Genetic Architecture of Quantitative Traits in Sugarcane

Antonio Augusto Franco Garcia
aafgarci@esalq.usp.br

Department of Genetics,
"Luiz de Queiroz" College of Agriculture
University of São Paulo

Workshop BIOEN on Sugarcane Improvement
March/19th/2009

Outline

Outline

Outline

Outline

Modern Sugarcane Cultivars

Complex aneuploid and polyploid genome

- $2n = 100 - 130$ (aneuploids)
- Interespecific crosses: *S. officinarum* (domesticated) and *S. spontaneum* (wild species)
- 80% *S. officinarum*, 10% *S. spontaneum*, 10% recombinants

Modern Sugarcane Cultivars

Complex aneuploid and polyploid genome

- $2n = 100 - 130$ (aneuploids)
- Interespecific crosses: *S. officinarum* (domesticated) and *S. spontaneum* (wild species)
- 80% *S. officinarum*, 10% *S. spontaneum*, 10% recombinants

Modern Sugarcane Cultivars

Complex aneuploid and polyploid genome

- $2n = 100 - 130$ (aneuploids)
- Interespecific crosses: *S. officinarum* (domesticated) and *S. spontaneum* (wild species)
- 80% *S. officinarum*, 10% *S. spontaneum*, 10% recombinants

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Sugarcane Breeding

Principles

- Crosses (polycrosses) between genotypes (commercial cultivars)
- Selection for identification of the superior ones
- Plant breeding is efficient
- 10 to 15 years

Limitations

- 10 to 15 years - long time
- Small gains for sugar content
- Genetic vulnerability
- Yield plateau

Quantitative Trait Loci (QTL)

Genetic Architecture

- Estimate number, positions, genetic effects and interaction (epistasis, QTL $\times$ E) of QTL
- Usefull information for genetics, plant breeding and marker assisted selection

Some results

- Cloning QTL (tomato, others)
- MAS for disease resistance in tobacco
- Genetic basis of heterosis in maize (dominance) and rice ($a \times a$ epistasis)
- Correlation (linkage or pleiotropy); stable QTL

Quantitative Trait Loci (QTL)

Genetic Architecture

- Estimate number, positions, genetic effects and interaction (epistasis, QTL $\times$ E) of QTL
- Usefull information for genetics, plant breeding and marker assisted selection

Some results

- Cloning QTL (tomato, others)
- MAS for disease resistance in tobacco
- Genetic basis of heterosis in maize (dominance) and rice ($a \times a$ epistasis)
- Correlation (linkage or pleiotropy); stable QTL

Quantitative Trait Loci (QTL)

Genetic Architecture

- Estimate number, positions, genetic effects and interaction (epistasis, QTL $\times$ E) of QTL
- Usefull information for genetics, plant breeding and marker assisted selection

Some results

- Cloning QTL (tomato, others)
- MAS for disease resistance in tobacco
- Genetic basis of heterosis in maize (dominance) and rice ($a \times a$ epistasis)
- Correlation (linkage or pleiotropy); stable QTL

Quantitative Trait Loci (QTL)

Genetic Architecture

- Estimate number, positions, genetic effects and interaction (epistasis, QTL $\times$ E) of QTL
- Usefull information for genetics, plant breeding and marker assisted selection

Some results

- Cloning QTL (tomato, others)
- MAS for disease resistance in tobacco
- Genetic basis of heterosis in maize (dominance) and rice ($a \times a$ epistasis)
- Correlation (linkage or pleiotropy); stable QTL

Quantitative Trait Loci (QTL)

Genetic Architecture

- Estimate number, positions, genetic effects and interaction (epistasis, QTL $\times$ E) of QTL
- Usefull information for genetics, plant breeding and marker assisted selection

Some results

- Cloning QTL (tomato, others)
- MAS for disease resistance in tobacco
- Genetic basis of heterosis in maize (dominance) and rice ($a \times a$ epistasis)
- Correlation (linkage or pleiotropy); stable QTL

Quantitative Trait Loci (QTL)

Genetic Architecture

- Estimate number, positions, genetic effects and interaction (epistasis, QTL $\times$ E) of QTL
- Usefull information for genetics, plant breeding and marker assisted selection

Some results

- Cloning QTL (tomato, others)
- MAS for disease resistance in tobacco
- Genetic basis of heterosis in maize (dominance) and rice ($a \times a$ epistasis)
- Correlation (linkage or pleiotropy); stable QTL

What is needed?

Genotype Molecular markers, good linkage maps

Phenotype Experimental design, statistical analysis

Statistical Genetics Models to associate genotype and phenotype

What is needed?

Genotype Molecular markers, good linkage maps

Phenotype Experimental design, statistical analysis

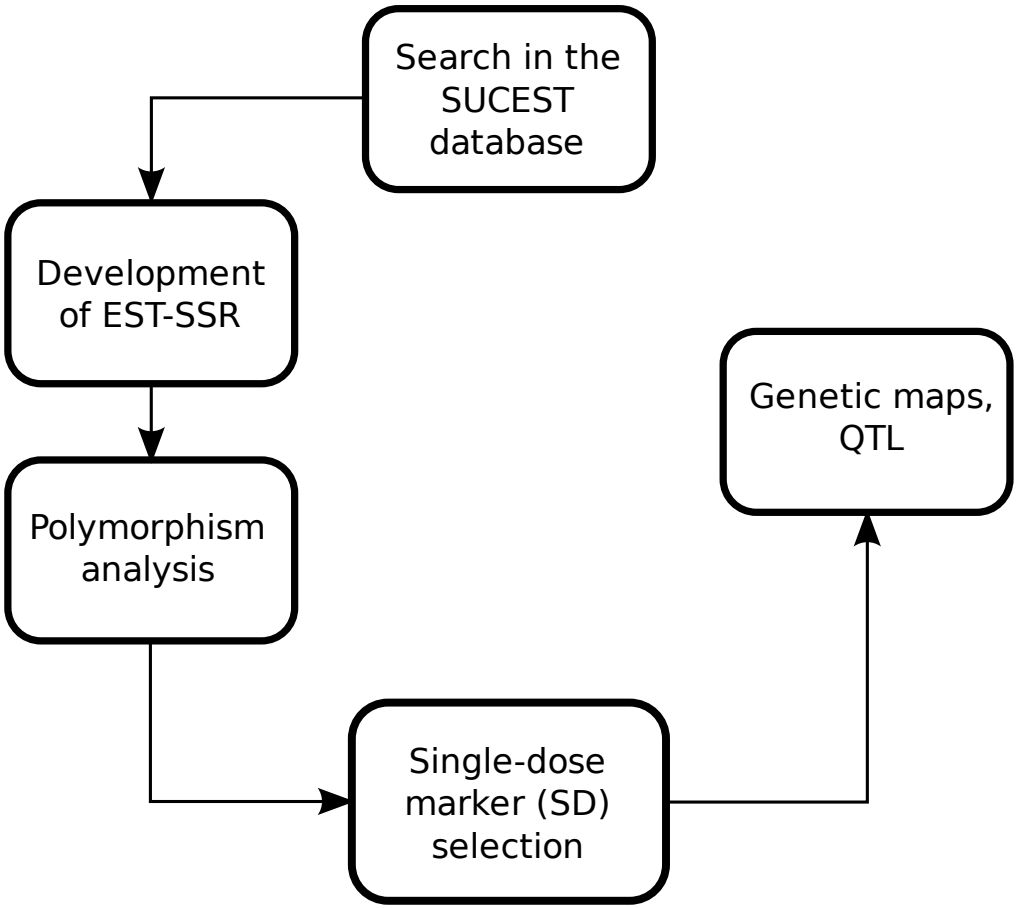
Statistical Genetics Models to associate genotype and phenotype

What is needed?

Genotype	Molecular markers, good linkage maps
Phenotype	Experimental design, statistical analysis
Statistical Genetics	Models to associate genotype and phenotype

DR. ANETE P. SOUZA, UNICAMP

STRATEGY



POLYPLOIDS AND SINGLE-DOSE MARKERS

- $AA- \times Aa-$ (D_1 type) or $Aa \times AA$ (D_2 type)
- It is "impossible" to test linkage between D_1 and D_2
- Pseudo-testcross strategy (1:1 segregation pattern)
- Need to estimate linkage phases
- Two subsets
- Two linkage maps; MAPMAKER/EXP
- Biological and statistical limitations

POLYPLOIDS AND SINGLE-DOSE MARKERS

- $AA- \times Aa-$ (D_1 type) or $Aa \times AA$ (D_2 type)
- It is "impossible" to test linkage between D_1 and D_2
- Pseudo-testcross strategy (1:1 segregation pattern)
- Need to estimate linkage phases
- Two subsets
- Two linkage maps; MAPMAKER/EXP
- Biological and statistical limitations

POLYPLOIDS AND SINGLE-DOSE MARKERS

- $AA- \times Aa-$ (D_1 type) or $Aa \times AA$ (D_2 type)
- It is "impossible" to test linkage between D_1 and D_2
- Pseudo-testcross strategy (1:1 segregation pattern)
- Need to estimate linkage phases
- Two subsets
- Two linkage maps; MAPMAKER/EXP
- Biological and statistical limitations

POLYPLOIDS AND SINGLE-DOSE MARKERS

- $AA- \times Aa-$ (D_1 type) or $Aa \times AA$ (D_2 type)
- It is "impossible" to test linkage between D_1 and D_2
- Pseudo-testcross strategy (1:1 segregation pattern)
- Need to estimate linkage phases
- Two subsets
- Two linkage maps; MAPMAKER/EXP
- Biological and statistical limitations

POLYPLOIDS AND SINGLE-DOSE MARKERS

- $AA- \times Aa-$ (D_1 type) or $Aa \times AA$ (D_2 type)
- It is "impossible" to test linkage between D_1 and D_2
- Pseudo-testcross strategy (1:1 segregation pattern)
- Need to estimate linkage phases
- Two subsets
- Two linkage maps; MAPMAKER/EXP
- Biological and statistical limitations

POLYPLOIDS AND SINGLE-DOSE MARKERS

- $AA- \times Aa-$ (D_1 type) or $Aa \times AA$ (D_2 type)
- It is "impossible" to test linkage between D_1 and D_2
- Pseudo-testcross strategy (1:1 segregation pattern)
- Need to estimate linkage phases
- Two subsets
- Two linkage maps; MAPMAKER/EXP
- Biological and statistical limitations

POLYPLOIDS AND SINGLE-DOSE MARKERS

- $AA- \times Aa-$ (D_1 type) or $Aa \times AA$ (D_2 type)
- It is "impossible" to test linkage between D_1 and D_2
- Pseudo-testcross strategy (1:1 segregation pattern)
- Need to estimate linkage phases
- Two subsets
- Two linkage maps; MAPMAKER/EXP
- Biological and statistical limitations

SINGLE-DOSE MARKERS IN BOTH PARENTS

- 1:1 and 3:1
- It is possible to integrate the maps
- Software designed for outcrossing (diploids) species (e.g. JoinMap)
- Not good results for our data

SINGLE-DOSE MARKERS IN BOTH PARENTS

- 1:1 and 3:1
- It is possible to integrate the maps
- Software designed for outcrossing (diploids) species (e.g. JoinMap)
- Not good results for our data

SINGLE-DOSE MARKERS IN BOTH PARENTS

- 1:1 and 3:1
- It is possible to integrate the maps
- Software designed for outcrossing (diploids) species (e.g. JoinMap)
- Not good results for our data

SINGLE-DOSE MARKERS IN BOTH PARENTS

- 1:1 and 3:1
- It is possible to integrate the maps
- Software designed for outcrossing (diploids) species (e.g. JoinMap)
- Not good results for our data

