[UPDATE:] Comparing and optimizing breeding strategies

Simulation results and recommendations for CIMMYT's GWP

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Introduction

> **Problem:** Ensure genetic gains and stability in **TPEs**

> **Ways:** Quantitative Genetics and Stochastic Simulations

> **Considering:** Historical data and Breeders' Experience

> **Inferences:** Components of the *Breeders' Equation*

> **Target:** Find an optimized strategy for *CIMMYT GWP*

Evaluate the outcomes from the Expert Panel Meeting
(January, 2020)

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Inputs

> Philomin *et al.,* 2020 – Frontiers in Plant Science

<doi: 10.3389/fpls.2020.580136>

... in special the *Supplementary Table 2*:

> grain yield *BLUPs* **GWP** lines;

> covering years/seasons from 2013 to 2017; and

> Stages one, two, three, **SABWGPY** plus **ESWYT**.

> Stages were taken as is

> and **SABWGPY** were taken as **TPEs**

> mean across **SABWGPY** is assumed as the **TBV**

Correlations on pairwise observations maybe biased upwards

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Methods

- ❯ *R* to simulate, analyze and summarize results
- ❯ *AlphaSimR* *R* package as simulation framework
- ❯ Using CIMMYT's *HPC* Infrastructure
- ❯ Took into account previous simulated works from **EiB**

- ❯ Results are based on 30 Monte Carlo Replicates
- ❯ Time spans a recurrent process along 30 years
- ❯ Data, codes and results are stored in the **EiB** repository (**GPL**)

Treatments

> **CCBS** – Current CIMMYT's Breeding Strategy

>> $F_{4:5}$ lines (selected bulk headrows) evaluated in 4 stages
>> recycling parents from first 3 stages (**SEs**)
>> releasing lines according to performance in **TPEs**

> **RBGA** – Rapid Bulk Generation Advancement

>> $F_{3:4}$ lines (speed breeding headrows) evaluated in 3 stages
>> recycling parents from stage 2 (**SEs** plus **TPEs**)
>> releasing lines according to performance in **TPEs**

> **RCRS** – Rapid cycle Recurrent Selection

>> $F_{3:4}$ lines (speed breeding headrows) evaluated in 2 stages
>> recycling parents from stage 1 (**SEs**)
>> releasing lines according to performance in **TPEs**

Selection Stages
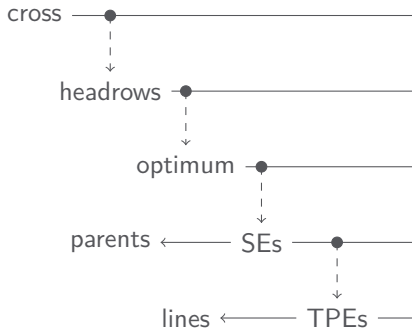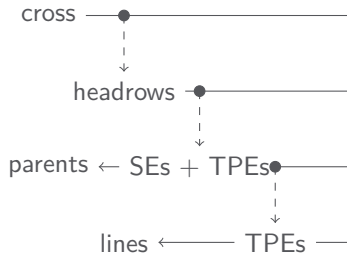
Scenarios

> selected bulks *vs* speed breeding: (selection of headrows)

> > negative correlated w/ **TBVs** ($\rho = -0.50$ and -0.25)

> > neutral effect on **TBV** ($\rho = 0.00$)

> > positive correlated w/ **TBVs** ($\rho = 0.25$ and 0.50)

> methods of analysis: (**TBVs** estimation)

> > without considering *kinship*

> > with markers (**GEBVs**)

> experimental designs:

> > **sparse testing . . . (needs further *brainstorn*)

