

KOREA 2021

# DISCOVERY SUMMIT

EXPLORING DATA  
INSPIRING INNOVATION



# JMP를 이용한 농업 재배 연구에서의 분할구 배치법 (split-plot design) 실험설계 및 분석



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# 개요

- 농업 (재배) 연구에 있어서의 실험설계는 자연상의 실제 재배 현장에서 진행되는 실험과정이기때문에 타 분야와 차별되는 실험 방법들이 존재함.
- 가장 대표적인 실험 설계 방법은 **분할구 배치법 (split-plot design)** 혹은 **세세구 배치법 (split-split plot design)** 이며, 이는 실제 재배지에서 구획을 나누어 실험처리를 계획하는 실험 방법임.
- 이럴 경우, 모든 실험인자가 fixed 하게 구성되는 것이 아니기 때문에 random 하게 구성되는 실험인자에 대한 분석이 요구됨.
- 기타 통계 프로그램과는 달리 JMP 는 random factor 에 대한 설정 및 통계 모델을 직접 구성할수 있어 분할구 배치법에 대한 심도있는 이해를 가능하게 함.
- JMP를 통한 분할구 배치법의 기본개념 및 통계모델 구성에 대한 방법 소개.



# Experimental design in agricultural field



*Bell-lloc d'Urgell, Spain (03/18/2019)*

# Randomized Complete Block Design (RCBD)

## Example

- ❑ Experimental factors: Genotype, Nitrogen level
  - **Genotype (4 levels):** Genotype A, Genotype B, Genotype C, Genotype D
  - **Nitrogen level (3 levels):** 0 kg·ha<sup>-1</sup>, 100 kg·ha<sup>-1</sup>, 200 kg·ha<sup>-1</sup>
- ❑ Replicates → 3 Blocks

Block I : (4 genotypes x 3 Nitrogen = 12, randomized)

Gen. A	Gen. A	Gen. C	Gen. D	Gen. D	Gen. A	Gen. B	Gen. B	Gen. D	Gen. C	Gen. C	Gen. B
200 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>

# Randomized Complete Block Design (RCBD)

## Block III

Gen. C	Gen. A	Gen. A	Gen. B	Gen. B	Gen. B	Gen. C	Gen. C	Gen. D	Gen. D	Gen. A	Gen. D
100 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>

## Block II

Gen. D	Gen. C	Gen. A	Gen. C	Gen. B	Gen. A	Gen. A	Gen. C	Gen. B	Gen. D	Gen. B	Gen. D
0 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>

## Block I

Gen. A	Gen. A	Gen. C	Gen. D	Gen. D	Gen. A	Gen. B	Gen. B	Gen. D	Gen. C	Gen. C	Gen. B
200 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>	100 kg·ha <sup>-1</sup>	200 kg·ha <sup>-1</sup>	0 kg·ha <sup>-1</sup>



# Bottleneck for RCBD

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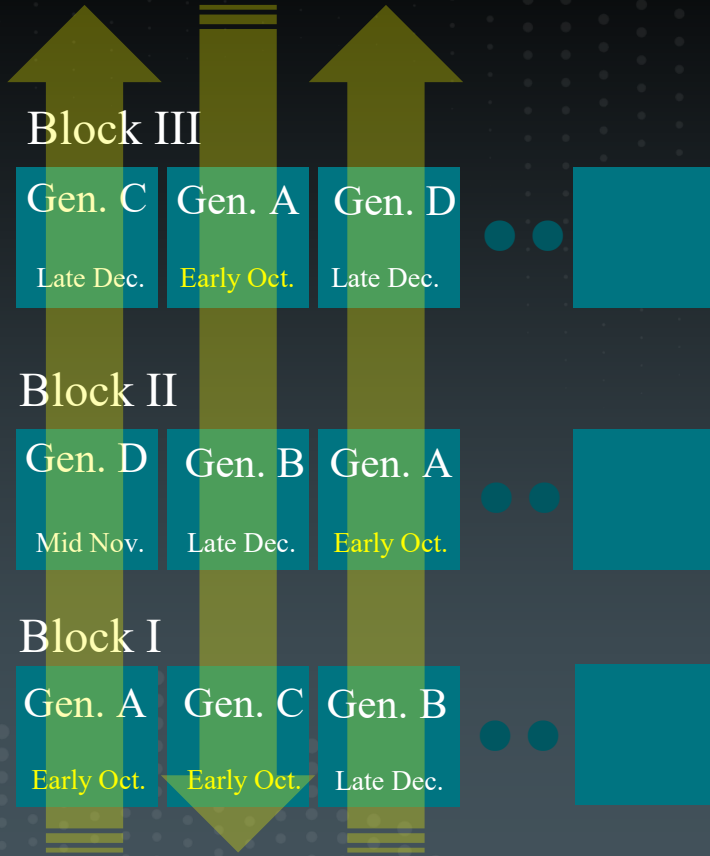
## Example 1

- ❑ Experimental factors: Genotype, **Sowing date** [파종시기]
  - **Genotype (4 levels)**: Genotype A, Genotype B, Genotype C, Genotype D
  - **Nitrogen level (3 levels)**: Early Oct., Mid Nov., Late Dec.
- ❑ Replicates → 3 Blocks

## Example 2

- ❑ Experimental factors: Genotype, **Virus inoculation** [식물 바이러스 접종]
  - **Genotype (4 levels)**: Genotype A, Genotype B, Genotype C, Genotype D
  - **Nitrogen level (3 levels)**: Control, Virus A, Virus B
- ❑ Replicates → 3 Blocks

# Example 1



*Bell-lloc d'Urgell, Spain (11/28/2019)*

*Physical barrier*

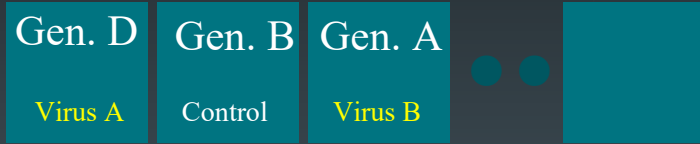


# Example 2

## Block III



## Block II



## Block I



Split-plot design  
[분할구 배치법]

*Biological damage*

# Split-plot design

## Block I (RCBD)

Gen. A	Gen. D	Gen. B	Gen. A	Gen. B	Gen. A	Gen. B	Gen. C	Gen. D	Gen. C	Gen. D	Gen. C
Early Oct.	Early Oct.	Late Dec.	Mid Nov.	Early Oct.	Late Dec.	Mid Nov.	Early Oct.	Late Dec.	Mid Nov.	Mid Nov.	Late Dec.

## Block I (Spilt-plot design)

Early Oct.				Mid Nov.				Late Dec.			
Gen. D	Gen. A	Gen. B	Gen. C	Gen. A	Gen. C	Gen. B	Gen. D	Gen. D	Gen. A	Gen. B	Gen. C
Early Oct.	Early Oct.	Early Oct.	Early Oct.	Mid Nov.	Mid Nov.	Mid Nov.	Mid Nov.	Late Dec.	Late Dec.	Late Dec.	Late Dec.