INTEGRATED MAP

- Likelihood-based approach

Wu, R.; C-X. Ma; I. Painter; Z.-B. Zeng, 2002
Simultaneous Maximum Likelihood Estimation of Linkage and Linkage Phases in Outcrossing Species.
Theor. Pop. Biology 61: 349-363

SP80-180 × SP80-4966

- 1118 markers (RFLP, SSR and AFLP)

	Linkage groups	Mapped markers	Map length (cM)
JoinMap	98	217	1340
Likelihood	131	357	2602

INTEGRATED MAP

- Likelihood-based approach

Wu, R.; C-X. Ma; I. Painter; Z.-B. Zeng, 2002
Simultaneous Maximum Likelihood Estimation of Linkage and Linkage Phases in Outcrossing Species.
Theor. Pop. Biology 61: 349-363

SP80-180 × SP80-4966

- 1118 markers (RFLP, SSR and AFLP)

	Linkage groups	Mapped markers	Map length (cM)
JoinMap	98	217	1340
Likelihood	131	357	2602

SOME RESULTS

RFLP, AFLP, SSR

Theor Appl Genet (2006) 112: 298–314
DOI 10.1007/s00122-005-0129-6

ORIGINAL PAPER

A. A. F. Garcia · E. A. Kido · A. N. Meza
H. M. B. Souza · L. R. Pinto · M. M. Pastina
C. S. Leite · J. A. G. da Silva · E. C. Ulian
A. Figueira · A. P. Souza

Development of an integrated genetic map of a sugarcane (*Saccharum* spp.) commercial cross, based on a maximum-likelihood approach for estimation of linkage and linkage phases

EST-SSR

Mol Breeding (2007) 20:189–208
DOI 10.1007/s11032-007-9082-1

Functional integrated genetic linkage map based on EST-markers for a sugarcane (*Saccharum* spp.) commercial cross

Karine M. Oliveira · Luciana R. Pinto · Thiago G. Marconi · Gabriel R. A. Margarido ·
Maria Marta Pastina · Laura Helena M. Teixeira · Antônio V. Figueira ·
Eugênio César Ulian · Antônio Augusto F. Garcia · Anete Pereira Souza

SOME RESULTS

SOFTWARE

Hereditas 144: 78–79 (2007)

OneMap: software for genetic mapping in outcrossing species

G. R. A. MARGARIDO[1], A. P. SOUZA[2] and A. A. F. GARCIA[1]

[1]*Department of Genetics, Escola Superior de Agricultura "Luiz de Queiroz", Universidade de São Paulo (USP), Piracicaba, São Paulo, Brazil*
[2]*Centro de Biologia Molecular e Engenharia Genética (CBMEG), Universidade Estadual de Campinas (UNICAMP), Campinas, São Paulo, Brazil*

OneMap

We need to go further

1. Maps can be integrated (with a number of 3:1)
2. Wu's et al. approach is based on pairwise (two-point) comparisons
3. We could do better if using multipoint estimates
4. Also, other segregation types must be included

OneMap

We need to go further

1. Maps can be integrated (with a number of 3:1)
2. Wu's et al. approach is based on pairwise (two-point) comparisons
3. We could do better if using multipoint estimates
4. Also, other segregation types must be included

OneMap

We need to go further

1. Maps can be integrated (with a number of 3:1)
2. Wu's et al. approach is based on pairwise (two-point) comparisons
3. We could do better if using multipoint estimates
4. Also, other segregation types must be included

OneMap

We need to go further

1. Maps can be integrated (with a number of 3:1)
2. Wu's et al. approach is based on pairwise (two-point) comparisons
3. We could do better if using multipoint estimates
4. Also, other segregation types must be included

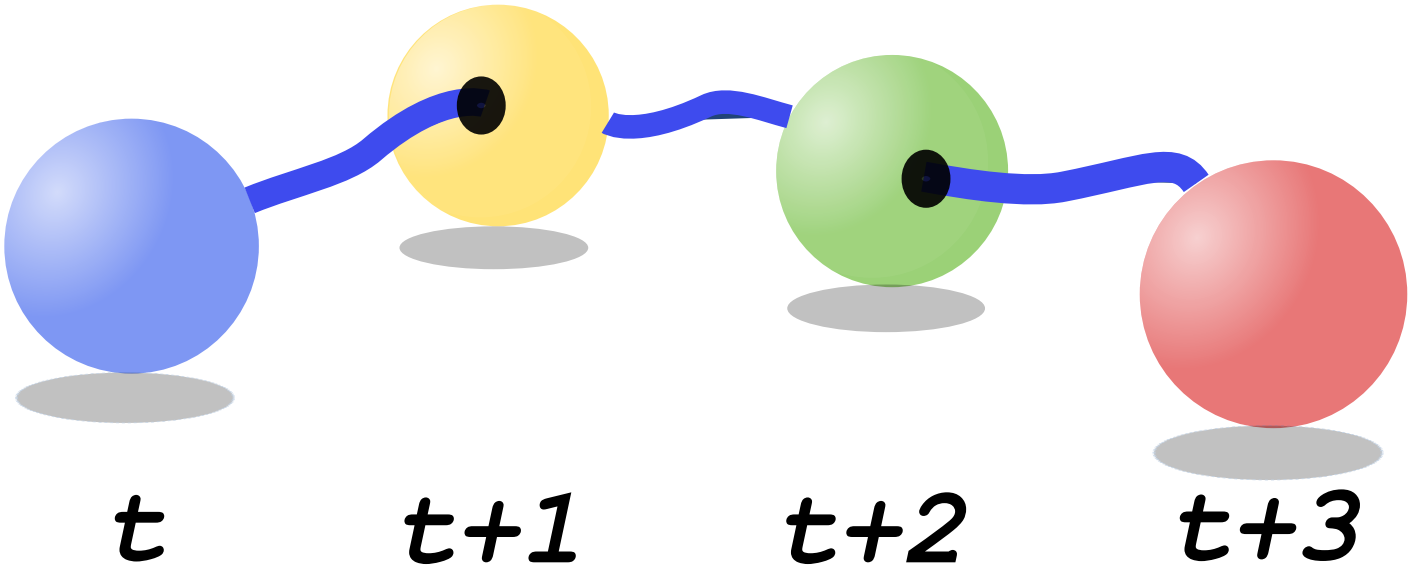
MULTIPOINT APPROACH

Lander, E.S.; Green, P., 1987
Construction of multilocus genetic linkage maps in human
Proc. Natl. Acad. Sci. USA 84: 2363-2367

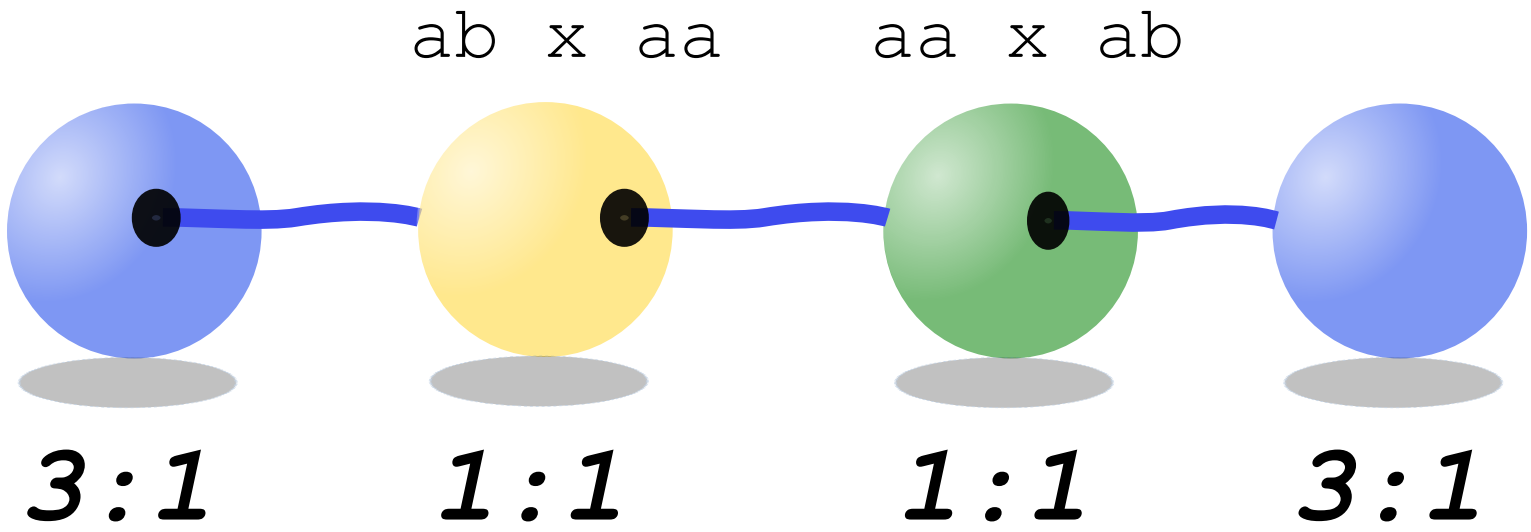
Jiang, C.; Zeng, Z.-B., 1997
Mapping quantitative trait loci with dominant and missing markers in various crosses from two inbred lines
Genetica 101: 47-58

Wu, R.; Ma, C.-X.; Wu, S. S.; Zeng, Z.-B., 2002
Linkage mapping of sex-specific differences
Genetical Research 79: 85-96

Markov Chains



Markov Chains



MULTIPOINT APPROACH

MULTIPOINT LIKELIHOOD

$$L = \prod_{j=1}^{n} \mathbf{q}' \mathbf{I}_{z_{j1}} \mathbf{H}^1_{w,r} \mathbf{I}_{z_{j2}} \mathbf{H}^2_{w,r} \mathbf{I}_{z_{j3}} \ldots \mathbf{H}^k_{w,r} \mathbf{I}_{z_{jm}} \mathbf{c}$$

ADVANTAGES

- By using all information, one can have better maps

MULTIPOINT APPROACH

MULTIPOINT LIKELIHOOD

$$L = \prod_{j=1}^{n} \mathbf{q}' \mathbf{I}_{z_{j1}} \mathbf{H}^1_{w,r} \mathbf{I}_{z_{j2}} \mathbf{H}^2_{w,r} \mathbf{I}_{z_{j3}} \ldots \mathbf{H}^k_{w,r} \mathbf{I}_{z_{jm}} \mathbf{c}$$

ADVANTAGES

- By using all information, one can have better maps

MULTIPOINT APPROACH

- Already implement in OneMap (Margarido, Mollinari, Garcia, 2009)

```
> grupo1

Printing map:

Markers                Position          Parent 1          Parent 2

AGGCAG100c                0.00          a |   | o         a |   | o
ACGCTA36c                23.61          o |   | a         o |   | a
SMC36C2                  24.46          a |   | o         a |   | o
AGGCTT89c                45.48          a |   | o         a |   | o
ACACTT87c                64.53          a |   | o         a |   | o
SG08A                    64.64          o |   | a         o |   | a
ACGCAA24c                93.93          o |   | a         o |   | a
ACGCTA15a               106.58          o |   | a         o |   | o
AACCAC16a               115.13          o |   | a         o |   | o
AGCCAG39c               127.15          o |   | a         o |   | a
ESTA10m2D1              154.29          o |   | a         o |   | o
ESTB40m2C               155.59          o |   | a         o |   | a
ESTB99m2D1              155.59          o |   | a         o |   | o
ESTB56m4D1              162.64          o |   | a         o |   | o
ESTC39m4D1              165.74          o |   | a         o |   | o

log-likelihood: -585.4868

>
-u:**  *R*          Bot L29717   (iESS [R]: run)----------------------------------
```

