



Spatial Analyses and Pedigree-based Relationship Matrix for Breeding Value Estimation for Root Yield in a Diallel Population of Autohexaploid Sweetpotato



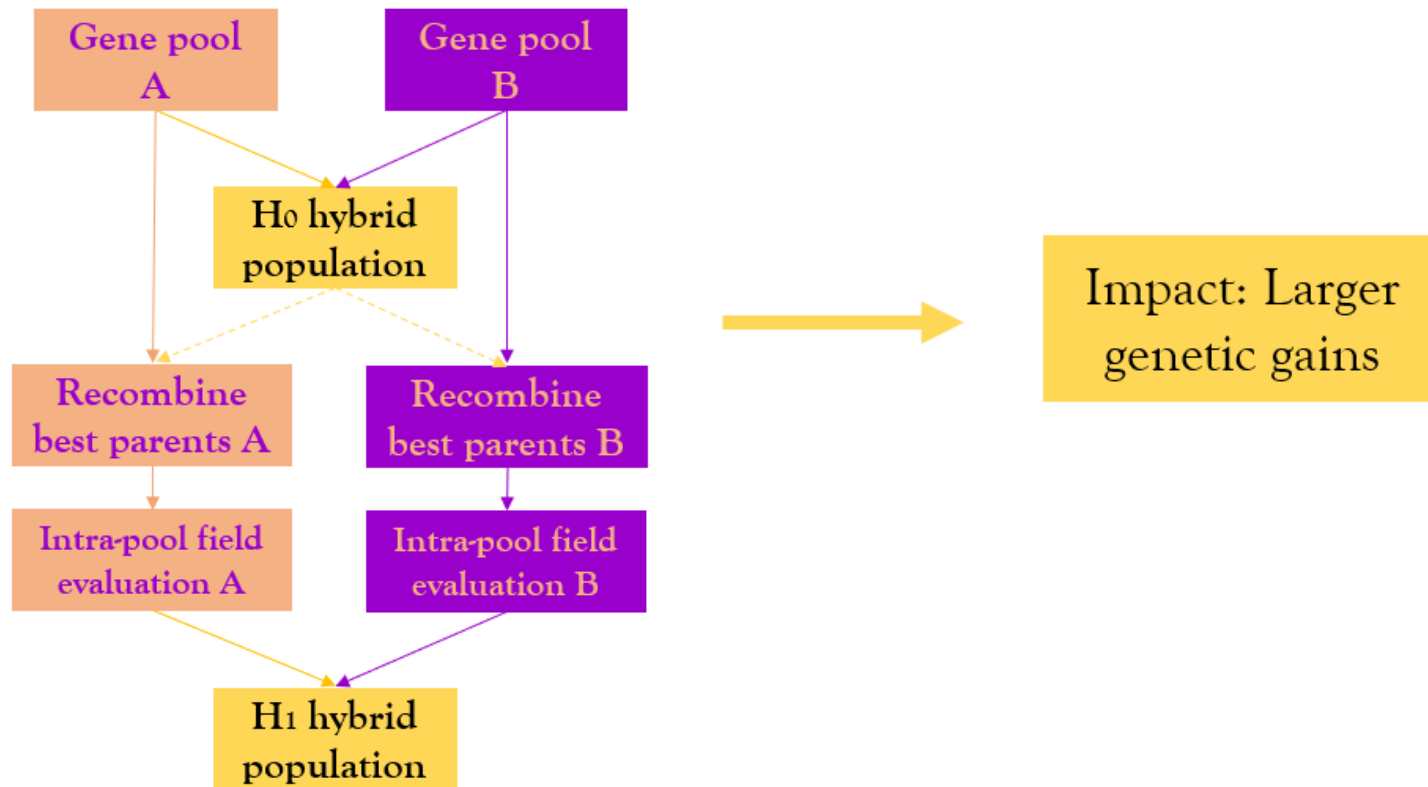
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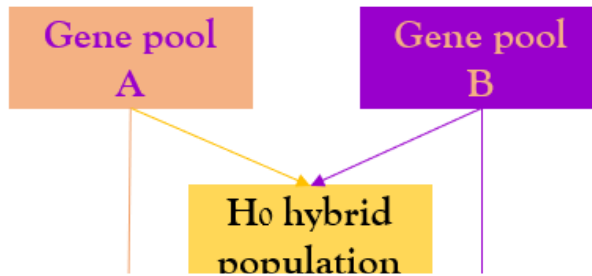
Introduction