Indirect Selection

... taking the traits evaluated and selected in Bulks as an index...
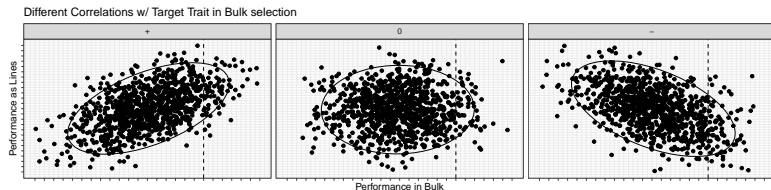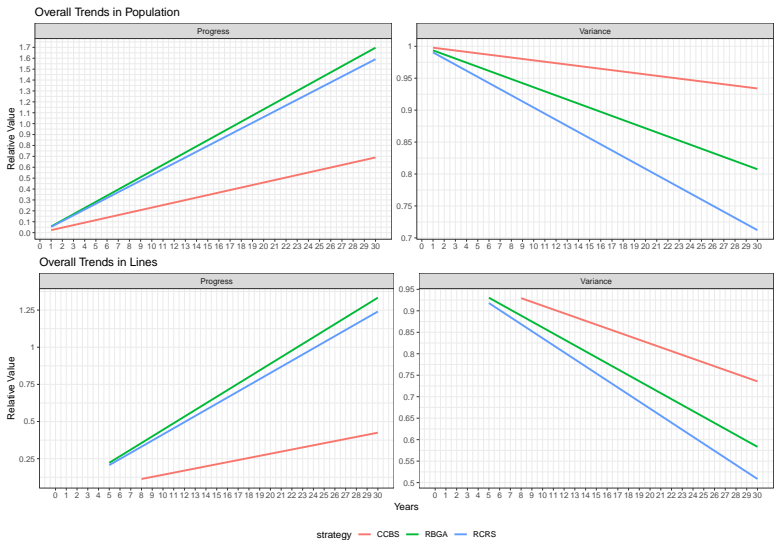

... taking the target traits also as an index.

How much the selection (sampling) in bulks affects the distribution of the lines?

Results I: *Overall trends in genetic progress*

Trends of mean/variance in each treatment for populations and lines

Results II: *Short and Long term comparisons*

Estimates for each treatment regarding mean/variances and gains

	Trends			5th year		
	CCBS	RBGA	RCRS	CCBS	RBGA	RCRS
CCBS	0.0283	<0.001	<0.001	0.0258	0.0006	0.0020
RBGA	-0.0376	0.0659	0.3818	-0.1151	0.1409	0.9107
RCRS	-0.0338	0.0038	0.0621	-0.1028	0.0123	0.1286

	Variance			10th year		
	CCBS	RBGA	RCRS	CCBS	RBGA	RCRS
CCBS	-0.0045	0.0013	<0.001	0.1670	<0.001	<0.001
RBGA	0.0037	-0.0082	0.2332	-0.3032	0.4700	0.3910
RCRS	0.0055	0.0017	-0.0100	-0.2721	0.0311	0.4390

Results III: *Advantages on the use of additional information*

Effects of analysis scenarios in each treatment on the mean/variance

CCBS	mean	SE	variance	SE
markers	0.205	0.026	-0.195	0.018
unknown	0.198	0.025	-0.167	0.017
p value	0.824		0.266	

RBGA	mean	SE	variance	SE
markers	0.832	0.025	-0.315	0.016
unknown	0.638	0.025	-0.223	0.016
p value	<0.001		<0.001	

RCRS	means	SE	variance	SE
markers	0.658	0.026	-0.326	0.017
unknown	0.715	0.025	-0.309	0.017
p value	0.110		0.477	

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Results IV: *Selected Bulks vs Speed Breeding*

Effect of varying bulk accuracy in each treatment on the mean/variance

Mean	effect	SE	lower	upper
CCBS	0.1138	0.106	-0.0954	0.3230
RBGA	0.0692	0.112	-0.1514	0.2900
RCRS	0.1367	0.113	-0.0852	0.3590

Variance	effect	SE	lower	upper
CCBS	0.0600	0.031	-0.0016	0.1216
RBGA	-0.0308	0.033	-0.0958	0.0342
RCRS	0.0742	0.033	0.0088	0.1395

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Recommendations

- **RBGA** seems to have clear advantages in comparison to **CCBS**
    - higher gains and acceptable higher impact on genetic variance
- **RCRS** do **not** provide additional gains for populational improvement
    - line performance is comparable to **RGBA**
- Indirect effects of *Speed Breeding* were evaluated **widely**
    - . . . **No **consequence of** negative** effect in bulk selection
- The use of Markers for estimation do improve efficiency . . .
    - In terms of **precision** of the measurements and **gains**

Pedigree may have the advantange to be free of charge!

Caveats

> Costs and logistics were not taken into account

> Pairwise cross were made at random!

> Experimental procedures need further brainstorm

> > reasonable strategy for sparse testing

> Practical use of markers/pedigree may change results...

> > Estimation *vs* Prediction

> Management of segregating progenies (e.g., $F_{3:4}$) were not considered

Breeding dimensions are smaller than what is common computer limitations

Outlook

> Optimize breeding dimensions i.e., crosses and progeny sizes

> Define objectives and methods for optimized crossing strategies

> > increasing divergence; or

> > ensuring some threshold of performance . . .

> Evaluate feasible strategies to use Genomics and Pedigree

> > May depend on item 2 or *vice-versa*

> Evolve the ideas for *improved* experimental designs

> > *sparse testing*;

> > spatial analysis; and . . .

Questions?

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