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Evaluation of alternative sugarcane selection strategies

Thesis submitted by

Vanja Calija-Zoppolato BSc(Hons) UK

in June 2004

for the degree of Doctor of Philosophy
in the Mathematics and Statistics and Tropical Plant Science within the Schools of
Mathematical and Physical Sciences and Tropical Biology
James Cook University of North Queensland

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Abstract

The international competitiveness and success of the Australian sugar industry, which is one of the world's largest exporters of raw sugar depends on increased cane yield and advanced farming practices. One of the key drivers for a sustainable sugar industry is therefore, to increase cane yield through designing efficient breeding programs, that aim at producing new and improved varieties of cane. Selection for superior genotypes is the most important aspect of sugarcane breeding programs, and is a long and expensive process. It consists of a number of stages where at each stage some genotypes are chosen for further selection and some are discarded from future selection. Designing a selection system is a complex task, with varying parameters at each stage. While studies have investigated different components of selection independently, there has not been a whole system approach to improve the process of selection.

The aim of this research was to develop a tool for the optimisation of selection systems. The problem of designing an efficient selection system has two components: firstly, evaluating the performance of selection systems and secondly, deciding on a combination of selection variables that will select the most promising genotypes. These two components were designated sub-objectives, one and two respectively.

To address the first sub-objective, data on previous selection trials was collected and used to predict gain for different selection designs. The value that is used to compare the performances of different selection systems is what was called in this thesis, the genetic gain for economic value $\widetilde{G}$, a measure based on the estimate of a potential economic value of a genotype if planted as a cultivar. The connection between $\widetilde{G}$ and choice taken for selection variables at various stages is complex and not expressible by a simple set of

formulas. Instead, a computer based stochastic simulation model SSSM (Sugarcane Selection Simulation Model) was developed.

To eliminate as many simplifying assumptions as possible and bring the study as close to real life as possible, the quantitative genetics of sugarcanes relevant to selection was studied. Furthermore, a specific sugarcane-breeding region was targeted, the Burdekin region (Australia). To ensure the accuracy of the SSSM, it performance was verified and the sensitivity analysis was performed to identify those variance parameters to which it is most sensitive.

By, developing the SSSM this study approached the problem as an integrated system, where if one parameter changes the state of the whole system changes. Furthermore, by creating an accurate selection simulation model a new methodology for evaluating alterative sugarcane selection strategies was obtained. A new methodology that tests the performance of different selection designs prior to their field trials and also tests the impact any change in the estimated variance components may have on selection, will be a potential money saver for the industry. Furthermore, the SSSM can be directly applied to any region targeted by sugarcane breeding programs or to other clonally propagated crops.

The second sub-objective was addressed by the development of the optimisation algorithm called ASSSO (Algorithm for the Sugarcane Selection Simulation Optimisation), a combination of dynamic programming and branch-and-bound. The ASSSO was applied to the Burdekin region to identify selection designs that maximise selection outputs. Apart from providing a new approach to the problem of optimising selection system, the ASSSO also presents a new application of dynamic programming and branch-and-bound.

The ASSSO identified a number of alternative selection systems that are significant improvements to the practices currently used in the Burdekin region. Nevertheless, the purpose of this research was not to suggest that the intuitions and experiences of plant breeders can be replaced by the set of guidelines obtained using a computer simulation,

but rather to validate the benefits of a joint venture between mathematicians and plant breeders.

Acknowledgments

First of all I wish to thank my family for helping me through all difficulties I encountered during this research. I am grateful to my supervisory team: Dr Leone Bielig, Prof Dr Danny Coomans, Dr Andrew Higgins and Dr Phillip Jackson. Their contribution to this research and constant guidance has been invaluable.

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List of Acronyms

Table 1

List of acronyms used throughout the thesis

ASSSO	Algorithm for Sugarcane Selection System, Optimisation
BSES	Bureau of Sugar Experiment Station
CCS	Commercial Cane Sugar
CSIRO	Commonwealth Scientific and Industrial Research Organisation
CSR	formerly known as Colonial Sugar Refinery and today the name of a privately owned sugar research company
DP	Dynamic Programming
MANOVA	Multivariate Analysis of Variance
NMG	Net Merit Grade
OR	Operations Research
SRDC	Sugar Research and Development Corporation
SSSM	Sugarcane Selection Simulation Model
TCH	Tonnes Cane per Hectare – cane yield
TSH	Tonnes Sugar per Hectare – sugar yield