- Heterosis exploiting breeding scheme



Introduction

- Heterosis exploiting breeding scheme



Early generation trials usually are composed of a large number of genotypes covering large experimental areas

The accuracy of genetic estimates is impacted by the lack of replicates.

The objective of this study was: **To use spatial correction and relatedness information to improve the estimation of genetic parameters in a autohexaploid breeding population**

Materials & Methods

Mwanga Diversity Panel (MDP)

- 8 parents from gene pool A × 8 parents from gene pool B;
- 64 families with ~30 offspring clones each;
- Trait: Storage root yield (t ha⁻¹);
- Sites: Namulonge and Serere (seasons A and B) in 2018 and 2019
- Westcott design: unreplicated parents and offspring clones planted between columns of two alternating check clones

Table 1. Description of genotypes used as parents in this study

| Name | Cultivar origin | pool |
|------------------|------------------------|-------------|
| Dimbuka Bukulula | Uganda | Male |
| Ejumula | Uganda | Male |
| Huarmeyano | Peru | Female |
| Magabali | Uganda | Female |
| Mugande | Rwanda/ Congo | Female |
| NASPOT 1 | Uganda | Male |
| NASPOT 10 O | Uganda | Male |
| NASPOT 11 | Uganda | Female |
| NASPOT 5 | Uganda | Female |
| NASPOT 7 | Uganda | Male |
| NASPOT5/58 | Uganda | Male |
| New Kawogo | Uganda | Female |
| NK259L | Uganda | Male |
| Resisto | USA | Female |
| SPK004 | Kenya | Male |
| Wagabolige | Uganda | Female |

Materials & Methods

- Spatial Analysis of field Trials with Splines (SpATS) mixed model to get BLUPs

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{W}\mathbf{s} + \mathbf{Z}\mathbf{g} + \mathbf{e}$$

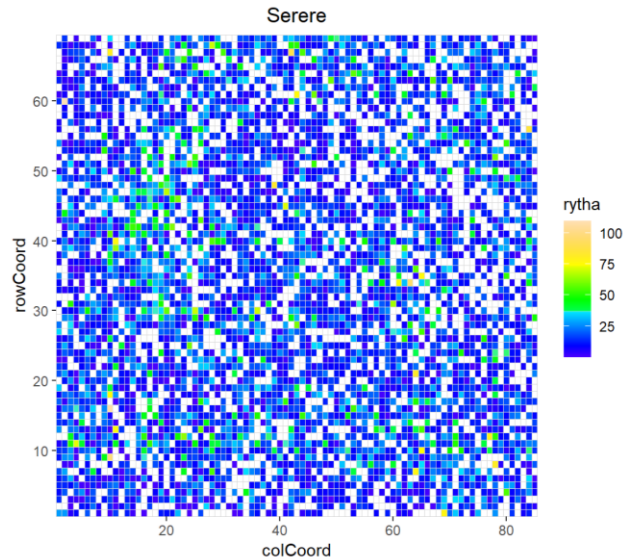
where \mathbf{y} refers to the vector of phenotypic observations, $\boldsymbol{\beta}$ is the vector of fixed effects of checks, and \mathbf{X} is the associated design matrix; \mathbf{s} is the vector containing the fixed (unpenalized) and random (penalized) components of the smooth spatial surface and the mutually independent sub-vectors of row and column effects, and \mathbf{W} is the associated design matrix that has an associated (co)variance matrix \mathbf{S} ; \mathbf{g} is the random vector of genotypic effects, $\mathbf{g} \sim N(0, \mathbf{H}\sigma_g^2)$, where \mathbf{H} is a combined relationship matrix and σ_g^2 is the additive genetic variance; \mathbf{e} is the random vector of spatially independent residuals, $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$, where \mathbf{I} is an identity matrix and σ_e^2 is the residual variance.

