



Change management
– upgrading
experimental designs,
biometrics and data
management at
CIP-NARS SweetGAINS
breeding network
Bert de Boeck & Hugo Campos

EiB Virtual Meeting 2021,
November 17th, 2021



CIP
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POTATO CENTER

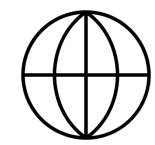


70% of organizational change attempts **Fail**

(McKinsey, 2008)



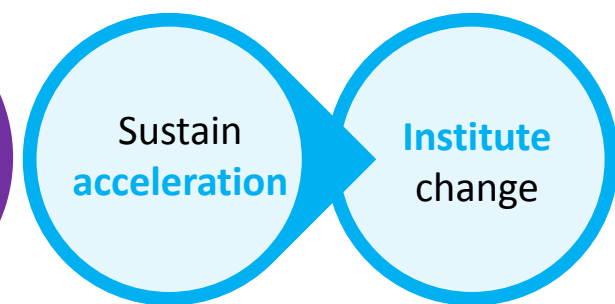
Creating a **climate** for change



Engaging and enabling the whole organization



Implementing and sustaining change



(John Kotter, Harvard University)



The five behaviors of **high-performing teams**

Creating a climate for change - Create a sense of urgency



Experimental designs

- RCBDs for large replicated experiments
- Westcott design for unreplicated experiments



Data analysis

- ANOVA – Least Square Means
- No spatial adjustments
- Compound symmetry V/COV by default



Breeding data management

- No naming convention for genotypes
- No global data curation rules
- Inconsistent trait ontology
- Plot row/column coordinates not recorded
- No global data management system

BEST LINEAR UNBIASED ESTIMATION AND PREDICTION UNDER A SELECTION MODEL

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SUMMARY

Mixed linear models are assumed in most animal breeding applications. Convenient methods for computing BLUE of the estimable linear functions of the fixed elements of the model and for computing best linear unbiased predictions of the random elements of the model have been available. Most data available to animal breeders, however, do not meet the usual requirements of random sampling, the problem being that the data arise either from selection experiments or from breeders' herds which are undergoing selection. Consequently, the usual methods are likely to yield biased estimates and predictions. Methods for dealing with such data are presented in this paper.

TECHNICAL NOTES

Best Linear Unbiased Prediction of Breeding Values Not in the Model for Records

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ABSTRACT

Methods for computing best linear unbiased predictions of random variables (breeding values or sire values) not appearing in the model for records are presented. One method involves taking

This paper describes how variables not in the model can be evaluated by BLUP. An application of these general principles to sire evaluation was presented by Henderson (2).

DERIVATION OF RESULTS

Creating a climate for change - Build a guiding coalition



Standard operating procedures for sweetpotato breeding data management

2020
SEPTEMBER

COP Breeding Data Management SweetGAINS

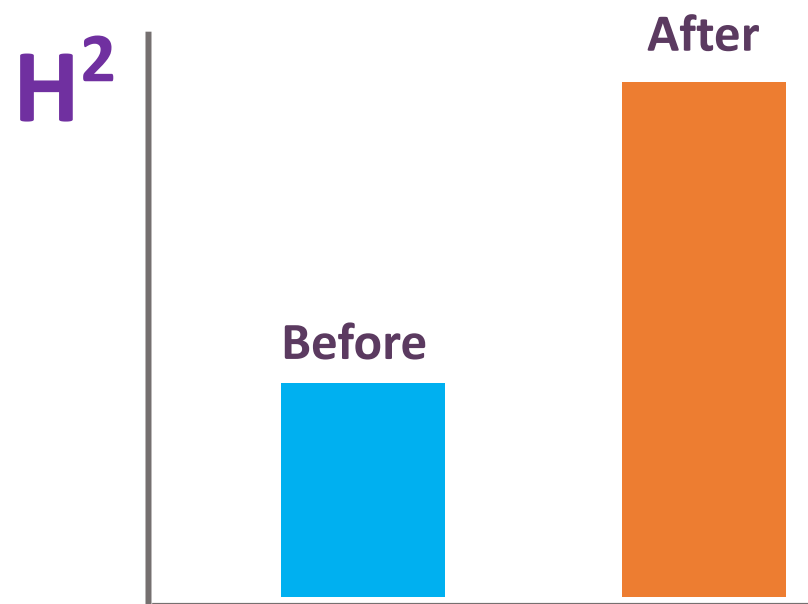
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Creating a climate for change - **Creating a vision**



To increase the **likelihood of success, and impact**, of CIP-NARS
SweetGAINS sweetpotato breeding network