ONEMAP

- Open source; R facilities

CRAN
Mirrors
What's new?
Task Views
Search

About R
R Homepage

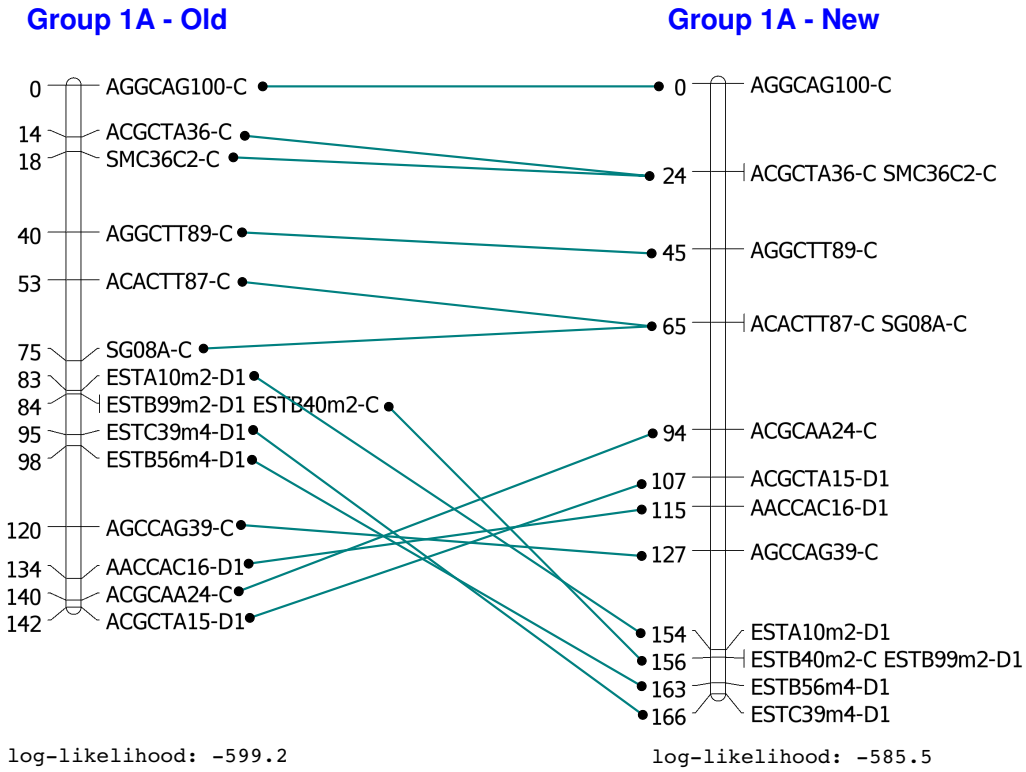
Software
R Sources
R Binaries
Packages
Other

ORMDR	ORMDR
Oarray	Arrays with arbitrary offsets
obsSens	Sensitivity analysis for Observational studies
oc	OC Roll Call Analysis Software
oce	Analysis of Oceanographic data
odesolve	Solvers for Ordinary Differential Equations
odfWeave	Sweave processing of Open Document Format (ODF) files
ofw	Optimal Feature Weighting algorithm
onemap	**Software for constructing genetic maps in outcrossing species**
openNLP	openNLP Interface
openNLPmodels	(English and Spanish) openNLP models
optmatch	Functions for optimal matching
orientlib	Support for orientation data
orloca	The package deals with Operations Research LOCational Analysis models
orth	Multivariate Logistic Regressions Using Orthogonalized Residuals

MULTIPOINT APPROACH

OLIVEIRA *et al.* 2007

- Likelihood 13.7 times greater



MULTIPOINT APPROACH

WE NEED TO GO FURTHER

1. Still not using all data available
2. Diploids, not polyploids
3. For sugarcane, we need to include other segregation patterns
4. This could lead to more saturated maps
5. Data from SNP's

MULTIPOINT APPROACH

WE NEED TO GO FURTHER

1. Still not using all data available
2. Diploids, not polyploids
3. For sugarcane, we need to include other segregation patterns
4. This could lead to more saturated maps
5. Data from SNP's

MULTIPOINT APPROACH

WE NEED TO GO FURTHER

1. Still not using all data available
2. Diploids, not polyploids
3. For sugarcane, we need to include other segregation patterns
4. This could lead to more saturated maps
5. Data from SNP's

MULTIPOINT APPROACH

WE NEED TO GO FURTHER

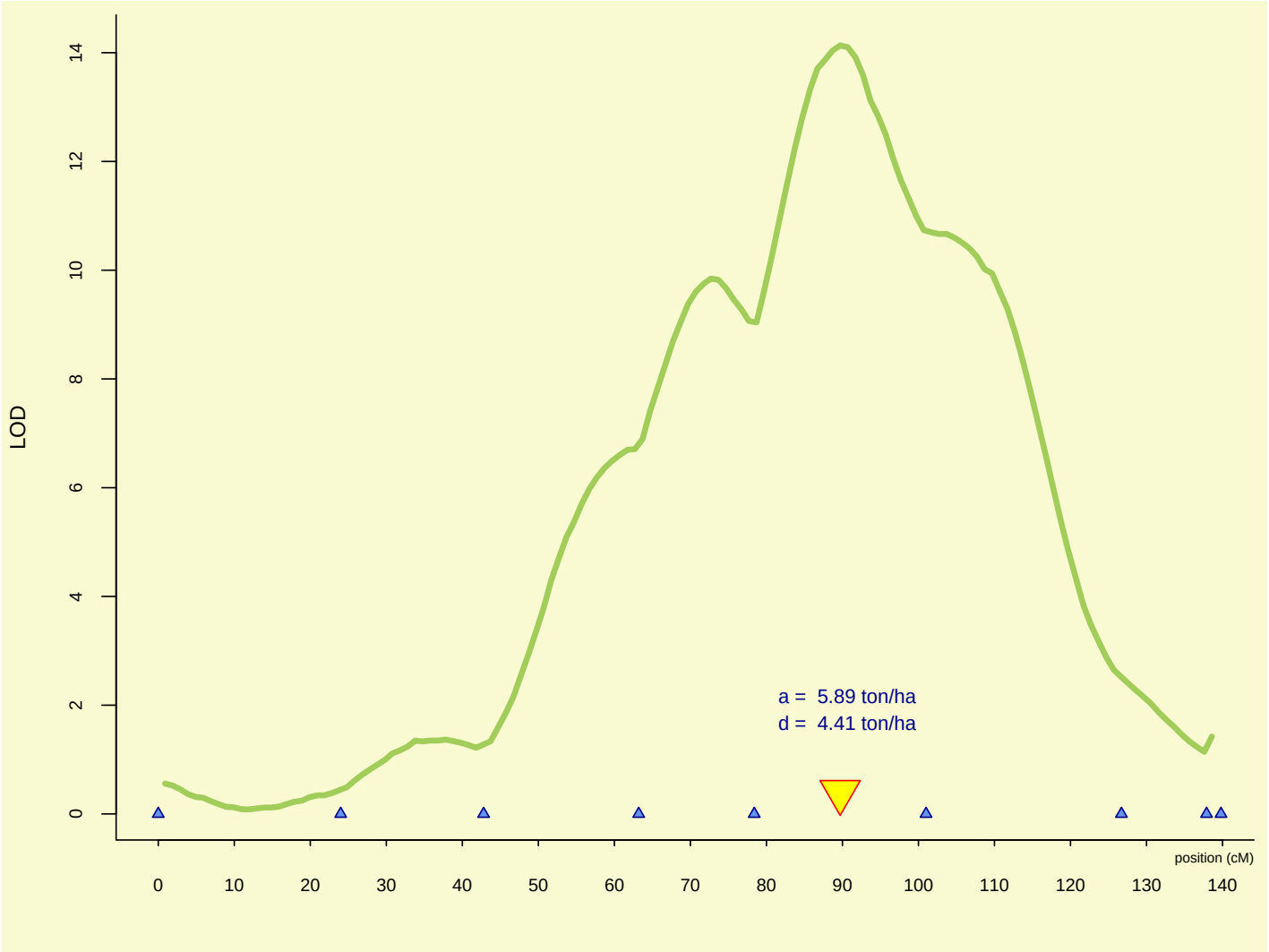
1. Still not using all data available
2. Diploids, not polyploids
3. For sugarcane, we need to include other segregation patterns
4. This could lead to more saturated maps
5. Data from SNP's

MULTIPOINT APPROACH

WE NEED TO GO FURTHER

1. Still not using all data available
2. Diploids, not polyploids
3. For sugarcane, we need to include other segregation patterns
4. This could lead to more saturated maps
5. Data from SNP's

QTL Mapping


LOD
0
2
4
6
8
10
12
14
a = 5.89 ton/ha
d = 4.41 ton/ha
0
10
20
30
40
50
60
70
80
90
100
110
120
130
140
position (cM)

Several (complex) statistical models

- Inbred-based populations: F_2, BC, Design III, RILs ...
  - Single Marker Analysis
  - Interval Mapping
  - Composite Interval Mapping
  - Multiple Interval Mapping
  - Mixed-models
  - Bayesian approach
  - ...
- Outcrossing species
  - Adaptation of these ideas

SUGARCANE (OUTCROSSING)

APPROACH - PSEUDO TESTCROSS

- Single Marker Analysis
  - Most of the papers
- Interval Mapping
  - Few results
- Composite Interval Mapping
  - Few results

LIMITATIONS

- Low statistical power
- In backcrosses, we do not estimate additive and dominance effects, but only a linear combination of them

Sugarcane (outcrossing)

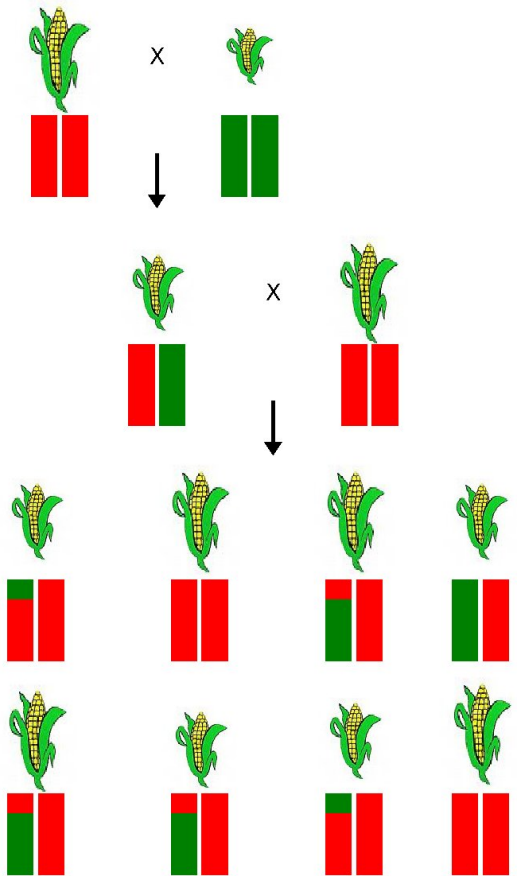
Approach - pseudo testcross

- Single Marker Analysis
  - Most of the papers
- Interval Mapping
  - Few results
- Composite Interval Mapping
  - Few results