Materials & Methods

- Spatial Analysis of field Trials with Splines (SpATS) mixed model to get BLUPs

$$y = X\beta + Ws + Zg + e$$

where y refers to the vector of phenotypic observations, β is the vector of fixed effects of checks, and X is the associated design matrix; s is the vector containing the fixed (unpenalized) and random (penalized) components of the smooth spatial surface and the mutually independent sub-vectors of row and column effects, and W is the associated design matrix that has an associated (co)variance matrix S ; g is the random vector of genotypic effects, $g \sim N(0, H\sigma_g^2)$, where H is a combined relationship matrix and σ_g^2 is the additive genetic variance; e is the random vector of spatially independent residuals, $e \sim N(0, I\sigma_e^2)$, where I is an identity matrix and σ_e^2 is the residual variance.

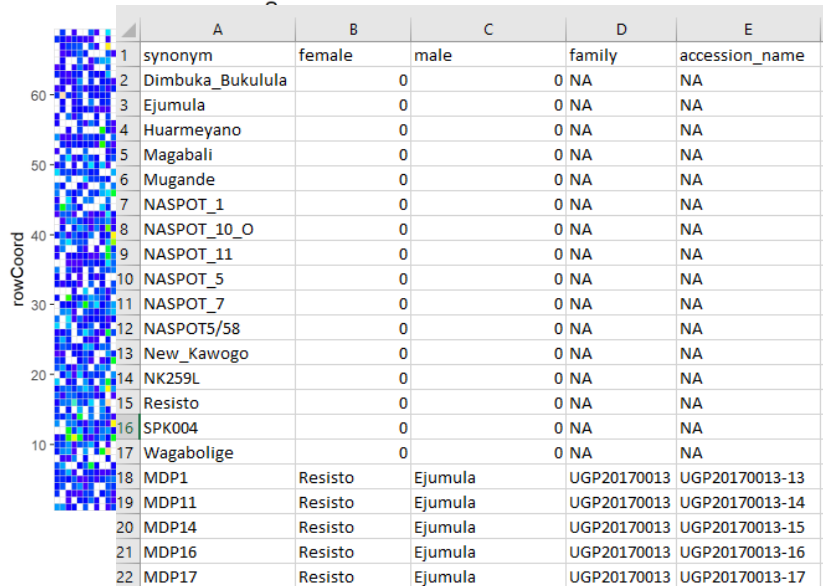


Materials & Methods

- Spatial Analysis of field Trials with Splines (SpATS) mixed model to get BLUPs

$$y = X\beta + Ws + Zg + e$$

where y refers to the vector of phenotypic observations, β is the vector of fixed effects of checks, and X is the associated design matrix; s is the vector containing the fixed (unpenalized) and random (penalized) components of the smooth spatial surface and the mutually independent sub-vectors of row and column effects, and W is the associated design matrix that has an associated (co)variance matrix S ; g is the random vector of genotypic effects, $g \sim N(0, H\sigma_g^2)$, where H is a combined relationship matrix and σ_g^2 is the additive genetic variance; e is the random vector of spatially independent residuals, $e \sim N(0, I\sigma_e^2)$, where I is an identity matrix and σ_e^2 is the residual variance.



