of fixed and random effects.

## APPENDIX

```

title 'Split Plot Design';
proc plan seed=37277;
  factors block=3 ordered Treat=2 Group=2 clones=11;
run;

```

```

data wue;
length Block Treat Group Clone 4. ;
retain Seed_1 0 Trait;
do Block=1 to 3 ;
  do treat=1 to 2;
    do group=1 to 2;
      do clone=1 to 11;
        call ranuni (Seed_1,Trait);
        output;
      end;
    end;
  end;
end;

```

```
                end;  
            end;  
        end;  
end;  
drop seed_1 ;  
if treat=1 then trait=trait+0.5;  
if group=2 then trait=trait+0.75 ;  
run;
```