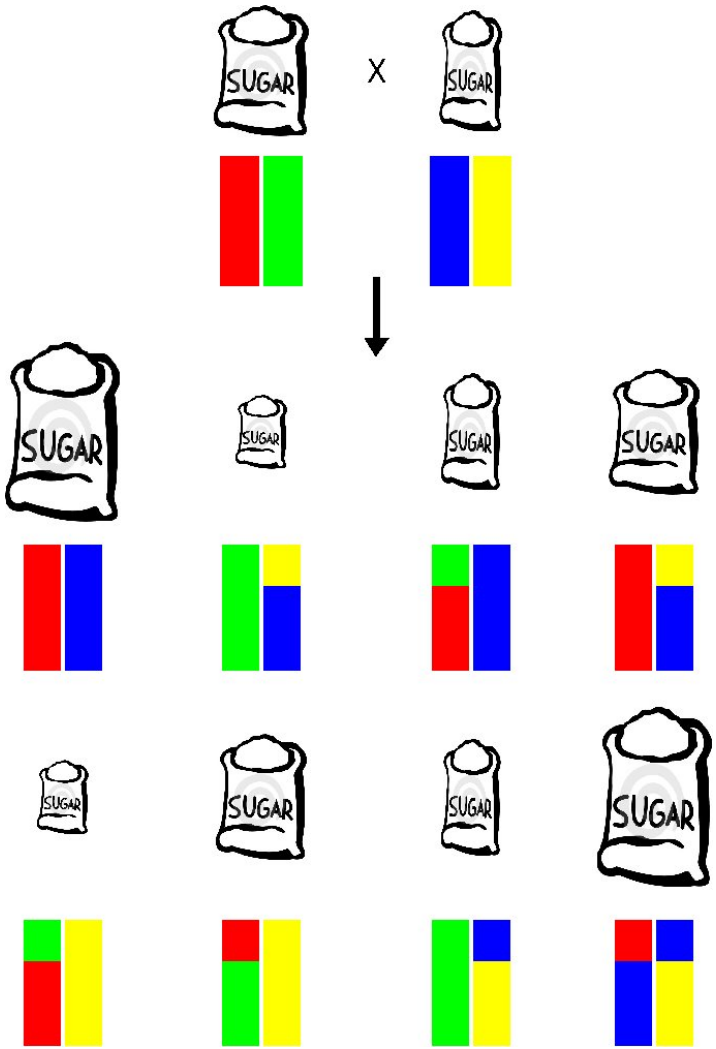
Limitations

- Low statistical power
- In backcrosses, we do not estimate additive and dominance effects, but only a linear combination of them

BACKCROSSES

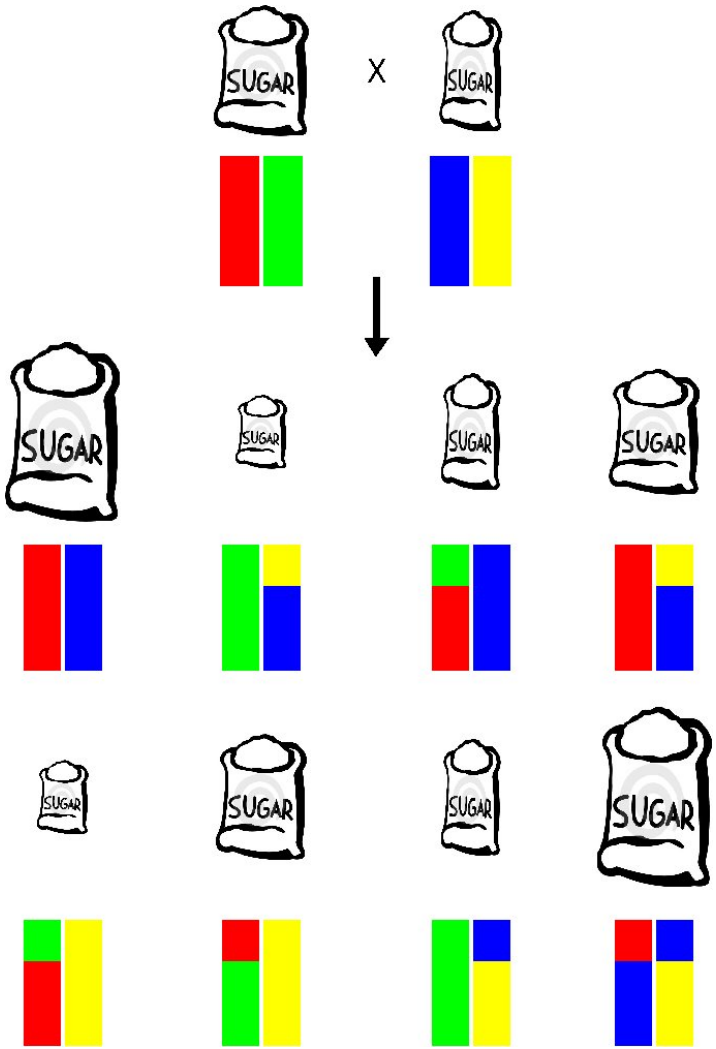


OUTCROSSING SPECIES



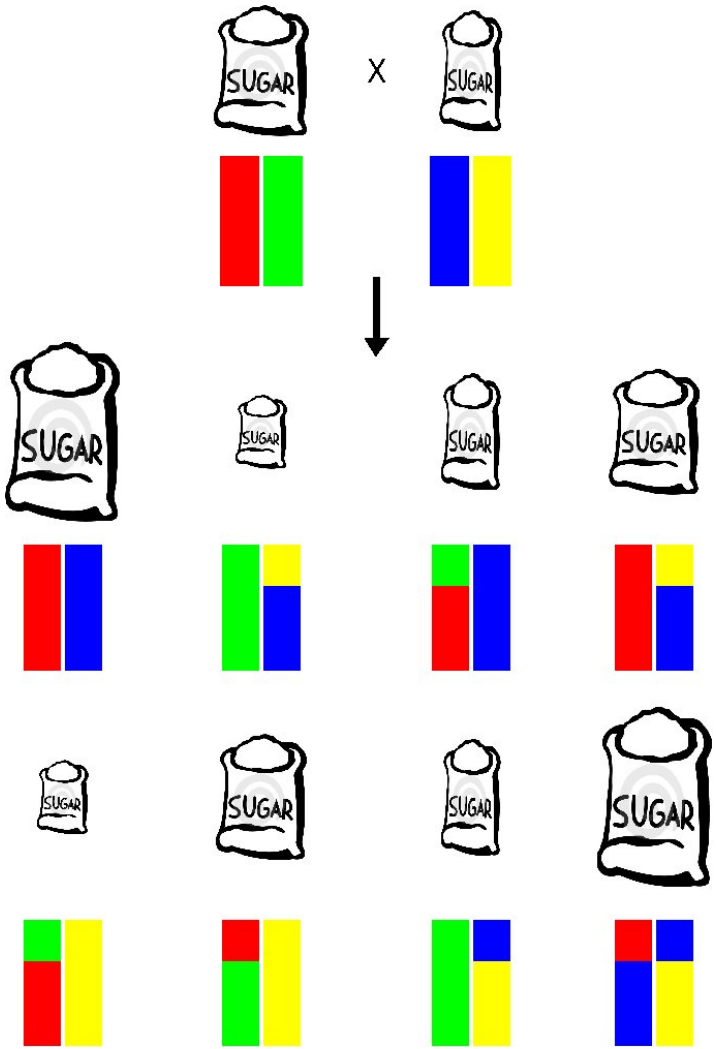
- Genetic effects?
- Red/Green?
- Blue/Yellow?
- Interactions!

OUTCROSSING SPECIES



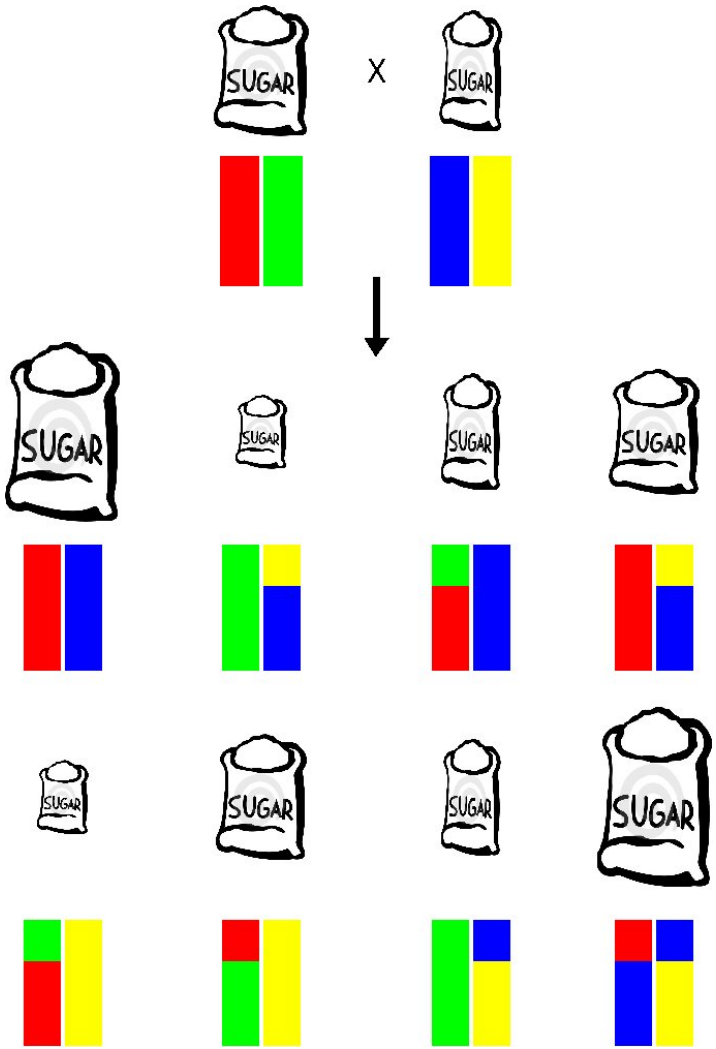
- Genetic effects?
- Red/Green?
- Blue/Yellow?
- Interactions!

OUTCROSSING SPECIES



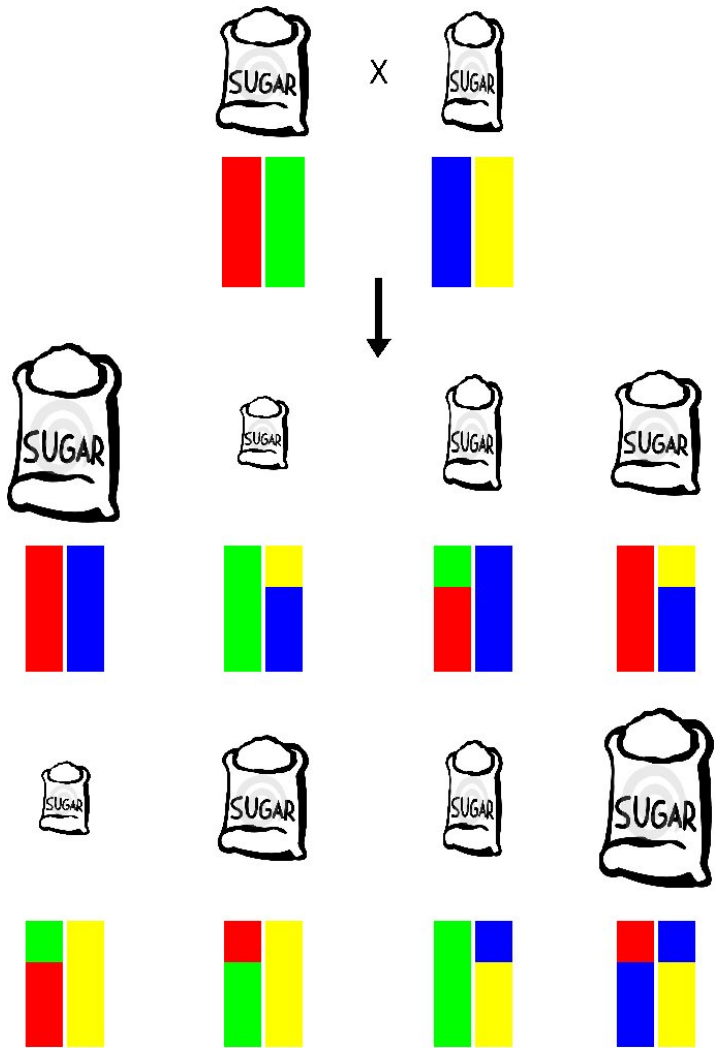
- Genetic effects?
- Red/Green?
- Blue/Yellow?
- Interactions!