| | A | B | C | D | E |
|----|------------------|---------|---------|-------------|----------------|
| 1 | synonym | female | male | family | accession_name |
| 2 | Dimbuka_Bukulula | 0 | 0 | NA | NA |
| 3 | Ejumula | 0 | 0 | NA | NA |
| 4 | Huarmeyano | 0 | 0 | NA | NA |
| 5 | Magabali | 0 | 0 | NA | NA |
| 6 | Mugande | 0 | 0 | NA | NA |
| 7 | NASPOT_1 | 0 | 0 | NA | NA |
| 8 | NASPOT_10_O | 0 | 0 | NA | NA |
| 9 | NASPOT_11 | 0 | 0 | NA | NA |
| 10 | NASPOT_5 | 0 | 0 | NA | NA |
| 11 | NASPOT_7 | 0 | 0 | NA | NA |
| 12 | NASPOT5/58 | 0 | 0 | NA | NA |
| 13 | New_Kawogo | 0 | 0 | NA | NA |
| 14 | NK259L | 0 | 0 | NA | NA |
| 15 | Resisto | 0 | 0 | NA | NA |
| 16 | SPK004 | 0 | 0 | NA | NA |
| 17 | Wagabolige | 0 | 0 | NA | NA |
| 18 | MDP1 | Resisto | Ejumula | UGP20170013 | UGP20170013-13 |
| 19 | MDP11 | Resisto | Ejumula | UGP20170013 | UGP20170013-14 |
| 20 | MDP14 | Resisto | Ejumula | UGP20170013 | UGP20170013-15 |
| 21 | MDP16 | Resisto | Ejumula | UGP20170013 | UGP20170013-16 |
| 22 | MDP17 | Resisto | Ejumula | UGP20170013 | UGP20170013-17 |

| | A | B | C | D | E | F | G |
|----|-------------|----------|-----------|--------------|--------------|------------|--------------|
| 1 | Mugande | Resisto | NASPOT_11 | New_Kawogo | NK259L | Wagabolige | |
| 2 | Mugande | 1.055609 | 0.014 | -0.098026767 | -0.131723483 | -0.08391 | -0.073481866 |
| 3 | Resisto | 0.014 | 0.961338 | -0.014737223 | -0.100732925 | -0.04219 | 0.024848095 |
| 4 | NASPOT_11 | -0.09803 | -0.01474 | 1.088882855 | 0.259963913 | -0.09862 | -0.056824155 |
| 5 | New_Kawogo | -0.13172 | -0.10073 | 0.259963913 | 0.877116736 | -0.18998 | -0.064440989 |
| 6 | NK259L | -0.08391 | -0.04219 | -0.098621193 | -0.189976452 | 1.139764 | -0.01359411 |
| 7 | Wagabolige | -0.07348 | 0.024848 | -0.056824155 | -0.064440989 | -0.01359 | 1.069581099 |
| 8 | NASPOT_1 | -0.07045 | -0.05642 | -0.095448133 | -0.166794666 | 0.061531 | -0.035783027 |
| 9 | NASPOT_7 | -0.13379 | -0.12848 | -0.01900687 | 0.083110083 | -0.14576 | -0.105401185 |
| 10 | NASPOT_5 | -0.03635 | -0.01848 | -0.05159409 | -0.000848564 | -0.01126 | -0.053655281 |
| 11 | SPK004 | -0.15901 | -0.11852 | -0.291389839 | -0.309476639 | -0.0281 | -0.115978995 |
| 12 | NASPOT_10_O | -0.21687 | -0.18303 | -0.08997155 | 0.106749198 | -0.18977 | -0.14637393 |
| 13 | Huarmeyano | 0.389472 | 0.02011 | -0.182049105 | -0.198091339 | -0.03574 | -0.087897984 |
| 14 | Magabali | -0.00351 | -0.02285 | 0.041205641 | 0.006811664 | -0.06996 | 0.018542514 |
| 15 | Fiumula | -0.07364 | -0.05277 | -0.089611619 | -0.149788645 | 0.067131 | -0.009985639 |