# Split-plot design [분할구 배치법]



Main plot : Sowing time

Sub plot : Genotype

# JMP for split-plot design

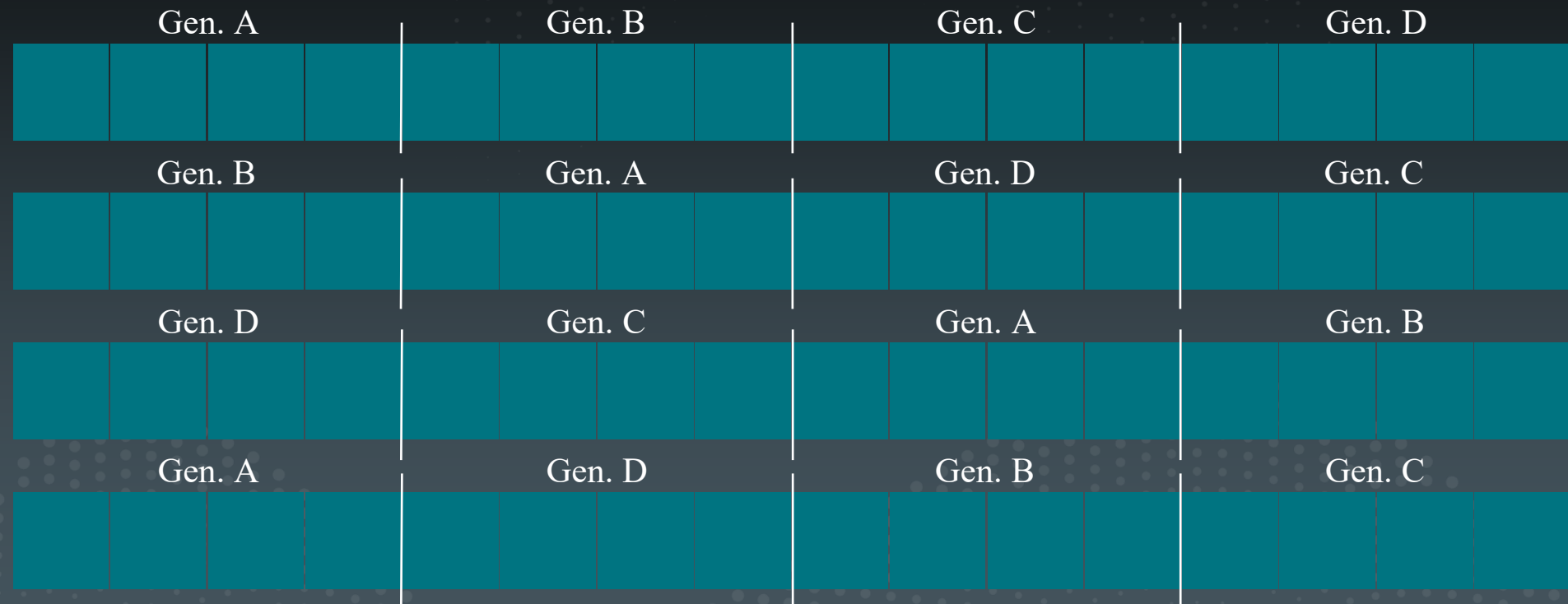
Genotype	Block	Control	Fertilizer 1	Fertilizer 2	Fertilizer 3
Gen. A	I	42.9	53.8	49.5	44.4
Gen. A	II	41.6	58.5	53.8	41.8
Gen. A	III	28.9	43.9	40.7	28.3
Gen. A	IV	30.8	46.3	39.4	34.7
Gen. B	I	53.3	57.6	59.8	64.1
Gen. B	II	69.6	69.6	65.8	57.4
Gen. B	III	45.4	42.4	41.4	44.1
Gen. B	IV	35.1	51.9	45.4	51.6
Gen. C	I	62.3	63.4	64.5	63.6
Gen. C	II	58.5	50.4	46.1	56.1
Gen. C	III	44.6	45.0	62.6	52.7
Gen. C	IV	50.3	46.7	50.3	51.8
Gen. D	I	75.4	70.3	68.8	71.6
Gen. D	II	65.6	67.3	65.3	69.4
Gen. D	III	54.0	57.6	45.6	56.6
Gen. D	IV	52.7	58.5	51.0	47.4

- ❑ Experimental factors:
  - Genotype (4 levels)
  - Fertilizer (4 levels)
- ❑ No. Experiment: 16 (= 4 x 4)
- ❑ Replicates: 4 blocks
- ❑ Experimental unit: 64 (= 16 x 4)



# Split-plot design

Main plot: Genotype



# Split-plot design

## Main plot: Genotype

Fit Model - JMP Pro

**Model Specification**

Select Columns  
4 Columns  
Genotype  
Block  
Fertilizer  
Yield

Pick Role Variables

Y: Yield (optional)

Weight: optional numeric

Freq: optional numeric

Validation: optional

By: optional

Personality: Standard Least Squares

Emphasis: Minimal Report

Method: EMS (Traditional)

Help Run

Recall  Keep dialog open

Remove

Construct Model Effects

Add Cross Nest Macros

Degree: 2

Attributes Transform

No Intercept

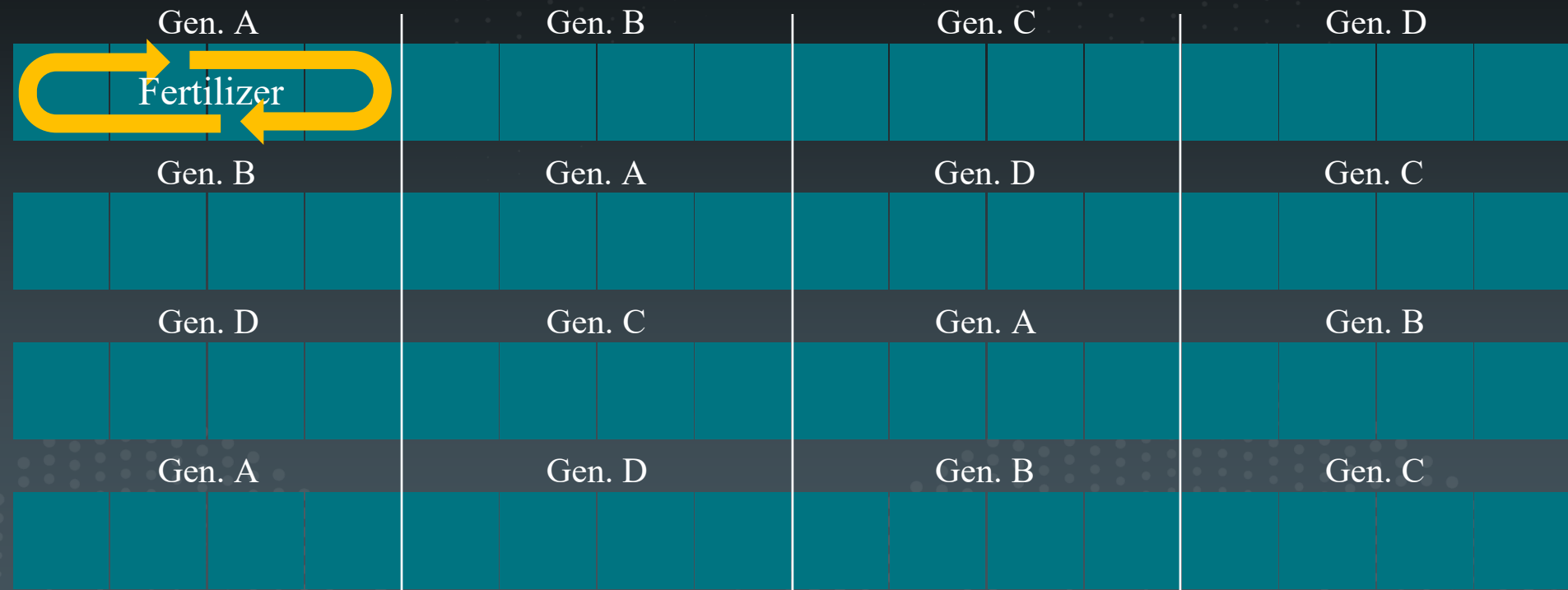
Block  
Genotype  
Genotype\*Block & Random