OUTCROSSING SPECIES



- Genetic effects?
- Red/Green?
- Blue/Yellow?
- Interactions!

NOTATION



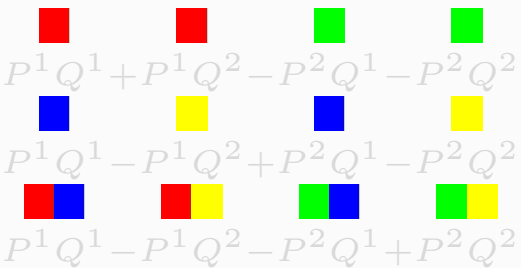
CROSS

$$\begin{array}{c|c|} & P \\ \hline M_1^k & M_2^k \\ \hline P_1 & P_2 \\ \hline M_1^{k+1} & M_2^{k+1} \\ \hline \end{array} \times \begin{array}{c|c|} & Q \\ \hline N_1^k & N_2^k \\ \hline Q_1 & Q_2 \\ \hline N_1^{k+1} & N_2^{k+1} \\ \hline \end{array}$$

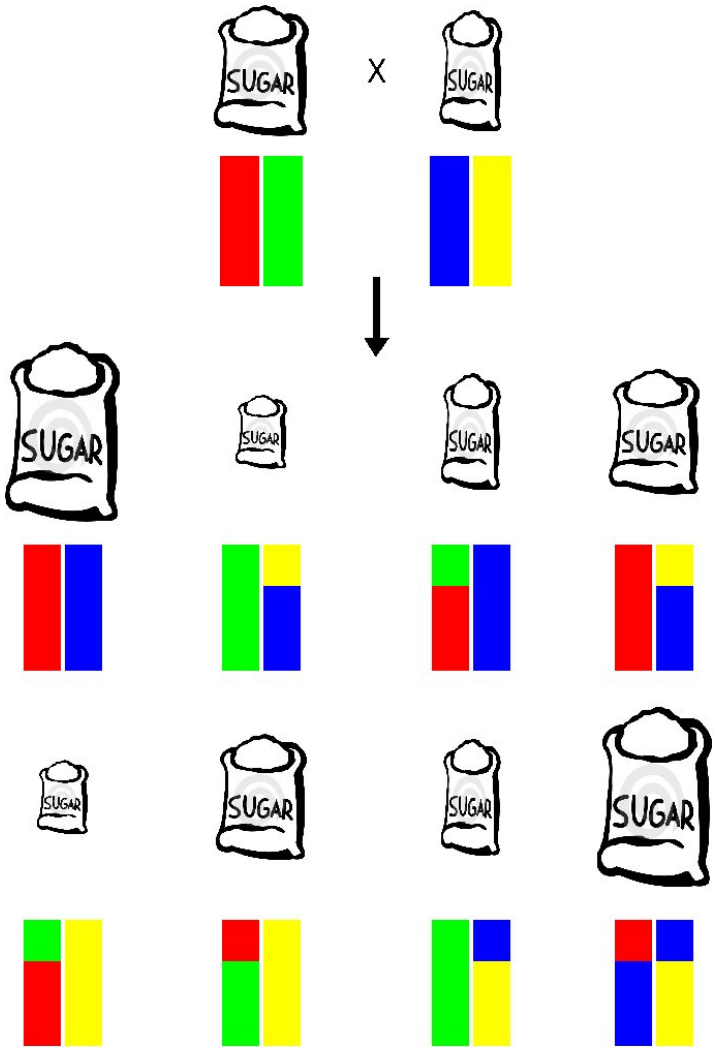
$$\downarrow$$

$$\underset{P_1Q_1}{1} : \underset{P_1Q_2}{1} : \underset{P_2Q_1}{1} : \underset{P_2Q_2}{1}$$

CONTRASTS



NOTATION



CROSS

$$\begin{array}{c|c|} & P \\ \hline M_1^k & M_2^k \\ P_1 & P_2 \\ M_1^{k+1} & M_2^{k+1} \\ \hline \end{array} \times \begin{array}{c|c|} & Q \\ \hline N_1^k & N_2^k \\ Q_1 & Q_2 \\ N_1^{k+1} & N_2^{k+1} \\ \hline \end{array}$$

$$\downarrow$$

$$\underset{P_1Q_1}{1} : \underset{P_1Q_2}{1} : \underset{P_2Q_1}{1} : \underset{P_2Q_2}{1}$$

CONTRASTS

$$P^1Q^1 + P^1Q^2 - P^2Q^1 - P^2Q^2$$

$$P^1Q^1 - P^1Q^2 + P^2Q^1 - P^2Q^2$$

$$P^1Q^1 - P^1Q^2 - P^2Q^1 + P^2Q^2$$

Composite Interval Mapping

Model

$$y_j = \boldsymbol{Z}_j\boldsymbol{\gamma} + \alpha_p^* x_{pj}^* + \alpha_q^* x_{qj}^* + \delta_{pq}^* x_{pj}^* x_{qj}^* + \epsilon_j$$

- y_j: phenotypic value;
- γ: intercept, cofactors;
- α_p: additive effect of QTL on parental P;
- α_q: additive effect of QTL on parental Q;
- δ_{pq}: intralocus interaction for additive effects (dominance);
- x_{pj}^*, x_{qj}^*, x_{pq}^*: indicator variables for QTL genotypes;
- ϵ_j: residual

Composite Interval Mapping

Likelihood, EM algorithm

$$L(\boldsymbol{\theta}, \boldsymbol{\gamma}, \sigma) = \prod_{j=1}^{n} \left[\sum_{k=1}^{2} \sum_{l=1}^{2} p_{klj} \phi \left(\frac{y_j - \mu_{klj}}{\sigma} \right) \right]$$

$$\hat{\alpha}_p^{*(t+1)} = \frac{1}{1' \Pi (D_1 \# D_1)} \left[\left(y - Z\gamma^t \right)' \Pi^t D_1 - 1' \Pi^t (D_1 \# D_2) \alpha_q^{*t} - 1' \Pi^t (D_1 \# D_3) \delta_{pq}^{*t} \right]$$

$$\hat{\alpha}_q^{*(t+1)} = \frac{1}{1' \Pi (D_2 \# D_2)} \left[\left(y - Z\gamma^t \right)' \Pi^t D_2 - 1' \Pi^t (D_2 \# D_1) \alpha_p^{*t} - 1' \Pi^t (D_2 \# D_3) \delta_{pq}^{*t} \right]$$

$$\hat{\delta}_{pq}^{*(t+1)} = \frac{1}{1' \Pi (D_3 \# D_3)} \left[\left(y - Z\gamma^t \right)' \Pi^t D_3 - 1' \Pi^t (D_3 \# D_1) \alpha_p^{*t} - 1' \Pi^t (D_3 \# D_2) \alpha_q^{*t} \right]$$

$$\hat{\gamma}^{(t+1)} = \left(Z' Z \right)^{-1} Z' \left(y - \Pi^t D \theta^{(t+1)} \right)$$

$$\hat{\sigma}^{2(t+1)} = (1/n) \left[\left(y - Z\gamma^{(t+1)} \right)' \left(y - Z\gamma^{(t+1)} \right) - 2 \left(y - Z\gamma^{(t+1)} \right)' \Pi^t D \theta^{(t+1)} + \theta'^{(t+1)} V^t \theta^{(t+1)} \right]$$

COMPOSITE INTERVAL MAPPING

LIKELIHOOD, EM ALGORITHM

$$L(\boldsymbol{\theta}, \boldsymbol{\gamma}, \sigma) = \prod_{j=1}^{n} \left[\sum_{k=1}^{2} \sum_{l=1}^{2} p_{klj} \phi \left(\frac{y_j - \mu_{klj}}{\sigma} \right) \right]$$

$$\hat{\alpha}_p^{*(t+1)} = \frac{1}{\mathbf{1}' \boldsymbol{\Pi} (\boldsymbol{D}_1 \# \boldsymbol{D}_1)} \left[\left(\boldsymbol{y} - \boldsymbol{Z} \boldsymbol{\gamma}^t \right)' \boldsymbol{\Pi}^t \boldsymbol{D}_1 - \mathbf{1}' \boldsymbol{\Pi}^t (\boldsymbol{D}_1 \# \boldsymbol{D}_2) \alpha_q^{*t} - \mathbf{1}' \boldsymbol{\Pi}^t (\boldsymbol{D}_1 \# \boldsymbol{D}_3) \delta_{pq}^{*t} \right]$$

$$\hat{\alpha}_q^{*(t+1)} = \frac{1}{\mathbf{1}' \boldsymbol{\Pi} (\boldsymbol{D}_2 \# \boldsymbol{D}_2)} \left[\left(\boldsymbol{y} - \boldsymbol{Z} \boldsymbol{\gamma}^t \right)' \boldsymbol{\Pi}^t \boldsymbol{D}_2 - \mathbf{1}' \boldsymbol{\Pi}^t (\boldsymbol{D}_2 \# \boldsymbol{D}_1) \alpha_p^{*t} - \mathbf{1}' \boldsymbol{\Pi}^t (\boldsymbol{D}_2 \# \boldsymbol{D}_3) \delta_{pq}^{*t} \right]$$

$$\hat{\delta}_{pq}^{*(t+1)} = \frac{1}{\mathbf{1}' \boldsymbol{\Pi} (\boldsymbol{D}_3 \# \boldsymbol{D}_3)} \left[\left(\boldsymbol{y} - \boldsymbol{Z} \boldsymbol{\gamma}^t \right)' \boldsymbol{\Pi}^t \boldsymbol{D}_3 - \mathbf{1}' \boldsymbol{\Pi}^t (\boldsymbol{D}_3 \# \boldsymbol{D}_1) \alpha_p^{*t} - \mathbf{1}' \boldsymbol{\Pi}^t (\boldsymbol{D}_3 \# \boldsymbol{D}_2) \alpha_q^{*t} \right]$$

$$\hat{\boldsymbol{\gamma}}^{(t+1)} = \left(\boldsymbol{Z}' \boldsymbol{Z} \right)^{-1} \boldsymbol{Z}' \left(\boldsymbol{y} - \boldsymbol{\Pi}^t \boldsymbol{D} \boldsymbol{\theta}^{(t+1)} \right)$$

$$\hat{\sigma}^{2(t+1)} = (1/n) \left[\left(\boldsymbol{y} - \boldsymbol{Z} \boldsymbol{\gamma}^{(t+1)} \right)' \left(\boldsymbol{y} - \boldsymbol{Z} \boldsymbol{\gamma}^{(t+1)} \right) - 2 \left(\boldsymbol{y} - \boldsymbol{Z} \boldsymbol{\gamma}^{(t+1)} \right)' \boldsymbol{\Pi}^t \boldsymbol{D} \boldsymbol{\theta}^{(t+1)} + \boldsymbol{\theta}'^{(t+1)} \boldsymbol{V}^t \boldsymbol{\theta}^{(t+1)} \right]$$

Composite Interval Mapping

QTL search

$$H_0 : \alpha_p^* = \alpha_q^* = \delta_{pq}^* = 0$$

H_a : at least one different from zero

Linkage phases (signs of α_p^* and α_q^*)

$$\begin{array}{|cc|} \hline M_1^k & M_2^k \\ P_1 & P_2 \\ M_1^{k+1} & M_2^{k+1} \\ \hline \end{array} \times \begin{array}{|cc|} \hline N_1^k & N_2^k \\ Q_1 & Q_2 \\ N_1^{k+1} & N_2^{k+1} \\ \hline \end{array}$$