Materials & Methods

- Correcting information - removing the fixed effect of checks and the random spatial variation:

$$\mathbf{y}^* = \hat{\mathbf{g}} + \hat{\mathbf{e}}$$

genotypic effect +
residuals used as input
in the following analyses

- General Combining Ability (GCA) effects for females and males, and Specific Combining Ability (SCA) effects for crosses:

$$\mathbf{y}^* = \mathbf{1}\mu + \mathbf{Z}_A\mathbf{g}_A + \mathbf{Z}_B\mathbf{g}_B + \mathbf{Z}_C\mathbf{g}_C + \mathbf{e}$$

where \mathbf{y}^* is the vector of corrected phenotypic observations, μ is the fixed intercept and $\mathbf{1}$ is a vector of ones; $\mathbf{g}_A, \mathbf{g}_B, \mathbf{g}_C$ are random vectors of GCA for male, GCA for female and SCA for crosses, respectively, with $\mathbf{g}_A \sim N(\mathbf{0}, \sigma_A^2)$, $\mathbf{g}_B \sim N(\mathbf{0}, \sigma_B^2)$, and $\mathbf{g}_C \sim N(\mathbf{0}, \sigma_C^2)$. $\sigma_A^2, \sigma_B^2, \sigma_C^2$ are genetic variances of males (pool A), females (pool B), and offsprings (A × B crosses), respectively

Results

Table 1. Storage root yield predictions (t ha⁻¹) of parents and average of offspring (n = 1897), genetic variance component and narrow-sense heritability (h²) estimates by environment.

| Parent | Namulonge | | | | Serere | | | | Average across environments |
|-------------------|-----------|--------|---------|--------|--------|--------|---------|--------|-----------------------------|
| | 2018A | 2018B | 2019A | 2019B | 2018A | 2018B | 2019A | 2019B | |
| Dimbuka Bukulula | 7.03 | 2.53 | 13.82 | 8.21 | 4.95 | 7.09 | 29.70 | 4.32 | 9.71 |
| Ejumula | 9.06 | 3.20 | 20.45 | 9.29 | 5.4 | 5.79 | 29.30 | 4.18 | 10.83 |
| Huarmeyano | 7.12 | 2.25 | 15.62 | 5.30 | 3.36 | 6.27 | 33.03 | 3.54 | 9.56 |
| Magabali | 8.44 | 2.89 | 16.82 | 11.34 | 4.18 | 7.7 | 25.23 | 4.81 | 10.18 |
| Mugande | 5.86 | 1.84 | 13.33 | 5.28 | 2.72 | 5.79 | 29.82 | 4.17 | 8.60 |
| NASPOT 1 | 8.56 | 2.95 | 11.74 | 8.48 | 5.10 | 5.99 | 30.10 | 4.78 | 9.71 |
| NASPOT 10 O | 8.99 | 2.21 | 18.61 | 11.10 | 4.61 | 6.27 | 32.63 | 6.38 | 11.35 |
| NASPOT 11 | 12.42 | 5.72 | 32.05 | 11.45 | 5.69 | 8.10 | 41.03 | 8.56 | 15.63 |
| NASPOT 5 | 4.18 | 1.83 | 4.28 | 3.72 | 3.14 | 5.07 | 15.67 | 4.59 | 5.31 |
| NASPOT 7 | 7.18 | 2.87 | 20.23 | 12.57 | 3.59 | 7.57 | 30.79 | 8.55 | 11.67 |
| NASPOT5/58 | 5.04 | 2.28 | 11.06 | 7.99 | 3.06 | 6.75 | 24.35 | 7.30 | 8.48 |
| New Kawogo | 12.48 | 3.63 | 28.34 | 9.74 | 6.39 | 7.13 | 34.4 | 6.55 | 13.58 |
| NK259L | 8.12 | 3.57 | 26.75 | 9.33 | 5.96 | 7.34 | 32.54 | 6.92 | 12.57 |
| Resisto | 9.17 | 3.14 | 10.63 | 8.91 | 7.49 | 6.98 | 32.28 | 5.66 | 10.53 |
| SPK004 | 5.93 | 2.32 | 13.05 | 8.47 | 1.96 | 6.63 | 27.46 | 5.25 | 8.88 |
| Wagabolige | 5.15 | 2.05 | 3.53 | 6.48 | 4.36 | 5.83 | 29.22 | 5.25 | 7.73 |
| Average parents | 7.80 | 2.83 | 16.27 | 8.60 | 4.50 | 6.64 | 29.85 | 5.68 | 10.27 |
| Average offspring | 7.79 | 2.83 | 16.26 | 8.61 | 4.49 | 6.65 | 29.87 | 5.67 | 10.27 |
| σ_g^2 | 6.39** | 1.31** | 71.10** | 5.62** | 2.84** | 1.31** | 38.50** | 3.08** | 16.27 |
| h^2 | 0.66 | 0.61 | 0.66 | 0.61 | 0.59 | 0.57 | 0.59 | 0.57 | 0.61 |