*Main plot*

Gen. A	Gen. B	Gen. C	Gen. D
Gen. B	Gen. A	Gen. D	Gen. C
Gen. D	Gen. C	Gen. A	Gen. B
Gen. A	Gen. D	Gen. B	Gen. C

# Split-plot design

Sub plot: Fertilizer



# Split-plot design

Fit Model - JMP Pro

**Model Specification**

Select Columns: 4 Columns  
Genotype, Block, Fertilizer, Yield

Pick Role Variables:  
Y: Yield (optional)  
Weight: optional numeric  
Freq: optional numeric  
Validation: optional  
By: optional

Personality: Standard Least Squares  
Emphasis: Minimal Report  
Method: EMS (Traditional)

Buttons: Help, Run, Recall, Remove, Keep dialog open (checked)

Construct Model Effects:  
Main plot: Block, Genotype, Genotype\*Block & Random, Fertilizer  
Sub plot: Fertilizer\*Genotype

Degree: 2  
Attributes: [v]  
Transform: [v]  
No Intercept: [ ]





Response Yield

Effect Summary

Summary of Fit

RSquare	0.906225
RSquare Adj	0.835893
Root Mean Square Error	4.506793
Mean of Response	52.80938
Observations (or Sum Wgts)	64

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	7066.1919	261.711	12.8851
Error	36	731.2025	20.311	Prob > F
C. Total	63	7797.3944		<.0001*

Parameter Estimates

Expected Mean Squares

Variance Component Estimates

Test Denominator Synthesis

Tests wrt Random Effects

Source	SS	MS	Num	DF	Ratio	Prob > F
Block	2842.87	947.624	3	13.7938	0.0010*	
Genotype	2848.02	949.341	3	13.8188	0.0010*	
Fertilizer	170.537	56.8456	3	2.7987	0.0539	
Fertilizer*Genotype	586.466	65.1628	9	3.2082	0.0059*	
Genotype*Block&Random	618.294	68.6994	9	3.3823	0.0042*	

Error b

Error a

Source of variation	df	SS	MS	F-ratio	Prob >F
Block	3	2842.87	947.624	13.7938	**
Genotype	3	2848.02	949.341	13.8188	**
Error a	9	618.294	68.6994		
Fertilizer	3	170.537	56.8456	2.7987	n.s.
Genotype x Fertilizer	9	586.466	65.1628	3.2082	**
Error b	36	731.2025	20.311		
Total	63	7797.3944			


# JMP for split-plot design

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## □ RCBD

$$y_{ijk} = \mu + \alpha_i + \beta_j + \delta_{ij} + \gamma_k + \varepsilon_{ijk}$$

$N(0, \sigma^2)$



## □ Split-plot

$$y_{ijk} = \mu + \alpha_i + \gamma_k + \eta_{ik} + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijk}$$

$N(0, \sigma^2)$

$N(0, \sigma^2)$

# Data partitioning

$$y_{ijk} = \mu + \alpha_i + \beta_j + \delta_{ij} + \gamma_k + \varepsilon_{ijk}$$