Segregation of QTL

- Step 1: H_{01}, H_{02} and H_{03}
- Step 2: H_{04}, H_{05} and H_{06}

Composite Interval Mapping

QTL search

$$H_0 : \alpha_p^* = \alpha_q^* = \delta_{pq}^* = 0$$

$$H_a : \text{at least one different from zero}$$

Linkage phases (signs of α_p^* and α_q^*)

$$\begin{vmatrix} M_1^k & M_2^k \\ P_1 & P_2 \\ M_1^{k+1} & M_2^{k+1} \end{vmatrix} \times \begin{vmatrix} N_1^k & N_2^k \\ Q_1 & Q_2 \\ N_1^{k+1} & N_2^{k+1} \end{vmatrix}$$

Segregation of QTL

- Step 1: H_{01}, H_{02} and H_{03}
- Step 2: H_{04}, H_{05} and H_{06}

Composite Interval Mapping

QTL search

$$H_0: \ \alpha_p^* = \alpha_q^* = \delta_{pq}^* = 0$$

$$H_a: \text{ at least one different from zero}$$

Linkage phases (signs of α_p^* and α_q^*)

$$\begin{vmatrix} M_1^k & M_2^k \\ P_1 & P_2 \\ M_1^{k+1} & M_2^{k+1} \end{vmatrix} \times \begin{vmatrix} N_1^k & N_2^k \\ Q_1 & Q_2 \\ N_1^{k+1} & N_2^{k+1} \end{vmatrix}$$

Segregation of QTL

- Step 1: H_{01}, H_{02} and H_{03}
- Step 2: H_{04}, H_{05} and H_{06}

PROCEDURE

Step 1	Step 2		Conclusion	
Rejected	Hypot. to test		Segregation	Phase
H_{01}: $\alpha_p^* = 0$	–	–	$1:1$	P^1P^2 or P^2P^1 (a)
H_{02}: $\alpha_q^* = 0$	–	–	$1:1$	Q^1Q^2 or Q^2Q^1 (b)
H_{03}: $\delta_{pq}^* = 0$	–	–	$1:1$	unknown

PROCEDURE

Step 1	Step 2		Conclusion	
Rejected	Hypot. to test		Segregation	Phase
H_{01}: $\alpha_p^* = 0$	–	–	$1:1$	P^1P^2 or P^2P^1 (a)
H_{02}: $\alpha_q^* = 0$	–	–	$1:1$	Q^1Q^2 or Q^2Q^1 (b)
H_{03}: $\delta_{pq}^* = 0$	–	–	$1:1$	unknown
H_{01} and H_{02}	H_{04}: $\alpha_p^* = \alpha_q^*$	R	$1:1:1:1$	$P^1P^2 \times Q^1Q^2$ (c)
	H_{04}: $-\alpha_p^* = -\alpha_q^*$	R	$1:1:1:1$	$P^2P^1 \times Q^2Q^1$ (d)
	H_{04}: $\alpha_p^* = -\alpha_q^*$	R	$1:1:1:1$	$P^1P^2 \times Q^2Q^1$ (e)
	H_{04}: $-\alpha_p^* = \alpha_q^*$	R	$1:1:1:1$	$P^2P^1 \times Q^1Q^2$ (f)
	H_{04}	NR	$1:2:1$	(c), (d), (e) e (f)

PROCEDURE

Step 1	Step 2		Conclusion	
Rejected	Hypot. to test		Segregation	Phase
H_{01}: $\alpha_p^* = 0$	–	–	$1:1$	P^1P^2 or P^2P^1 (a)
H_{02}: $\alpha_q^* = 0$	–	–	$1:1$	Q^1Q^2 or Q^2Q^1 (b)
H_{03}: $\delta_{pq}^* = 0$	–	–	$1:1$	unknown
H_{01} and H_{02}	H_{04}: $\alpha_p^* = \alpha_q^*$	R	$1:1:1:1$	$P^1P^2 \times Q^1Q^2$ (c)
	H_{04}: $-\alpha_p^* = -\alpha_q^*$	R	$1:1:1:1$	$P^2P^1 \times Q^2Q^1$ (d)
	H_{04}: $\alpha_p^* = -\alpha_q^*$	R	$1:1:1:1$	$P^1P^2 \times Q^2Q^1$ (e)
	H_{04}: $-\alpha_p^* = \alpha_q^*$	R	$1:1:1:1$	$P^2P^1 \times Q^1Q^2$ (f)
	H_{04}	NR	$1:2:1$	(c), (d), (e) e (f)
H_{01} and H_{03}	H_{05}: $\alpha_p^* = \delta_{pq}^*$ or $-\alpha_p^* = -\delta_{pq}^*$	R	$1:1:1:1$	(a)
	H_{05}: $\alpha_p^* = -\delta_{pq}^*$ or $-\alpha_p^* = \delta_{pq}^*$	R	$1:1:1:1$	(a)
	H_{05}	NR	$1:2:1$	(a)

PROCEDURE

Step 1	Step 2		Conclusion	
Rejected	Hypot. to test		Segregation	Phase
H_{01}: $\alpha_p^* = 0$	–	–	$1:1$	P^1P^2 or P^2P^1 (a)
H_{02}: $\alpha_q^* = 0$	–	–	$1:1$	Q^1Q^2 or Q^2Q^1 (b)
H_{03}: $\delta_{pq}^* = 0$	–	–	$1:1$	unknown
H_{01} and H_{02}	H_{04}: $\alpha_p^* = \alpha_q^*$	R	$1:1:1:1$	$P^1P^2 \times Q^1Q^2$ (c)
	H_{04}: $-\alpha_p^* = -\alpha_q^*$	R	$1:1:1:1$	$P^2P^1 \times Q^2Q^1$ (d)
	H_{04}: $\alpha_p^* = -\alpha_q^*$	R	$1:1:1:1$	$P^1P^2 \times Q^2Q^1$ (e)
	H_{04}: $-\alpha_p^* = \alpha_q^*$	R	$1:1:1:1$	$P^2P^1 \times Q^1Q^2$ (f)
	H_{04}	NR	$1:2:1$	(c), (d), (e) e (f)
H_{01} and H_{03}	H_{05}: $\alpha_p^* = \delta_{pq}^*$ or $-\alpha_p^* = -\delta_{pq}^*$	R	$1:1:1:1$	(a)
	H_{05}: $\alpha_p^* = -\delta_{pq}^*$ or $-\alpha_p^* = \delta_{pq}^*$	R	$1:1:1:1$	(a)
	H_{05}	NR	$1:2:1$	(a)
H_{02} and H_{03}	H_{06}: $\alpha_q^* = \delta_{pq}^*$ or $-\alpha_q^* = -\delta_{pq}^*$	R	$1:1:1:1$	(b)
	H_{06}: $\alpha_q^* = -\delta_{pq}^*$ or $-\alpha_q^* = \delta_{pq}^*$	R	$1:1:1:1$	(b)
	H_{06}	NR	$1:2:1$	(b)

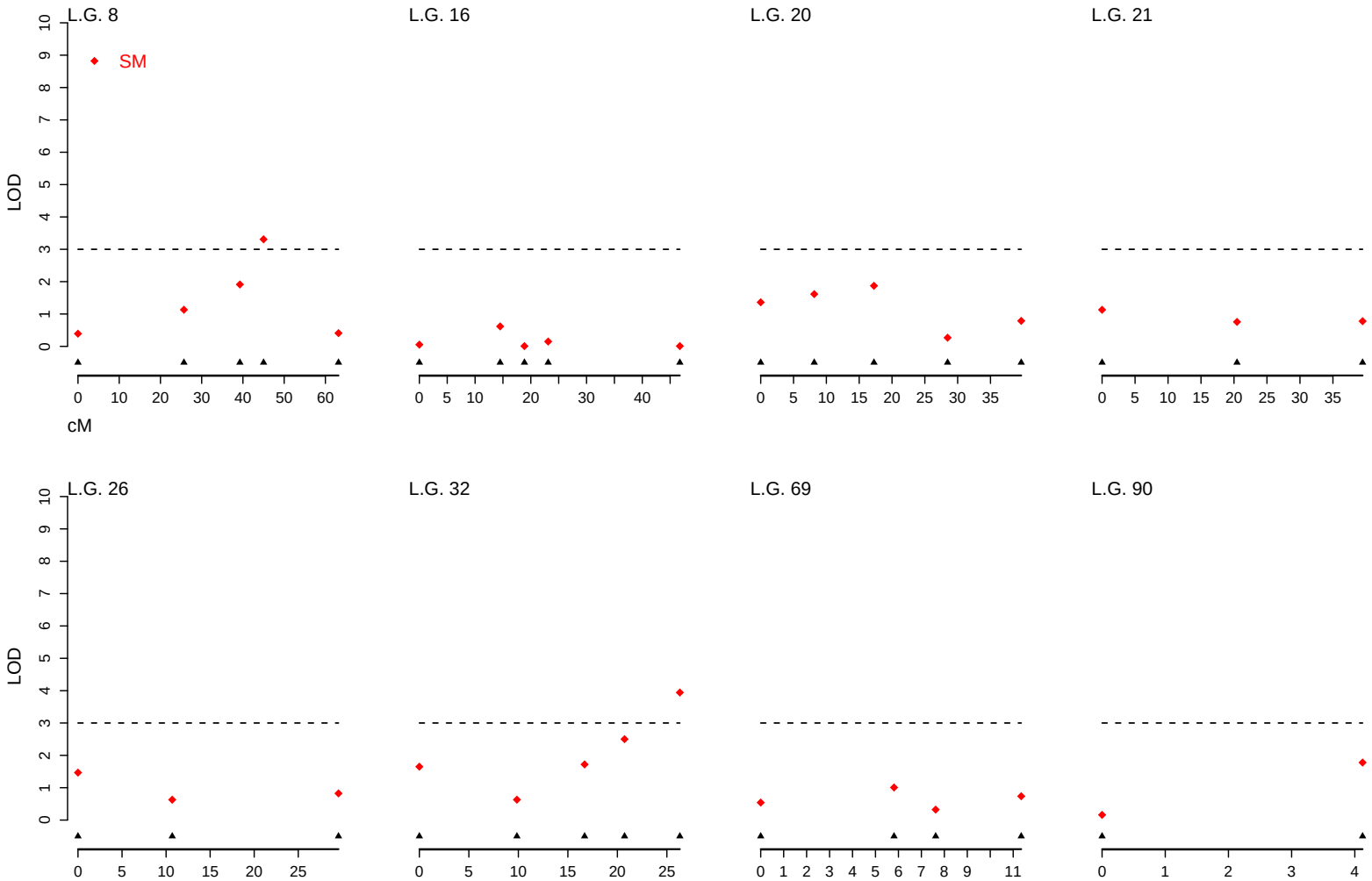
PROCEDURE

Step 1	Step 2		Conclusion	
Rejected	Hypot. to test		Segregation	Phase
H_{01}: $\alpha_p^* = 0$	–	–	$1:1$	P^1P^2 or P^2P^1 (a)
H_{02}: $\alpha_q^* = 0$	–	–	$1:1$	Q^1Q^2 or Q^2Q^1 (b)
H_{03}: $\delta_{pq}^* = 0$	–	–	$1:1$	unknown
H_{01} and H_{02}	H_{04}: $\alpha_p^* = \alpha_q^*$	R	$1:1:1:1$	$P^1P^2 \times Q^1Q^2$ (c)
	H_{04}: $-\alpha_p^* = -\alpha_q^*$	R	$1:1:1:1$	$P^2P^1 \times Q^2Q^1$ (d)
	H_{04}: $\alpha_p^* = -\alpha_q^*$	R	$1:1:1:1$	$P^1P^2 \times Q^2Q^1$ (e)
	H_{04}: $-\alpha_p^* = \alpha_q^*$	R	$1:1:1:1$	$P^2P^1 \times Q^1Q^2$ (f)
	H_{04}	NR	$1:2:1$	(c), (d), (e) e (f)
H_{01} and H_{03}	H_{05}: $\alpha_p^* = \delta_{pq}^*$ or $-\alpha_p^* = -\delta_{pq}^*$	R	$1:1:1:1$	(a)
	H_{05}: $\alpha_p^* = -\delta_{pq}^*$ or $-\alpha_p^* = \delta_{pq}^*$	R	$1:1:1:1$	(a)
	H_{05}	NR	$1:2:1$	(a)
H_{02} and H_{03}	H_{06}: $\alpha_q^* = \delta_{pq}^*$ or $-\alpha_q^* = -\delta_{pq}^*$	R	$1:1:1:1$	(b)
	H_{06}: $\alpha_q^* = -\delta_{pq}^*$ or $-\alpha_q^* = \delta_{pq}^*$	R	$1:1:1:1$	(b)
	H_{06}	NR	$1:2:1$	(b)
H_{01}, H_{02} and H_{03}	H_{04}, H_{05} e H_{06}	R (1 or 3)	$1:1:1:1$	(c), (d), (e), (f)
H_{01}, H_{02} and H_{03}	H_{04}, H_{05} e H_{06}	R (2)	$1:2:1$	(c), (d), (e), (f)
H_{01}, H_{02} and H_{03}	H_{04}, H_{05} e H_{06}	NR	$3:1$	(c), (d), (e), (f)

