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Population hybrid breeding and the use of new statistical tools for sweetpotato

Keywords: orange-fleshed sweetpotato, reciprocal recurrent selection, population hybrid breeding, restricted maximum likelihood, spatial analysis

Introduction

Sweetpotato is a highly heterozygous hybrid, and populations of orange-fleshed sweetpotato (OFSP) have a considerable importance for food security and health. Population hybrid breeding (PHB) has been recently introduced for sweetpotato in the Peruvian, Ugandan, and Mozambican breeding platform by the International Potato Center (CIP). In addition, PHB was accompanied by intensifying the use of more modern statistical tools like (generalized) linear mixed models that account for spatial trends in the field.

Reciprocal Recurrent Selection

At the International Potato Center (CIP) in Peru a Reciprocal Recurrent Selection (RRS) based breeding scheme for PHB was implemented since 2010, to systematically exploit heterosis and to enhance genetic gains. RRS is a cyclic breeding procedure where the hybrid performance from crosses between two parental pools is improved by the selection of the best combining parents in each pool to generate new parents by recombination in each parental pool for the next cycle. The parental pools should be genetically distinct in order to exploit heterosis. A schematic overview of the adopted RRS breeding scheme is shown in Figure 1. Two heterogenic OFSP breeding foundation pools were developed in Peru, called PJ and PZ. From these base populations/pools, three different OFSP populations were developed in the first complete RRS cycle, aiming at three different product profiles, respectively.

Three product profiles

- O-WAE: OFSP for wide adaptation and earliness (very short crop duration)
- O-NSSP: non-sweet OFSP with no or low sweet taste after cooking
- O-HIFE: OFSP double biofortified with high iron