Genotype	Fertilizer	Interaction	Block	Mean					Treatment			(9) Block	(10) Residual	(11) Total	
				Yield	(1) Gran	(2) Genotype	(3) Fertilizer	(4) Interaction	(5) Block	(6) Genotype	(7) Fertilizer				(8) Interaction
				$Y_{ijk}$	$\bar{Y}_{i..}$	$\bar{Y}_{i.}$	$\bar{Y}_{ij.}$	$\bar{Y}_{i.k}$	$\bar{Y}_{i..} - \bar{Y}_{i..}$	$\bar{Y}_{ij.} - \bar{Y}_{i..}$	$\bar{Y}_{ij.} - \bar{Y}_{i..} - \bar{Y}_{.j.} + \bar{Y}_{i..}$				$\bar{Y}_{i.k} - \bar{Y}_{i..}$
$\alpha_i$	$\beta_j$	$\delta_{ij}$	$\gamma_k$	$\varepsilon_{ijk}$											
Gen. C	Fertilizer 1	Gen. C_Fertilizer 1	IV	46.7	52.8	54.3	55.2	51.4	46.5	1.5	2.4	-5.3	-6.3	1.6	-6.1
Gen. C	Fertilizer 2	Gen. C_Fertilizer 2	I	64.5	52.8	54.3	53.1	55.9	60.3	1.5	0.3	1.3	7.5	1.1	11.7
Gen. C	Fertilizer 2	Gen. C_Fertilizer 2	II	46.1	52.8	54.3	53.1	55.9	58.6	1.5	0.3	1.3	5.7	-15.5	-6.7
Gen. C	Fertilizer 2	Gen. C_Fertilizer 2	III	62.6	52.8	54.3	53.1	55.9	45.9	1.5	0.3	1.3	-6.9	13.7	9.8
Gen. C	Fertilizer 2	Gen. C_Fertilizer 2	IV	50.3	52.8	54.3	53.1	55.9	46.5	1.5	0.3	1.3	-6.3	0.7	-2.5
Gen. C	Fertilizer 3	Gen. C_Fertilizer 3	I	63.6	52.8	54.3	52.2	56.1	60.3	1.5	-0.6	2.3	7.5	0.0	10.8
Gen. C	Fertilizer 3	Gen. C_Fertilizer 3	II	56.1	52.8	54.3	52.2	56.1	58.6	1.5	-0.6	2.3	5.7	-5.7	3.3
Gen. C	Fertilizer 3	Gen. C_Fertilizer 3	III	52.7	52.8	54.3	52.2	56.1	45.9	1.5	-0.6	2.3	-6.9	3.6	-0.1
Gen. C	Fertilizer 3	Gen. C_Fertilizer 3	IV	51.8	52.8	54.3	52.2	56.1	46.5	1.5	-0.6	2.3	-6.3	2.1	-1.0
Gen. D	Control	Gen. D_Control	I	75.4	52.8	61.1	50.7	61.9	60.3	8.3	-2.1	3.0	7.5	6.0	22.6
Gen. D	Control	Gen. D_Control	II	65.6	52.8	61.1	50.7	61.9	58.6	8.3	-2.1	3.0	5.7	-2.1	12.8
Gen. D	Control	Gen. D_Control	III	54.0	52.8	61.1	50.7	61.9	45.9	8.3	-2.1	3.0	-6.9	-1.0	1.2
Gen. D	Control	Gen. D_Control	IV	52.7	52.8	61.1	50.7	61.9	46.5	8.3	-2.1	3.0	-6.3	-2.9	-0.1
Gen. D	Fertilizer 1	Gen. D_Fertilizer 1	I	70.3	52.8	61.1	55.2	63.4	60.3	8.3	2.4	0.0	7.5	-0.6	17.5
Gen. D	Fertilizer 1	Gen. D_Fertilizer 1	II	67.3	52.8	61.1	55.2	63.4	58.6	8.3	2.4	0.0	5.7	-1.9	14.5
Gen. D	Fertilizer 1	Gen. D_Fertilizer 1	III	57.6	52.8	61.1	55.2	63.4	45.9	8.3	2.4	0.0	-6.9	1.1	4.8
Gen. D	Fertilizer 1	Gen. D_Fertilizer 1	IV	58.5	52.8	61.1	55.2	63.4	46.5	8.3	2.4	0.0	-6.3	1.4	5.7
Gen. D	Fertilizer 2	Gen. D_Fertilizer 2	I	68.8	52.8	61.1	53.1	57.7	60.3	8.3	0.3	-3.7	7.5	3.6	16.0
Gen. D	Fertilizer 2	Gen. D_Fertilizer 2	II	65.3	52.8	61.1	53.1	57.7	58.6	8.3	0.3	-3.7	5.7	1.9	12.5
Gen. D	Fertilizer 2	Gen. D_Fertilizer 2	III	45.6	52.8	61.1	53.1	57.7	45.9	8.3	0.3	-3.7	-6.9	-5.1	-7.2
Gen. D	Fertilizer 2	Gen. D_Fertilizer 2	IV	51.0	52.8	61.1	53.1	57.7	46.5	8.3	0.3	-3.7	-6.3	-0.4	-1.8
Gen. D	Fertilizer 3	Gen. D_Fertilizer 3	I	71.6	52.8	61.1	52.2	61.3	60.3	8.3	-0.6	0.8	7.5	2.8	18.8
Gen. D	Fertilizer 3	Gen. D_Fertilizer 3	II	69.4	52.8	61.1	52.2	61.3	58.6	8.3	-0.6	0.8	5.7	2.4	16.6
Gen. D	Fertilizer 3	Gen. D_Fertilizer 3	III	56.6	52.8	61.1	52.2	61.3	45.9	8.3	-0.6	0.8	-6.9	2.3	3.8
Gen. D	Fertilizer 3	Gen. D_Fertilizer 3	IV	47.4	52.8	61.1	52.2	61.3	46.5	8.3	-0.6	0.8	-6.3	-7.5	-5.4
Sum of squares =SUMSQ()				186282.5	178485.1	181333.1	178655.7	182090.2	181328.0	2848.02	170.54	586.47	2842.87	1349.50	7797.39

				Mean							
				(1)	(2)	(3)	(4)	(5)			
Yield	Gran	Genotype	Fertilizer	Interaction	Block						
Genotype	Fertilizer	Interaction	Block	$\bar{Y}_{ijk}$	$\bar{Y}_{i..}$	$\bar{Y}_{.j.}$	$\bar{Y}_{ij.}$	$\bar{Y}_{..k}$			
Sum of squares =SUMSQ()				186282.5	178485.1	181333.1	178655.7	182090.2	181328.0		

Treatment						(9)	(10)	(11)
(6)	(7)	(8)	Block	Residual	Total			
Genotype	Fertilizer	Interaction				Block	Residual	Total
$\bar{y}_{i..} - \bar{y}_{...}$	$\bar{y}_{.j.} - \bar{y}_{...}$	$\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...}$	$\bar{y}_{..k} - \bar{y}_{...}$	$y_{ijk} - \bar{y}_{ij.} - \bar{y}_{..k} + \bar{y}_{...}$	$y_{ijk} - \bar{y}_{...}$			
$\alpha_i$	$\beta_j$	$\delta_{ij}$	$\gamma_k$	$\epsilon_{ijk}$				
2848.02	170.54	586.47	2842.87	1349.50	7797.39			

$$SS_{Total} = SS_{Treatment} + SS_{Block} + SS_{Error}$$

$$7797.39 = 2848.02 + 170.54 + 586.47 + 2842.87 + 1349.50$$

$$y_{ijk} = \mu + \alpha_i + \beta_j + \delta_{ij} + \gamma_k + \epsilon_{ijk}$$

Source of variation	df	SS	MS	F-ratio	Prob >F
Genotype	3	2848.02	949.3	31.66	***
Fertilizer	3	170.54	56.8	1.90	n.s.
Genotype x Fertilizer	9	586.47	65.2	2.17	*
Block	3	2842.87	947.6	31.60	***
Residual	45	1349.50	30.0		
Total	63	7797.39			



## □ RCBD

$$y_{ijk} = \mu + \alpha_i + \beta_j + \delta_{ij} + \gamma_k + \varepsilon_{ijk}$$

Source of variation	df	SS	MS	F-ratio	Prob >F
Genotype	3	2848.02	949.3	31.66	***
Fertilizer	3	170.54	56.8	1.90	n.s.
Genotype x Fertilizer	9	586.47	65.2	2.17	*
Block	3	2842.87	947.6	31.60	***
Residual	45	1349.50	30.0		
Total	63	7797.39			

## □ Split-plot

$$y_{ijk} = \mu + \alpha_i + \gamma_k + \eta_{ik} + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijk}$$

Source of variation	df	SS	MS	F-ratio	Prob >F
Block	3	2842.87	947.624	13.7938	**
Genotype	3	2848.02	949.341	13.8188	**
Error a	9	618.294	68.6994		
Fertilizer	3	170.537	56.8456	2.7987	n.s.
Genotype x Fertilizer	9	586.466	65.1628	3.2082	**
Error b	36	731.2025	20.311		
Total	63	7797.3944			

## □ RCBD

$$y_{ijk} = \mu + \alpha_i + \beta_j + \delta_{ij} + \gamma_k + \epsilon_{ijk}$$

Source of variation	df	SS	MS	F-ratio	Prob >F
Genotype	3	2848.02	949.3	31.66	***
Fertilizer	3	170.54	56.8	1.90	n.s.
Genotype x Fertilizer	9	586.47	65.2	2.17	*
Block	3	2842.87	947.6	31.60	***
Residual	45	1349.50	30.0		
Total	63	7797.39			