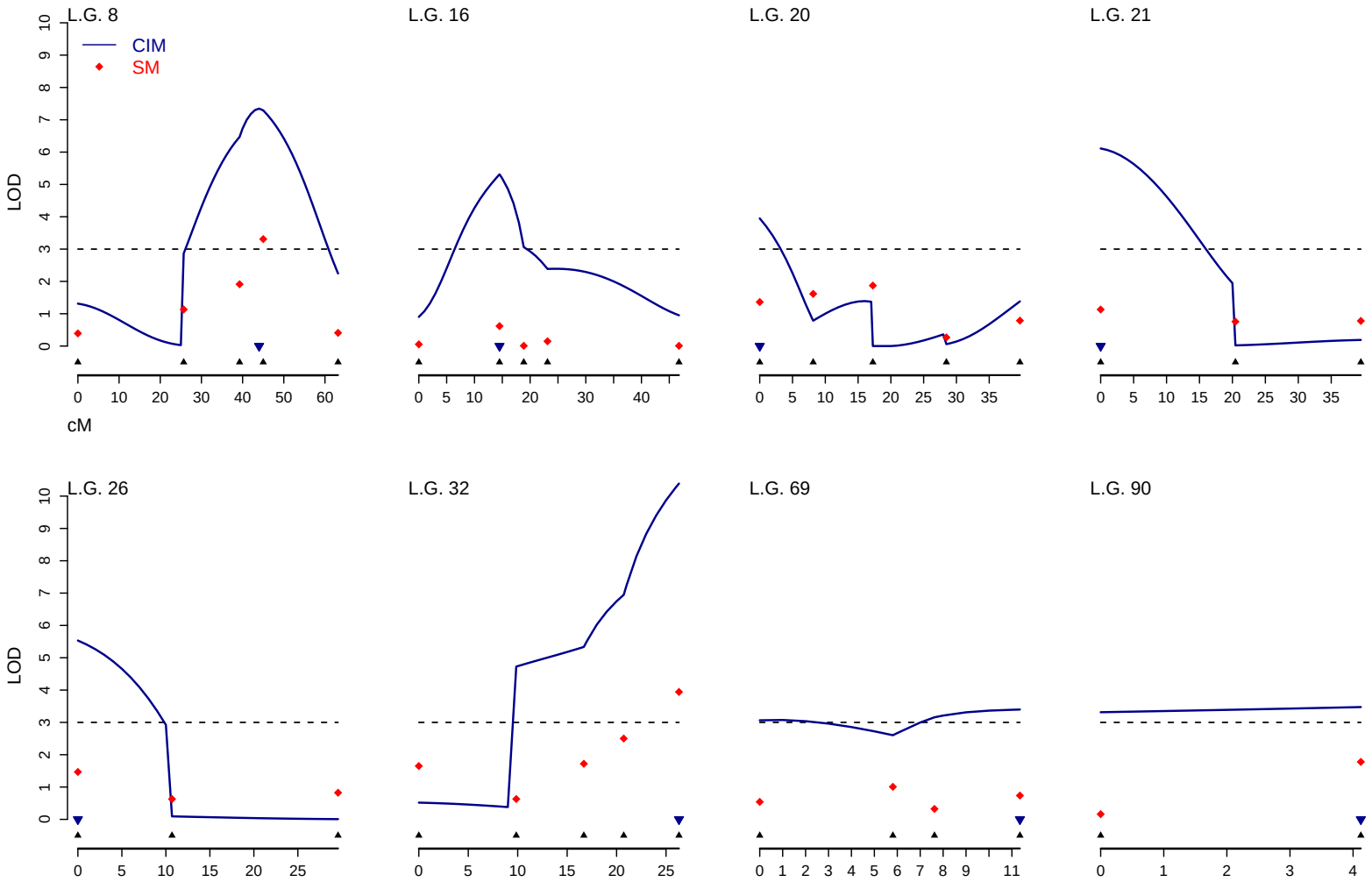
COMMERCIAL CROSS

- SP80-180 $\times$ SP80-4966
- $n = 100$
- 2 replications, plant and ratoon crop
  - Tons of cane per hectare (TCH), POL, tons of POL per hectare (TPH), fiber content
- 740 Marcadores (188 RFLP, 37 EST-SSR, 515 EST-RFLP)
- Multipoint approach (new version of `OneMap`)
- Single Marker *vs* new CIM model

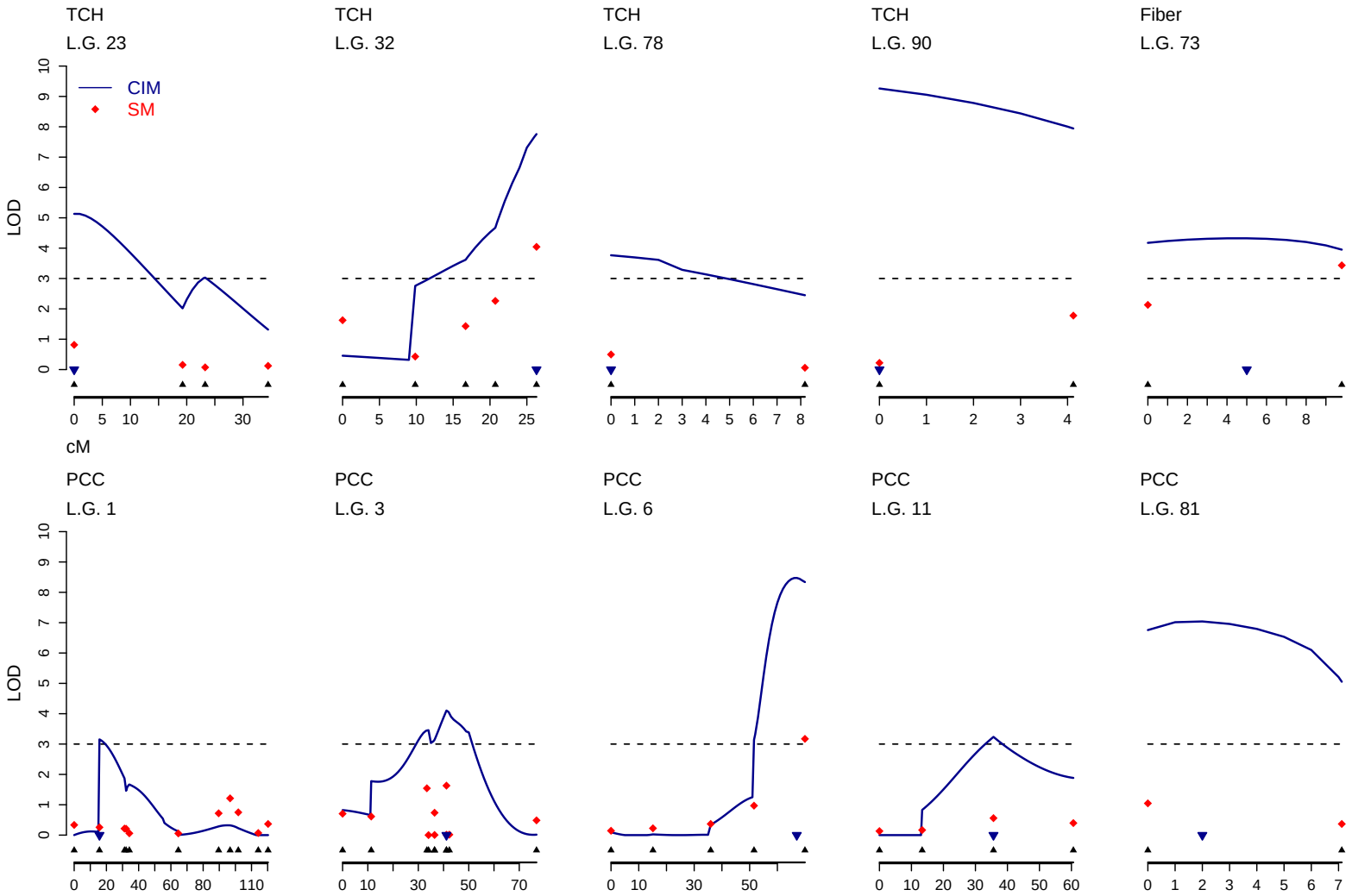
TPH (PLANT CROP)



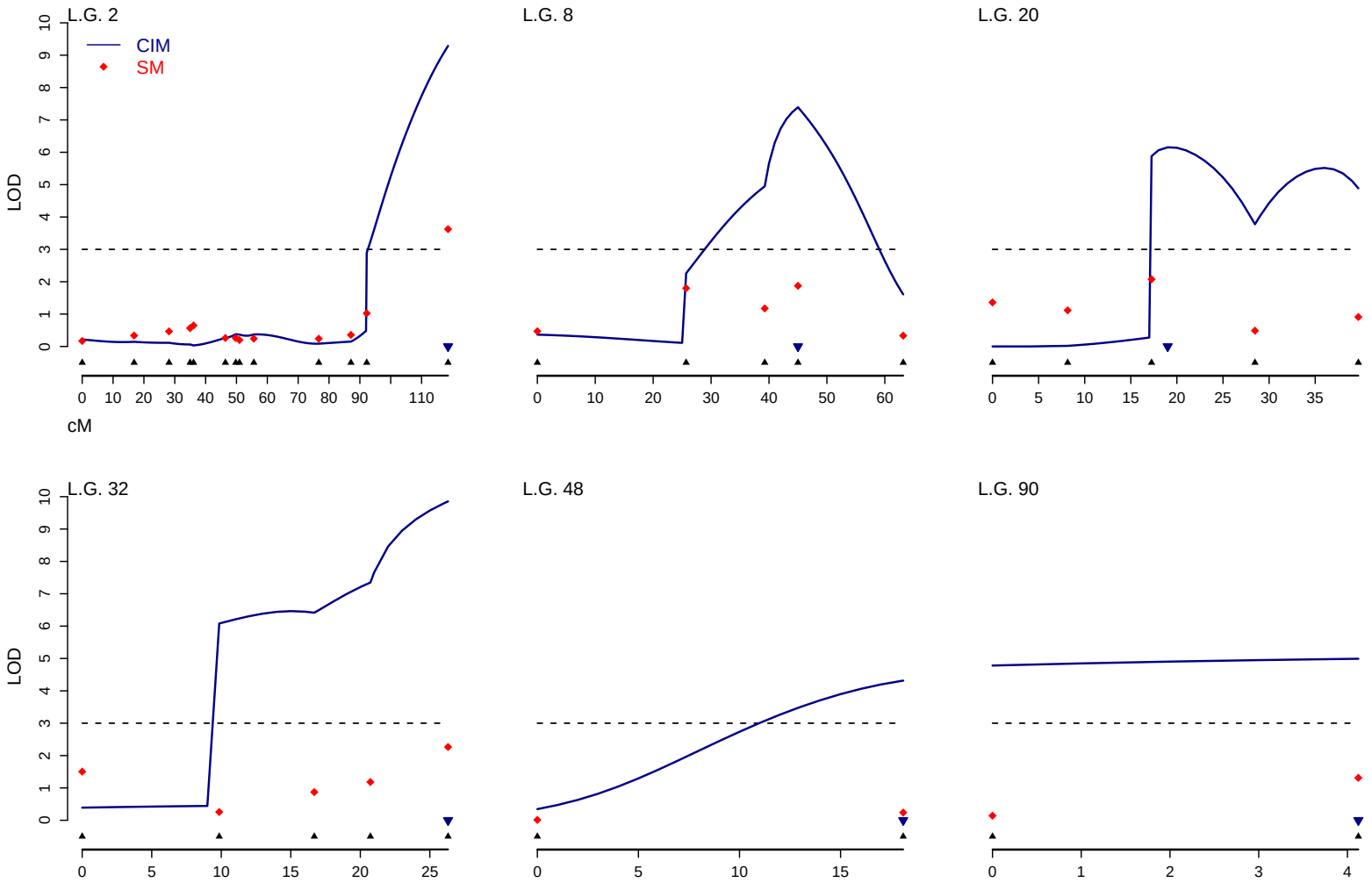
TPH (RATOON CROP)