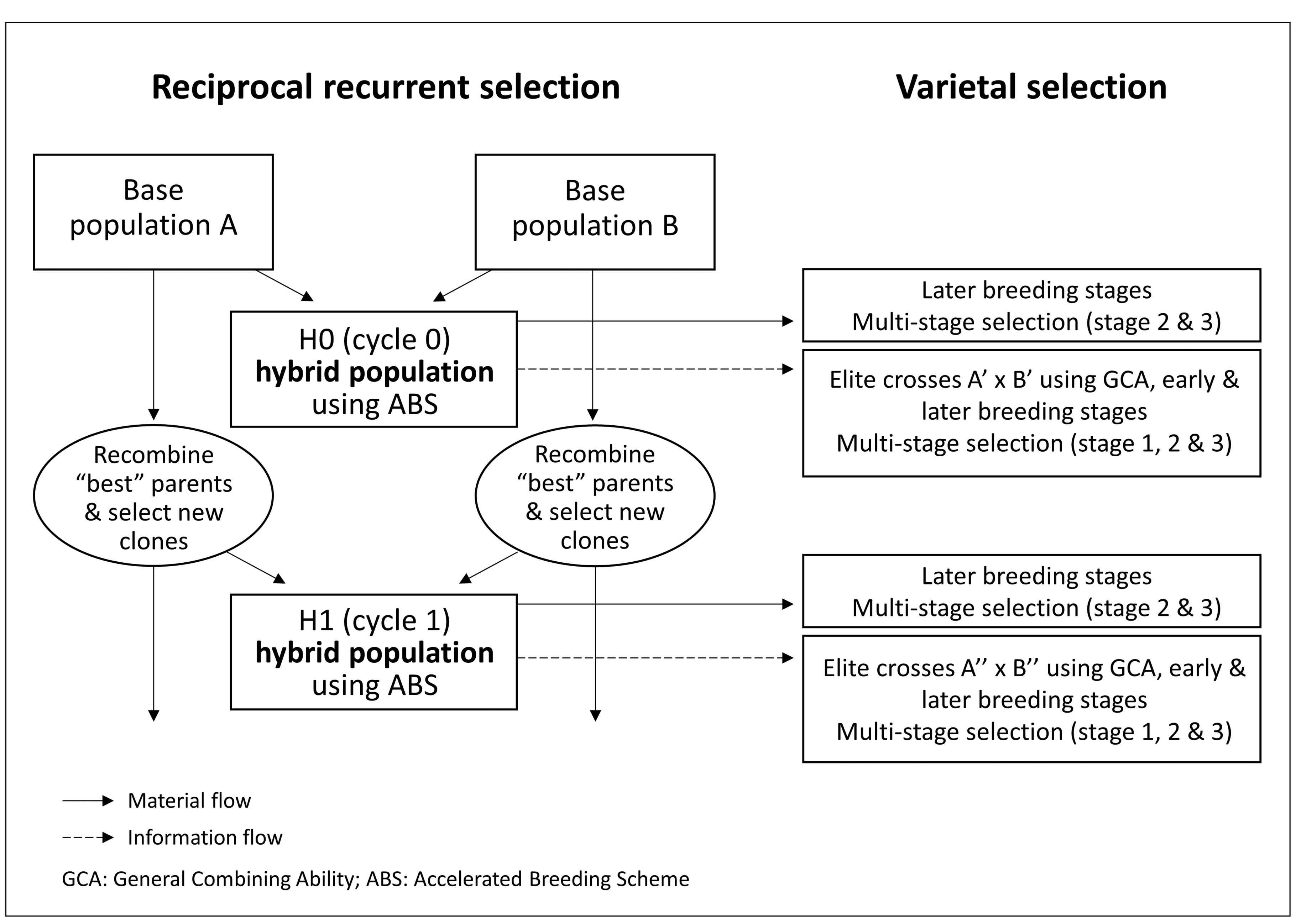

Figure 1. CIP's approach to PHB with RRS (left) and hybrid variety selection (right).

Figure 2. Illustrative picture demonstrating heterosis by comparing the root yield of a single plant harvest of one of the hybrid progeny, PH17.19120, with its parents PJ14.00044 and PZ14.09781, from the two parental pools PJ' and PZ', respectively.

Experiments

PHB has been studied at the Peruvian breeding platform for a complete reciprocal recurrent selection (RRS) cycle, for each of the three product profiles/populations, by simultaneously evaluating:

- founder clones (PJ and PZ; common across all three populations),
- parents (PJ' and PZ'; specific for the three populations),
- and the hybrid population (H1; specific for the three populations)

at two contrasting locations in Peru:

- Satipo : humid tropics of the Amazon basin (11°15'S; 74°38'W)
- Cañete: arid Pacific coast (13°04'S; 76°23'W)

Statistical methodology

The data were analyzed using modern statistical approaches using mixed models fitted with restricted maximum likelihood (REML), correcting for spatial variation in the field, using the R package "SpATS" for single-trial analysis, and allowing for heterogeneity of genetic (co)variances in the tested environments, using the R package "asreml" for multi-environment trial analysis. In contrast to previous approaches this leads to more precise estimates of model parameters, and to higher heritabilities because spatial noise is removed from the genetic signal.

Results

Heterosis increment and total genetic gain were estimated after one RRS cycle in the three populations, both for yield and quality traits. Results for storage root yield are presented in Table 1. For all other results, the reader is referred to Grüneberg et al. (2022). In conclusion we argue that PHB is a tool to achieve large genetic gains in sweetpotato yield and most likely all other clonally propagated crops. Moreover, PHB allows a rapid global dissemination of true seed that is generated from elite crosses (an intermediate reproducible product generated in isolations), thus, avoiding costly and time-consuming virus cleaning of elite clones transferred as vegetative plantlets.

	Foundation clones (PJ + PZ)/2 [t/ha]	Parental clones (PJ' + PZ')/2 [t/ha]	Hybrid clones H1 [t/ha]	Genetic Gain due to heterosis increment (%)	Total Genetic Gain after one RRS cycle (%)
O-WAE	7.8	13.2	17.0	28.5%	118.8%
O-NSSP	12.7	20.8	29.4	41.2%	132.4%
O-HIFE	22.6	32.3	44.6	38.0%	97.1%

Table 1. Estimates for total root yield in ton/ha for the different genotype groups, heterosis and total genetic gain after one complete RRS cycle.

More information

Grüneberg W. J., De Boeck B., Diaz F., Eyzaguirre R., Low J. W., Reif J. C., Campos H. (2022). Heterosis and Responses to Selection in Orange-Fleshed Sweetpotato (Ipomoea batatas L.) Improved Using Reciprocal Recurrent Selection. *Frontiers in Plant Science* 13. https://doi.org/10.3389/fpls.2022.793904.

Acknowledgement

The transition to more modern statistical tools at CIP was enabled by the Centre for International Migration and Development (CIM), a joint operation of GIZ and the German Federal Employment Agency, by funding the position of plant breeding statistician and resulting capacity building in statistics.