## □ Split-plot

$$y_{ijk} = \mu + \alpha_i + \gamma_k + \eta_{ik} + \beta_j + (\alpha\beta)_{ij} + \epsilon_{ijk}$$

Source of variation	df	SS	MS	F-ratio	Prob >F
Block	3	2842.87	947.624	13.7938	**
Genotype	3	2848.02	949.341	13.8188	**
<b>Error a</b>	<b>9</b>	<b>618.294</b>	<b>68.6994</b>		
Fertilizer	3	170.537	56.8456	2.7987	n.s.
Genotype x Fertilizer	9	586.466	65.1628	3.2082	**
<b>Error b</b>	<b>36</b>	<b>731.2025</b>	<b>20.311</b>		
Total	63	7797.3944			

# Data partitioning

$$y_{ijk} = \mu + \alpha_i + \beta_j + \delta_{ij} + \gamma_k + \varepsilon_{ijk}$$

Genotype	Fertilizer	Interaction	Block	Mean					Treatment				(10) Residual	(11) Total	
				Yield	(1) Gran	(2) Genotype	(3) Fertilizer	(4) Interaction	(5) Block	(6) Genotype	(7) Fertilizer	(8) Interaction			(9) Block
				$V_{ijk}$	$\bar{Y}...$	$\bar{Y}i..$	$\bar{Y}.j.$	$\bar{Y}ij.$	$\bar{Y}..k$	$\bar{Y}i.. - \bar{Y}...$	$\bar{Y}.j. - \bar{Y}...$	$\bar{Y}ij. - \bar{Y}i.. - \bar{Y}.j. + \bar{Y}...$			$\bar{Y}..k - \bar{Y}...$
Gen. C	Fertilizer 1	Gen. C_Fertilizer 1	IV	46.7	52.8	54.3	55.2	51.4	46.5	1.5	2.4	-5.3	-6.3	1.6	-6.1
Gen. C	Fertilizer 2	Gen. C_Fertilizer 2	I	64.5	52.8	54.3	53.1	55.9	60.3	1.5	0.3	1.3	7.5	1.1	11.7
Gen. C	Fertilizer 2	Gen. C_Fertilizer 2	II	46.1	52.8	54.3	53.1	55.9	58.6	1.5	0.3	1.3	5.7	-15.5	-6.7
Gen. C	Fertilizer 2	Gen. C_Fertilizer 2	III	62.6	52.8	54.3	53.1	55.9	45.9	1.5	0.3	1.3	-6.9	13.7	9.8
Gen. C	Fertilizer 2	Gen. C_Fertilizer 2	IV	50.3	52.8	54.3	53.1	55.9	46.5	1.5	0.3	1.3	-6.3	0.7	-2.5
Gen. C	Fertilizer 3	Gen. C_Fertilizer 3	I	63.6	52.8	54.3	52.2	56.1	60.3	1.5	-0.6	2.3	7.5	0.0	10.8
Gen. C	Fertilizer 3	Gen. C_Fertilizer 3	II	56.1	52.8	54.3	52.2	56.1	58.6	1.5	-0.6	2.3	5.7	-5.7	3.3
Gen. C	Fertilizer 3	Gen. C_Fertilizer 3	III	52.7	52.8	54.3	52.2	56.1	45.9	1.5	-0.6	2.3	-6.9	3.6	-0.1
Gen. C	Fertilizer 3	Gen. C_Fertilizer 3	IV	51.8	52.8	54.3	52.2	56.1	46.5	1.5	-0.6	2.3	-6.3	2.1	-1.0
Gen. D	Control	Gen. D_Control	I	75.4	52.8	61.1	50.7	61.9	60.3	8.3	-2.1	3.0	7.5	6.0	22.6
Gen. D	Control	Gen. D_Control	II	65.6	52.8	61.1	50.7	61.9	58.6	8.3	-2.1	3.0	5.7	-2.1	12.8
Gen. D	Control	Gen. D_Control	III	54.0	52.8	61.1	50.7	61.9	45.9	8.3	-2.1	3.0	-6.9	-1.0	1.2
Gen. D	Control	Gen. D_Control	IV	52.7	52.8	61.1	50.7	61.9	46.5	8.3	-2.1	3.0	-6.3	-2.9	-0.1
Gen. D	Fertilizer 1	Gen. D_Fertilizer 1	I	70.3	52.8	61.1	55.2	63.4	60.3	8.3	2.4	0.0	7.5	-0.6	17.5
Gen. D	Fertilizer 1	Gen. D_Fertilizer 1	II	67.3	52.8	61.1	55.2	63.4	58.6	8.3	2.4	0.0	5.7	-1.9	14.5
Gen. D	Fertilizer 1	Gen. D_Fertilizer 1	III	57.6	52.8	61.1	55.2	63.4	45.9	8.3	2.4	0.0	-6.9	1.1	4.8
Gen. D	Fertilizer 1	Gen. D_Fertilizer 1	IV	58.5	52.8	61.1	55.2	63.4	46.5	8.3	2.4	0.0	-6.3	1.4	5.7
Gen. D	Fertilizer 2	Gen. D_Fertilizer 2	I	68.8	52.8	61.1	53.1	57.7	60.3	8.3	0.3	-3.7	7.5	3.6	16.0
Gen. D	Fertilizer 2	Gen. D_Fertilizer 2	II	65.3	52.8	61.1	53.1	57.7	58.6	8.3	0.3	-3.7	5.7	1.9	12.5
Gen. D	Fertilizer 2	Gen. D_Fertilizer 2	III	45.6	52.8	61.1	53.1	57.7	45.9	8.3	0.3	-3.7	-6.9	-5.1	-7.2
Gen. D	Fertilizer 2	Gen. D_Fertilizer 2	IV	51.0	52.8	61.1	53.1	57.7	46.5	8.3	0.3	-3.7	-6.3	-0.4	-1.8
Gen. D	Fertilizer 3	Gen. D_Fertilizer 3	I	71.6	52.8	61.1	52.2	61.3	60.3	8.3	-0.6	0.8	7.5	2.8	18.8
Gen. D	Fertilizer 3	Gen. D_Fertilizer 3	II	69.4	52.8	61.1	52.2	61.3	58.6	8.3	-0.6	0.8	5.7	2.4	16.6
Gen. D	Fertilizer 3	Gen. D_Fertilizer 3	III	56.6	52.8	61.1	52.2	61.3	45.9	8.3	-0.6	0.8	-6.9	2.3	3.8
Gen. D	Fertilizer 3	Gen. D_Fertilizer 3	IV	47.4	52.8	61.1	52.2	61.3	46.5	8.3	-0.6	0.8	-6.3	-7.5	-5.4
Sum of squares =SUMSQ()				186282.5	178485.1	181333.1	178655.7	182090.2	181328.0	2848.02	170.54	586.47	2842.87	1349.50	7797.39

