

**Universidade de São Paulo  
Escola Superior de Agricultura “Luiz de Queiroz”**

**Mapeamento de QTLs e estudo da interação entre QTLs, ambientes e cortes em  
cana-de-açúcar, usando a abordagem de modelos mistos**

**Maria Marta Pastina**

Tese apresentada para obtenção do título de Doutor  
em Ciências. Área de concentração: Genética e  
Melhoramento de Plantas

**Piracicaba  
2010**

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Engenheira Agrônoma**

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sem eles não chegaria tão longe. . .

**Dedico.**

“The best of all things is to learn.

Money can be lost or stolen, health and strength may fail but what you have committed to your mind is yours forever.”

**Louis L'Amour** (22/03/1908 - 10/07/1988)

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## SUMMARY

RESUMO . . . . .	9
ABSTRACT . . . . .	11
1 INTRODUCTION . . . . .	13
2 REVIEW . . . . .	15
2.1 General Aspects of Sugarcane . . . . .	15
2.2 Genetic Mapping . . . . .	17
2.2.1 Molecular Markers and Linkage Maps . . . . .	17
2.2.2 QTL Mapping . . . . .	22
2.2.2.1 Statistical Models . . . . .	23
2.2.2.2 QTL Mapping in Sugarcane . . . . .	26
2.3 Mixed Models . . . . .	30
2.3.1 Mixed Models for Multi-Environment Trials . . . . .	33
2.3.2 Mixed Models and QTL Mapping . . . . .	38
3 MATERIAL AND METHODS . . . . .	41
3.1 Material . . . . .	41
3.1.1 Plant Material . . . . .	41
3.1.2 Molecular Data . . . . .	41
3.1.3 Phenotypic Data . . . . .	41
3.2 Methods . . . . .	42
3.2.1 Linkage Map . . . . .	42
3.2.2 Genetic Predictors . . . . .	43
3.2.3 Multi-Harvest-Location Phenotypic Analysis . . . . .	45
3.2.4 QTL Analysis . . . . .	46
4 RESULTS . . . . .	49
4.1 Linkage Map . . . . .	49
4.2 Multi-Harvest-Location Phenotypic Analysis . . . . .	49
4.3 QTL Analysis . . . . .	51
5 DISCUSSION . . . . .	61
6 CONCLUSION . . . . .	65



REFERENCES . . . . . 67

## RESUMO

### **Mapeamento de QTLs e estudo da interação entre QTLs, ambientes e cortes em cana-de-açúcar, usando a abordagem de modelos mistos**

Os programas de melhoramento da cana-de-açúcar demandam aproximadamente 12 anos para a obtenção de um novo cultivar. Assim, os marcadores moleculares podem ser usados como uma ferramenta valiosa, uma vez que possibilitam o estudo da arquitetura genética de caracteres quantitativos, ajudando a reduzir este tempo. Embora a cana-de-açúcar seja uma cultura perene, para a qual o desempenho genotípico é avaliado através de ensaios estabelecidos ao longo de diferentes locais e cortes, a maior parte dos estudos de mapeamento de QTLs ignora a existência de interação entre QTLs, corte e local ( $QTL \times H \times L$ ). Neste contexto, o presente trabalho apresenta uma estratégia que foi desenvolvida para a detecção de QTLs em cana-de-açúcar, com base em modelos mistos e mapeamento por intervalo, considerando diferentes estruturas de (co)variância que permitem supor heterogeneidade de variâncias genéticas e existência de correlações genéticas entre cortes e locais. A metodologia de modelos mistos foi aplicada aos dados de uma população segregante obtida a partir do cruzamento entre dois cultivares pré-comerciais de cana-de-açúcar, constituída por 100 indivíduos avaliados em dois locais (Piracicaba e Jaú, SP, Brasil) e em três cortes para produção (toneladas de cana por hectare, TCH), produção de açúcar (toneladas de Pol por hectare, TPH), porcentagem de fibra e Pol (teor de sacarose). A análise fenotípica resultou na seleção do modelo não-estruturado, que assume heterogeneidade de variâncias e existência de correlação genética específica para cada combinação de corte e local, para todos os caracteres avaliados. Na análise de mapeamento, foram detectados 50 QTLs, incluindo 14 QTLs para TCH, 15 para TSH, 10 para Pol e 11 para Fibra. Além disso, os resultados mostram que os efeitos das interações entre QTL e corte ( $QTL \times H$ ), QTL e local ( $QTL \times L$ ) e QTL, corte e local ( $QTL \times H \times L$ ) foram importantes para todos os caracteres avaliados. Do total de QTLs identificados, 33 (66 %) apresentaram algum tipo de interação e apenas 17 (34 %) mostraram mesmo efeito entre as diferentes combinações de corte e local. Estes resultados fornecem informações importantes para o entendimento da base genética de caracteres quantitativos relacionados com produção e teor de sacarose em cana-de-açúcar.

Palavras-chave: Poliplóides; Progenie de irmãos completos; Mapa genético integrado; Análise multiponto; Mapeamento por intervalo;  $QTL \times E$



## ABSTRACT

**A mixed-model QTL analysis for sugarcane multiple-harvest-location trial data**

Sugarcane breeding programs take at least twelve years to develop new commercial cultivars. Thus, molecular markers can be used as a valuable tool since they offer the possibility to study the genetic architecture of quantitative traits, helping to reduce this time. Although the performance of genotypes in sugarcane breeding programs has been evaluated across a range of locations and harvest years, since sugarcane is a perennial crop, many of the QTL detection methods ignore QTL by harvest by location interaction ( $QTL \times H \times L$ ). In this work, a strategy for QTL detection in sugarcane was developed, based on mixed models and interval mapping, considering different (co)variance structures for the modeling of heterogeneous genetic variances and genetic correlations between harvests and locations. The mixed model approach was applied to a data set provided by a segregating population developed from a cross between two pre-commercial Brazilian cultivars, consisted of 100 individuals planted in two locations in 2003 (Piracicaba and Jaú, SP, Brazil) and evaluated in the first, second and third subsequent harvest years for cane yield (tonnes of cane per hectare, TCH), sugar yield (tonnes of sugar per hectare, TSH), fiber percent and Pol (sucrose content). Phenotypic analysis provided the selection of the unstructured model, which allows the assumption of heterogeneity of variance and presence of a specific genetic correlation for each combination of harvest and location. In the QTL mapping procedure, 50 QTLs were detected, including 14 QTLs for TCH, 15 for TSH, 10 for Pol and 11 for Fiber. In addition, the results show that QTL by harvest ( $QTL \times H$ ), QTL by location ( $QTL \times L$ ) and QTL by harvest by location ( $QTL \times H \times L$ ) interaction effects were important for all evaluated traits. From the total of QTLs identified, 33 (66%) had some interaction and only 17 (34%) showed stable effects across the different combinations of harvest and location. These results can provide useful information to understand the genetic control of complex traits related with sugarcane production and sucrose content.

Keywords: Polyploids; Full-sib progeny; Integrated linkage map; Multipoint analysis; Interval mapping;  $QTL \times E$

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