List of Symbols

Table 2

List of the symbols frequently used throughout the thesis

k	starting number of genotypes in the case of clonal selection or starting number of genotypes per family in case of family selection;
f	number of families to start selection;
b	family selection to be used in stage one $\in \{TRUE, FALSE\}$;
n	number of stages;
p_z	plot size for each stage $z = 1,2,...,n$;
s_z	number of sites (locations) for each stage $z = 1,2,...,n$;
r_z	number of replications per location for each stage $z = 1,2,...,n$;
d_z	selection index for each stage $z = 1,2,...,n$;
t_z	selection intensity for each stage $z = 1,2,...,n$;
y_{ijk}	phenotypic (observed) value of a genotype i being planted in the environment j in plot size k;
μ	grand mean of the trait observed;
g_i	genetic effect of genotype i;
v_{ij}	environmental effect of genotype i being planted in environment j
c_{ik}	competition effect of genotype i being planted in plot size k;
x_{ij}	genotype by environment interaction effect of genotype i being planted in environment j;
e_{ijk}	error effect;
σ_P^2	phenotypic variance;
σ_g^2	genetic variance (true yield);
σ_f^2	between-family genetic variance;
σ_w^2	within-family genetic variance;
σ_v^2	environmental variance;
σ_x^2	genotype by environment interaction variance;
σ_c^2	competition variance;
σ_τ^2	genotype by competition interaction variance;
σ_e^2	error variance;
σ_A^2	additive genetic variance (breeding value);
σ_D^2	dominance part of the non-additive genetic variance;
σ_I^2	epistasis part of the non-additive genetic variance;
$\text{cov}(g, v)$	covariance between genotype and environment;
$\text{cov}(g, c)$	covariance between genotype and competition;
H^2	broad sense heritability of a trait;

h^2	narrow sense heritability of a trait;
R	response to selection;
S	selection differential;
δ	proportion of the genetic variability attributable to the between families;
$\rho_{g,g+c}$	genetic correlation between a plot size and pure stand;
$\rho_{g,c}$	genetic correlation between genotype and competition;
$\rho_{CCS,TCH}$	phenotypic correlation between CCS and cane yield (TCH);
E_i	economic value of genotype i;
R_i	return from sugar produced when growing genotype i commercially;
C_i	costs associated with growing genotype i commercially;
G_i	genetic effect for economic value of genotype i;
$\overline{G}$	mean genetic effect for economic value of a population;
$\widetilde{G}$	genetic gain for economic value;
$\widetilde{G}_o$	the highest genetic gain for economic value given all optimisation constraints;
$\widetilde{G}_z$	the highest genetic gain for economic value obtained through stages $1,2,3,...,z$;
U_{z,P_0}	upper bound for selection stage z given the starting population of genotypes P_0;
A_z	alternative combination of parameters to be used at stage z;
$\overline{B}$	budget available to perform selection system;
C_z	cost of stage z;
$\overline{C}_z$	cost of stages $1,2,3,...,z$;
N	the total number of nodes to be branched;
$\widehat{M}_z$	planting material required to plant stage z;
$\breve{M}_z$	planting material available for stage z;
P_z	population of genotypes selected through stages $1,2,3,...,z$;

Statement of Sources

Declaration

I declare that this thesis is my own work and has not been submitted in any form for another degree or diploma at any university or other institution of tertiary education. Information derived from the published or unpublished work of others has been acknowledged in the text and a list of references is given.

16-08-2005

Vanja Calija-Zoppolato

Date

Publications Arising From the Thesis

Referred International Journal Publications

V. Calija, A.J. Higgins, P.A. Jackson, L.M. Bielig, and D. Coomans, An Operations Research Approach to the Problem of the Sugarcane Selection, Annals of Operations Research 108 (2001) 123-142.

Refereed Conference Papers

V. Calija, P. Jackson, A.J. Higgins, L. Bielig, and D. Coomans, Simulating and optimising sugarcane selection In: *Proceedings of the 15th National Conference of the Australian Society of Operations Research Inc. ASOR Queensland Branch and ORSJ Hokkaido Chapter Joint Workshop on Operations research from theory to real life: Contributed papers,* Ed. E. Kozan, School of Mathematical Sciences, Queensland University of Technology, Brisbane Vol. I (1999) 260-268

V. Calija, P. Jackson, A. Higgins and L. Bielig, Simulating and optimising selection systems, 11th Australian Plant Breeding Conference, Adelaide, SA, April 19-23, 1999