# JMP

# R

Source of variation	df	SS	MS	F-ratio	Prob >F
Block	3	2842.87	947.624	13.7938	**
Genotype	3	2848.02	949.341	13.8188	**
<b>Error a</b>	<b>9</b>	<b>618.294</b>	<b>68.6994</b>		
Fertilizer	3	170.537	56.8456	2.7987	<i>n.s.</i>
Genotype x Fertilizer	9	586.466	65.1628	3.2082	**
<b>Error b</b>	<b>36</b>	<b>731.2025</b>	<b>20.311</b>		
Total	63	7797.3944			

Block	<i>Main plot</i>
Genotype	
Genotype*Block & Random	
Fertilizer	<i>Sub plot</i>
Fertilizer*Genotype	

## Analysis of Variance Table

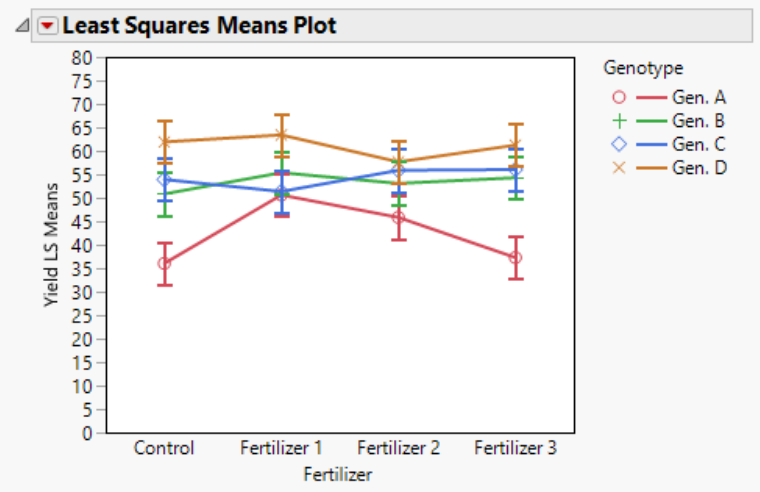
Response: dependent.var

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
block	3	2842.87	947.62	13.7938	0.001029	**
main.plot	3	2848.02	949.34	13.8188	0.001022	**
<b>Ea</b>	<b>9</b>	<b>618.29</b>	<b>68.70</b>			
sub.plot	3	170.54	56.85	2.7987	0.053859	.
main.plot:sub.plot	9	586.47	65.16	3.2082	0.005945	**
<b>Eb</b>	<b>36</b>	<b>731.20</b>	<b>20.31</b>			

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

splitplot (Yield[4], Yield\$Block, Yield\$Genotype, Yield\$Fertilizer, 1)





# Test slices

Untitled 11 - Fit Least Squares - JMP Pro

Response Yield

Effect Summary

Summary of Fit

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	7066.1919	261.711	12.8851
Error	36	731.2025	20.311	Prob > F
C. Total	63	7797.3944		<.0001*

Parameter Estimates

Expected Mean Squares

Variance Component Estimates

Test Denominator Synthesis

Tests wrt Random Effects

Source	SS	MS Num	DF Num	F Ratio	Prob > F
Block	2842.87	947.624	3	13.7938	0.0010*
Genotype	2848.02	949.341	3	13.8188	0.0010*
Fertilizer	170.537	56.8456	3	2.7987	0.0539
Genotype*Fertilizer	586.466	65.1628	9	3.2082	0.0059*
Genotype*Block&Random	618.294	68.6994	9	3.3823	0.0042*

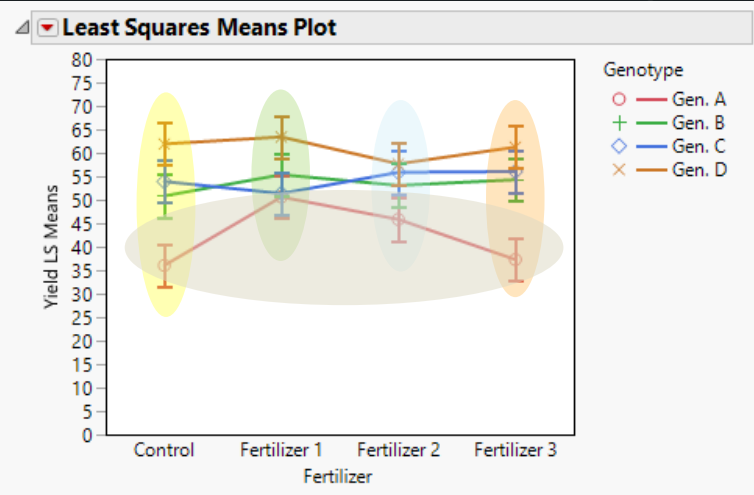
Effect Details

- Block
- Genotype
- Fertilizer
- Genotype\*Fertilizer**
  - LSMeans table
  - LSMeans Plot
  - LSMeans Contrast...
  - LSMeans Student's t
  - LSMeans Tukey HSD
  - LSMeans Dunnett
  - Test Slices**
  - Power Analysis

Runs a customized F-test for each level of both factors in an interaction term.

# Test slices

# Tukey



▼ Slice Genotype=Gen. A

▶ Test Detail

SS	NumDF	DenDF	F Ratio	Prob > F
583.5	3	36	9.5759	<.0001*

▼ Slice Fertilizer=Control

▶ Test Detail

SS	NumDF	DenDF	F Ratio	Prob > F
1404	3	36	23.0445	<.0001*

▼ Slice Fertilizer=Fertilizer 1

▶ Test Detail

SS	NumDF	DenDF	F Ratio	Prob > F
413	3	36	6.7774	0.0010*

▼ Slice Fertilizer=Fertilizer 2

▶ Test Detail

SS	NumDF	DenDF	F Ratio	Prob > F
324.8	3	36	5.3298	0.0038*

▼ Slice Fertilizer=Fertilizer 3

▶ Test Detail

SS	NumDF	DenDF	F Ratio	Prob > F
1293	3	36	21.2128	<.0001*



Level		Least Sq Mean
Gen. D,Fertilizer 1	A	63.425000
Gen. D,Control	A B	61.925000
Gen. D,Fertilizer 3	A B	61.250000
Gen. D,Fertilizer 2	A B	57.675000
Gen. C,Fertilizer 3	A B C	56.050000
Gen. C,Fertilizer 2	A B C	55.875000
Gen. B,Fertilizer 1	A B C	55.375000
Gen. B,Fertilizer 3	A B C	54.300000
Gen. C,Control	A B C	53.925000
Gen. B,Fertilizer 2	A B C	53.100000
Gen. C,Fertilizer 1	B C	51.375000
Gen. B,Control	B C	50.850000
Gen. A,Fertilizer 1	B C	50.625000
Gen. A,Fertilizer 2	C D	45.850000
Gen. A,Fertilizer 3	D	37.300000
Gen. A,Control	D	36.050000