Results

| Male parents | Female parents | | | | | | | |
|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-------------------|------------------|
| | Huarmeyano | Magabali | Mugande | NASPOT_11 | NASPOT_5 | New_Kawogo | Resisto | Wagabolige |
| SPK004 | 9.29 (-1.81%) | 9.74 (-0.82%) | 8.39 (-3.24%) | 12.33 (2.23%) | 6.96 (-5.05%) | 12.43 (3.34%) | 10.07 (-0.28%) | 7.95 (-3.89%) |
| NK259L | 10.73 (0.07%) | 11.65 (2.08%) | 9.9 (-1.02%) | 14.39 (4.99%) | 8.19 (-3.22%) | 12.73 (2.34%) | 12.48 (3.73%) | 10.8 (1.74%) |
| NASPOT5/58 | 9.07 (-2.08%) | 8.78 (-2.95%) | 9.25 (-0.72%) | 11.3 (0.22%) | 6.78 (-5.27%) | 11.24 (0.93%) | 9.17 (-2.21%) | 8.11 (-3.18%) |
| NASPOT_7 | 11.41 (2.23%) | 11.05 (1.22%) | 10.39 (0.71%) | 13.63 (3.94%) | 8.01 (-3.18%) | 12.08 (1.44%) | 11.78 (2.68%) | 8.88 (-2.51%) |
| NASPOT_10_O | 10.99 (1.58%) | 10.4 (0.02%) | 9.8 (-0.4%) | 12.25 (1.32%) | 7.84 (-3.31%) | 13.25 (4.36%) | 10.62 (0.28%) | 9.28 (-1.18%) |
| NASPOT_1 | 9.63 (-1.1%) | 10.39 (0.62%) | 9.01 (-1.79%) | 12.79 (3.09%) | 6.96 (-5.18%) | 11.62 (1.35%) | 10.06 (-0.44%) | 8.98 (-1.31%) |
| Ejumula | 10.91 (1.25%) | 9.84 (-1.43%) | 9.83 (-0.46%) | 13.41 (3.67%) | 8.03 (-2.9%) | 12.77 (3.16%) | 10.04 (-1.21%) | 9.26 (-1.34%) |
| Dimbuka_Bukulula | 9.67 (-1.29%) | 10.67 (1.01%) | 8.78 (-2.67%) | 14.27 (6.01%) | 6.85 (-5.78%) | 11.79 (1.45%) | 10.62 (0.61%) | 8.7 (-2.35%) |

Figure 2. Predictions of storage root yield (t ha⁻¹) of 64 families and heterosis increments in brackets on basis of family prediction – mid-parent value evaluated in eight environments in Uganda.

Take-home message

- Although partially-replicated experiments challenge the accurate estimation of genetic parameters, the correction of spatial effects and the inclusion of relatedness improve the quality of the genetic estimates.
- BLUPs can be further employed in estimating general and specific combining abilities and training genomic prediction models when molecular markers become available for the whole population.



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