Engaging and enabling the whole organization

- Communicate the vision & Empowering others to act

Computer exercises: variance covariance models

Daniela Bustos-Korts, Fred van Eeuwijk
09 December 2020



WAGENINGEN UNIVERSITY & RESEARCH

Introduction to case studies

Daniela Bustos-Korts, Fred van Eeuwijk
10 December 2020



WAGENINGEN UNIVERSITY & RESEARCH



The International Potato Center (CIP) and the CGIAR Research Program on Roots, Tubers and Bananas grant this certificate to

RANJANA BHATTACHARJEE

for its participation in the virtual statistical training on **PHENOTYPIC MODELLING OF MULTI-ENVIRONMENT TRIALS**, which took place in six weeks between November 30th, 2020 and March 17th, 2021, with a total of 30 hours of theory and practice lectures. This training was dictated by the Wageningen University & Research (WUR).

March 17, 2021

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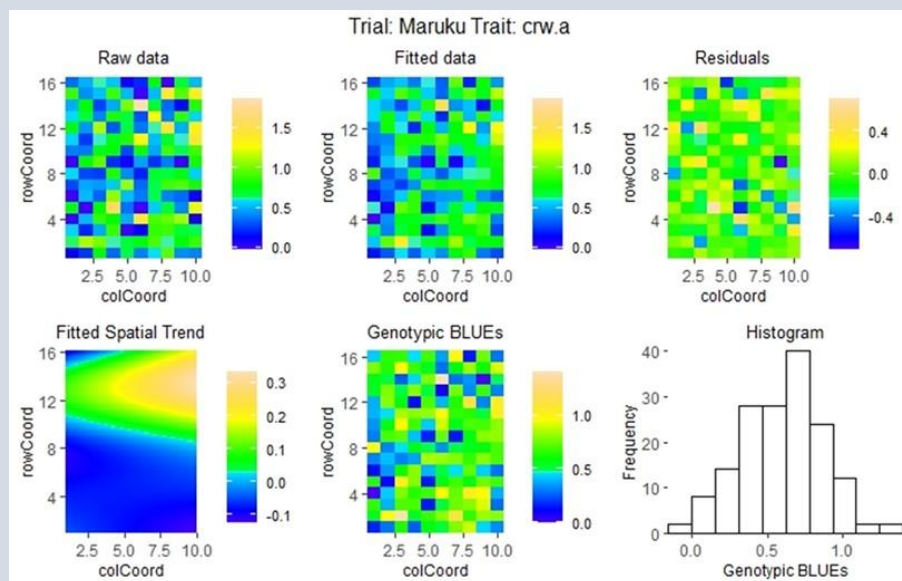
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Engaging and enabling the whole organization

- Generate short-term wins



Breeding program	Row and column coordinates recorded	Augmented row-column designs	Augmented p-rep design	Resolvable row-column designs
NaCRRI (Uganda)	12	0	0	12
CIP (Uganda)	7	1	6	0
Mozambique (CIP + NARS)	25	0	0	25
Malawi	3	0	0	3
Zambia	3	0	0	3
Zimbabwe	6	0	0	6
Tanzania	10	5	0	5
Rwanda	4	0	0	4
Total # trials	70	6	6	58
Percentage of total # trials	100%	9%	9%	82%

Implementing and sustaining change - Sustain acceleration

The screenshot displays the SweetPotatoBase website with a navigation menu including SweetPotatoBase, Search, Manage, Analyze, Genomes, and About. A dropdown menu is open under 'Analyze', listing tools such as Selection Index, HIDAP (Disability Index), Genomic Selection, Mixed Models, Compare Trials, GWAS, Heritability, Stability AMMI, Graphical Filter, and BoxPlotter Tool. The 'Mixed Model Analysis' tool is highlighted, showing a four-step process: 1. Choose Dataset, 2. Choose Dependent Variable, 3. Build Model, and 4. Results. The current step is 'Choose the dataset for your analysis', which includes a search bar and a table with columns for 'Select', 'Dataset Name', and 'Contents'. The table is currently empty, displaying 'No data available in table'. The website footer mentions that SweetPotatoBase is located at the Boyce Thompson Institute for Plant Research, established as part of the GT4SP and SweetGAINS projects.

Implementing and sustaining change - Institute change

- From 2022 onwards, **100% of breeding trials** using modern designs
- From 2022 onwards, **100% of advancement decisions** based on BLUPs
- Piloting **sparse designs** begins in 2022
- **Technical support** to designs trials, analyze datasets, and data management
- **Sustain and institutionalize** through EiB's BRIN



Change is hard,
but it is within reach



Weebale,
Asante sana,
Muito obrigado,
Thank you!

BILL & MELINDA
GATES foundation