# Split split-plot design [세세구 배치법]

Sowing_date	Block	Genotype	nitrogen	Yield
October	I	Genotype A	0 kg ha <sup>-1</sup>	25
October	II	Genotype A	0 kg ha <sup>-1</sup>	22
October	III	Genotype A	0 kg ha <sup>-1</sup>	20
October	I	Genotype A	200 kg ha <sup>-1</sup>	40
October	II	Genotype A	200 kg ha <sup>-1</sup>	41
October	III	Genotype A	200 kg ha <sup>-1</sup>	42
October	I	Genotype B	0 kg ha <sup>-1</sup>	30
October	II	Genotype B	0 kg ha <sup>-1</sup>	30
October	III	Genotype B	0 kg ha <sup>-1</sup>	29
October	I	Genotype B	200 kg ha <sup>-1</sup>	48
October	II	Genotype B	200 kg ha <sup>-1</sup>	47
October	III	Genotype B	200 kg ha <sup>-1</sup>	46
November	I	Genotype A	0 kg ha <sup>-1</sup>	25
November	II	Genotype A	0 kg ha <sup>-1</sup>	27
November	III	Genotype A	0 kg ha <sup>-1</sup>	26
November	I	Genotype A	200 kg ha <sup>-1</sup>	41
November	II	Genotype A	200 kg ha <sup>-1</sup>	41
November	III	Genotype A	200 kg ha <sup>-1</sup>	42
November	I	Genotype B	0 kg ha <sup>-1</sup>	38
November	II	Genotype B	0 kg ha <sup>-1</sup>	39
November	III	Genotype B	0 kg ha <sup>-1</sup>	42
November	I	Genotype B	200 kg ha <sup>-1</sup>	57
November	II	Genotype B	200 kg ha <sup>-1</sup>	59
November	III	Genotype B	200 kg ha <sup>-1</sup>	60

- ❑ Experimental factors:
  - Sowing date (2 levels)
  - Genotype (2 levels)
  - Fertilizer (2 levels)
- ❑ No. Experiment: 8 (= 2 x 2 x 2)
- ❑ Replicates: 3 blocks
- ❑ Experimental unit: 24 (= 8 x 3)

# Split split-plot design

Main plot: Sowing date

Sowing date: Oct.



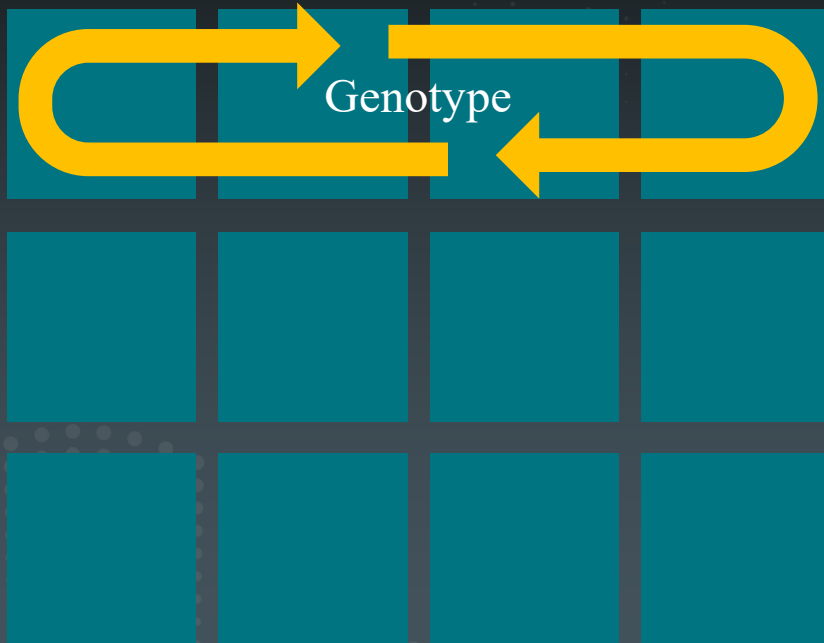
Sowing date: Nov.



# Split split-plot design

Sub plot: Genotype

Sowing date: Oct.

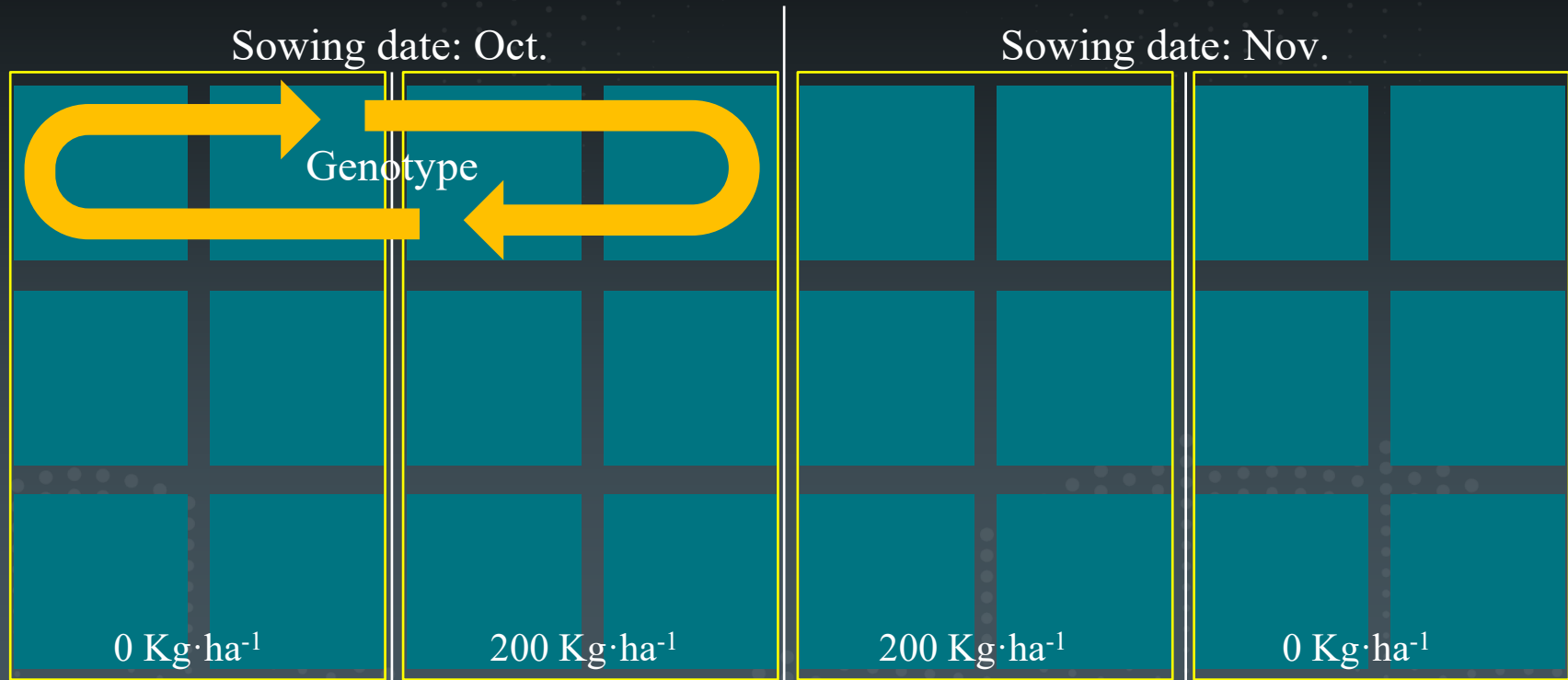


Sowing date: Nov.



# Split split-plot design

tertiary plot: Nitrogen



# Split split-plot design

Fit Model - JMP Pro

**Model Specification**

Select Columns: 5 Columns

- Sowing\_date
- Block
- Genotype
- Nitrogen
- Yield

Pick Role Variables

Y: Yield (optional)

Weight: optional numeric

Freq: optional numeric

Validation: optional

By: optional

Personality: Standard Least Squares

Emphasis: Minimal Report

Method: EMS (Traditional)

Help Run

Recall  Keep dialog open

Remove

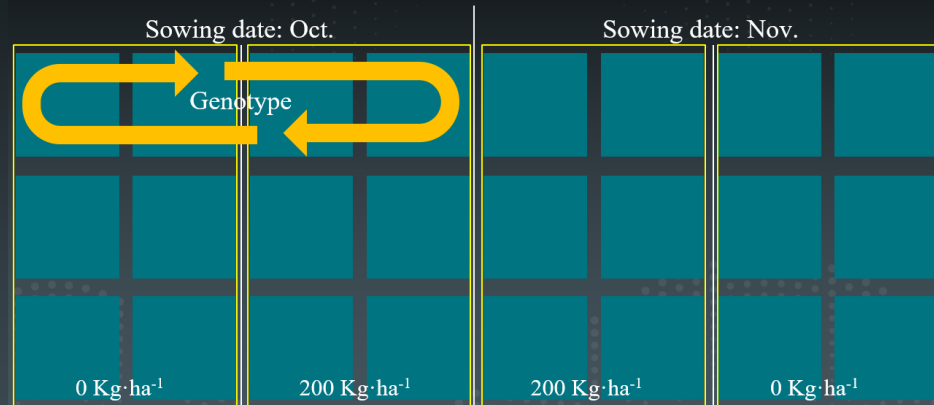
**Construct Model Effects**

- Add: Block
- Cross: Sowing\_date, Sowing\_date\*Block & Random
- Nest: Genotype
- Macros: Sowing\_date\*Genotype, Sowing\_date\*Block\*Genotype & Random
- Degree: 2
- Attributes: Nitrogen
- Transform: Sowing\_date\*Nitrogen, Genotype\*Nitrogen, Sowing\_date\*Genotype\*Nitrogen
- No Intercept

Main plot

Sub plot

Tertiary plot



Source of variation	df	SS	MS	F-ratio	Prob >F
Sowing date	1	247.042	247.042	35.0828	*
Block	2	0.58333	0.29167	0.0414	<i>n.s.</i>
<b>Error a</b>	<b>2</b>	<b>14.0833</b>	<b>7.04167</b>		
Genotype	1	737.042	737.042	707.56	**
Genotype x Sowing date	1	117.042	117.042	112.36	**
<b>Error b</b>	<b>2</b>	<b>2.08333</b>	<b>1.04167</b>		
Nitrogen	1	1855.04	1855.04	1118.618	***
Nitrogen x Sowing date	1	1.04167	1.04167	0.6281	<i>n.s.</i>
Nitrogen x Genotype	1	2.04167	2.04167	1.2312	<i>n.s.</i>
<b>Sowing date x Genotype x Nitrogen</b>	<b>1</b>	<b>9.375</b>	<b>9.375</b>	<b>5.6533</b>	*
<b>Error c</b>	<b>10</b>	<b>16.5833</b>	<b>1.658</b>		
<b>Total</b>	<b>23</b>	<b>2985.374</b>			

## □ Split split-plot design

Source of variation	df	SS	MS	F-ratio	Prob >F
Sowing date	1	247.042	247.042	35.0828	*
Block	2	0.58333	0.29167	0.0414	n.s.
<b>Error a</b>	<b>2</b>	<b>14.0833</b>	<b>7.04167</b>		
Genotype	1	737.042	737.042	707.56	**
Genotype x Sowing date	1	117.042	117.042	112.36	**
<b>Error b</b>	<b>2</b>	<b>2.08333</b>	<b>1.04167</b>		
Nitrogen	1	1855.04	1855.04	1118.618	***
Nitrogen x Sowing date	1	1.04167	1.04167	0.6281	n.s.
Nitrogen x Genotype	1	2.04167	2.04167	1.2312	n.s.
<b>Sowing date x Genotype x Nitrogen</b>	<b>1</b>	<b>9.375</b>	<b>9.375</b>	<b>5.6533</b>	<b>*</b>
<b>Error c</b>	<b>10</b>	<b>16.5833</b>	<b>1.658</b>		
<b>Total</b>	<b>23</b>	<b>2985.374</b>			

## □ RCBD

Source of variation	df	SS	MS	F-ratio	Prob >F
Sowing date	1	247.0417	247.042	105.6056	***
Genotype	1	737.0417	737.042	315.0712	***
Nitrogen	1	1855.042	1855.042	792.9949	***
Sowing date x Genotype	1	117.0417	117.042	50.0331	***
Sowing date x Nitrogen	1	1.0417	1.042	0.4453	n.s.
Genotype x Nitrogen	1	2.0417	2.042	0.8728	n.s.
<b>Sowing date x Genotype x Nitrogen</b>	<b>1</b>	<b>9.375</b>	<b>9.375</b>	<b>4.0076</b>	<b>n.s.</b>
Block	2	0.5833	0.292	0.1247	n.s.
<b>Error</b>	<b>14</b>	<b>32.75</b>	<b>2.339</b>		
<b>Total</b>	<b>23</b>	<b>3001.959</b>			

*Error 32.75 = 14.0833 (Main plot) + 2.0833 (sub plot) + 16.5833 (tertiary plot)*



# 결론

- 농업 (재배) 연구에 있어서 분할구 배치법 (split-plot design), 세세구 배치법 (split-split plot design) 은 실험요인의 재배지 배치시 물리적, 생물학적 한계를 극복할수 있게 하는 중요한 실험설계 중 하나임.
- Split(-spilt) plot design 에서는 Main plot 에 위치한 요인의 효과를 측정하는 정확도가 감소되는 반면 sub plot 의 요인의 정확도는 높아짐. 뿐만 아니라 Main plot 의 요인과 Sub plot 의 요인 간의 상호작용의 정확도 역시 일반적인 분산분석의 결과보다 높아짐.
- 이는 일반적 분산분석시 발생하는 오차의 분산 (MSE) 이 Split(-spilt) plot design 에서는 분할되어 상호작용의 통계적 유의성이 상대적으로 높아짐. 실험 인자간의 상호작용이 더 중요하게 평가되는 경우 실험계획 설계시 Split(-spilt) plot design 으로 설계하는 것이 더 효과적임.
- JMP 의 경우 기타 통계 프로그램과는 달리 직접 random factor 를 지정하며 모델을 구성해야 되는 구조여서 Split(-spilt) plot design 및 데이터의 구조를 이해하는 것에 가장 효율적인 프로그램으로 판단됨.

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*Thank you*