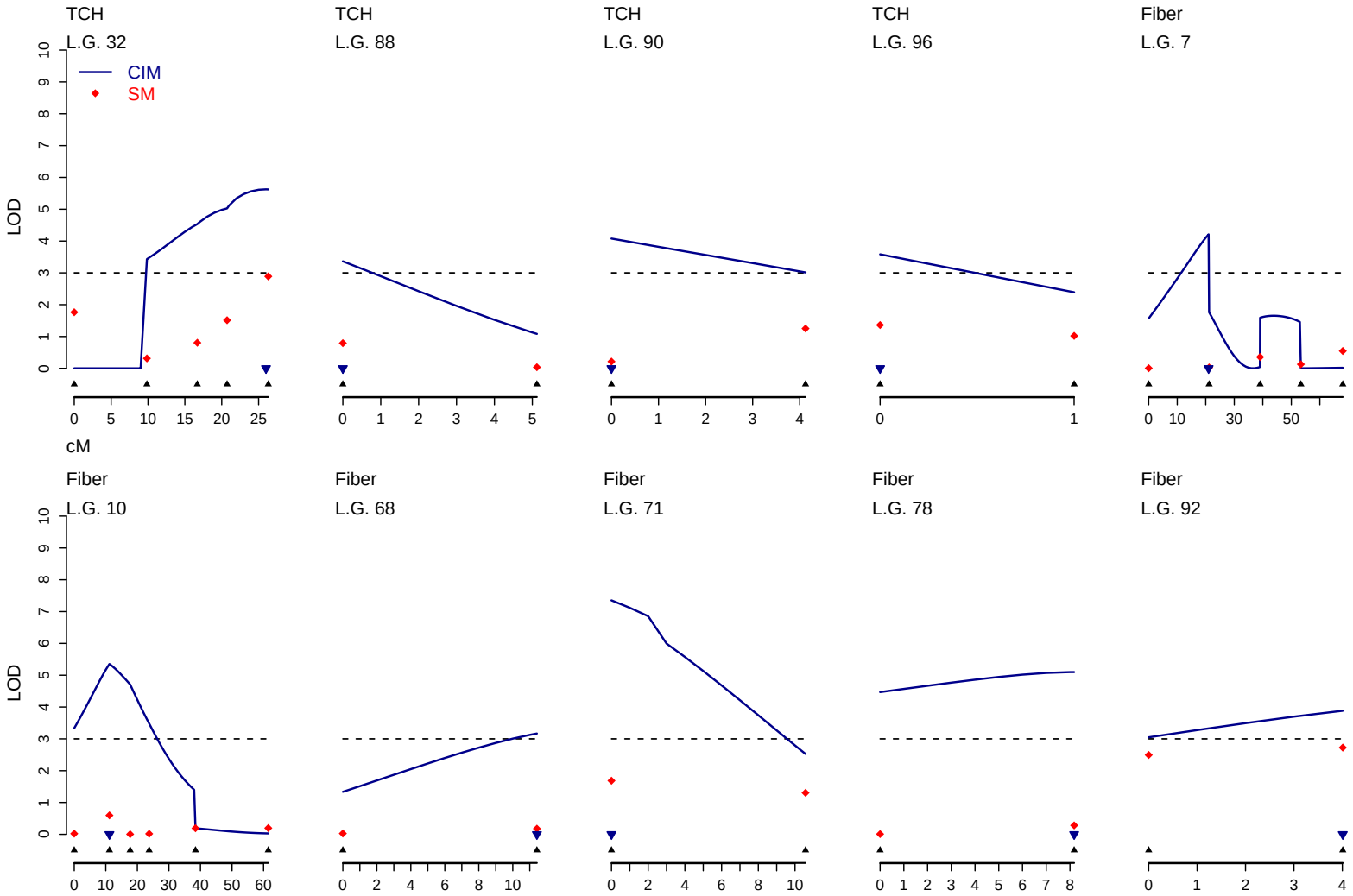
TCH, POL, Fiber (plant crop)



TPH (RATTON CROP)



TCH, Fiber (ratton crop)



PLANT CROP

Trait	L.G.	cM	LOD	$\hat{\mu}$	$\hat{\alpha}_p^*$	$\hat{\alpha}_q^*$	$\hat{\delta}_{pq}^*$	Segregation	Linkage Phase	R^2
TPH	8	44,0	7,3	9,38	0,00	0,70	0,00	1:1	Q^1Q^2	0,55%
	16	14,5	5,3	9,53	-0,31	-0,31	0,36	1:1	n.d.	**12,84%**
	20	0,0	4,0	9,34	0,00	-0,52	0,00	1:1	Q^2Q^1	0,53%
	21	0,0	6,1	9,40	-0,59	0,00	0,00	1:1	P^2P^1	0,58%
	26	0,0	5,5	9,38	0,00	0,57	0,00	1:1	Q^1Q^2	0,53%
	32	26,3	10,4	9,46	-0,03	-0,73	0,03	1:1	Q^2Q^1	**8,89%**
	69	11,3	3,3	9,38	-0,25	-0,25	0,27	3:1	$P^2P^1 \times Q^2Q^1$	**29,00%**
	90	4,1	3,4	9,43	-0,06	-0,33	0,33	1:2:1	Q^2Q^1	1,96%
										54,92%
TCH	23	0,0	5,1	50,93	0,00	3,44	0,00	1:1	Q^1Q^2	0,52%
	32	26,3	7,8	52,80	-0,83	-3,58	0,65	1:1	Q^2Q^1	**8,31%**
	78	0,0	3,7	51,90	3,20	-0,16	-0,29	1:1	P^1P^2	**16,87%**
	90	0,0	9,3	51,72	1,39	-4,72	4,42	1:2:1	Q^2Q^1	**29,19%**
										54,89%
POL	1	15,7	3,2	14,00	0,00	-0,30	0,00	1:1	Q^2Q^1	0,83%
	3	41,2	4,1	14,48	-0,02	-0,19	0,36	1:1	n.d.	3,91%
	6	67,0	8,4	14,28	0,26	0,26	-0,35	1:1	n.d.	**19,70%**
	11	35,6	3,1	13,44	0,00	-0,26	0,00	1:1	Q^2Q^1	0,91%
	81	2,0	6,7	14,42	0,00	-0,42	0,00	1:1	Q^2Q^1	0,86%
										26,1%
Fiber	73	5,0	4,3	0,09†	-2,67†	0,00	0,00	1:1	P^1P^2	1,10%

RATOON CROP

Trait	L.G.	cM	LOD	$\hat{\mu}$	$\hat{\alpha}_p^*$	$\hat{\alpha}_q^*$	$\hat{\delta}_{pq}^*$	Segregation	Phase	R^2
TPH	2	118,6	9,3	10,02	0,28	0,92	-0,10	1:1:1:1	$P^1P^2 \times Q^1Q^2$	6,12%
	8	45,0	7,2	9,88	0,00	0,93	0,00	1:1	Q^1Q^2	0,92%
	20	19,0	6,2	11,18	0,00	-0,93	0,00	1:1	Q^2Q^1	0,95%
	32	26,3	9,9	10,22	-0,24	-0,99	0,17	1:1	Q^2Q^1	3,81%
	48	18,1	4,3	10,03	-0,68	0,00	0,00	1:1	P^2P^1	0,87%
	90	5,0	5,0	9,92	0,14	-0,55	0,54	1:2:1	Q^2Q^1	2,99%
TCH	32	26,0	5,6	103,81	-1,51	-5,11	0,95	1:1	Q^2Q^1	9,83%
	88	0,0	3,4	118,83	0,00	-3,77	0,00	1:1	Q^2Q^1	0,61%
	90	0,0	4,1	165,07	7,53	-3,00	3,35	1:1	P^1P^2	**35,06%**
	96	0,0	3,6	76,02	-4,44	0,00	0,00	1:1	P^2P^1	0,56%
POL	1	101,8	3,4	14,11	0,00	0,23	0,00	1:1	Q^1Q^2	0,83%
	3	33,0	7,2	14,67	0,12	-0,34	0,13	1:1	Q^2Q^1	2,67%
	6	14,0	5,1	13,94	0,22	0,22	-0,20	3:1	$P^1P^2 \times Q^1Q^2$	**18,39%**
	30	21,0	4,1	14,29	0,00	0,26	0,00	1:1	Q^1Q^2	0,88%
	35	23,0	4,1	14,11	-0,25	0,00	0,00	1:1	P^2P^1	0,87%
	67	0,0	4,2	14,84	0,00	-0,25	0,00	1:1	Q^2Q^1	0,80%
	81	2,0	3,7	13,72	0,00	-0,31	0,00	1:1	Q^2Q^1	0,88%
Fiber	7	21,0	4,2	0,10	0,00	2,11†	0,00	1:1	Q^1Q^2	1,22%
	10	11,2	5,4	0,11	0,77†	-2,00	1,96†	1:2:1	Q^2Q^1	3,44%
	68	11,4	3,2	0,11	0,00	-2,00†	0,00	1:1	Q^2Q^1	0,95%
	71	0,0	7,4	0,11	-3,82†	0,00	0,00	1:1	P^2P^1	0,95%
	78	8,2	5,1	0,11	-0,06†	2,30	2,00†	1:2:1	Q^1Q^2	3,06%
	92	4,0	3,9	0,10	0,00	2,41†	0,00	1:1	Q^1Q^2	0,95%

SUMMARY

- 43 QTL with CIM *vs* 11 QTL with Single Marker
- Plant crop: 18 QTL
  - 8 for TPH; 4 for TCH; 5 for POL; 1 for Fiber
  - Most QTL on SP80-4966 (high sugar)
  - Segregation: 15 (1:1), 2 (1:2:1) e 1 (3:1)
- Ratoon crop: 23 QTL
  - 6 for TPH; 4 for TCH; 7 for POL; 6 for fiber
  - Segregation: 18 (1:1), 3 (1:2:1), 1 (3:1) e 1 (1:1:1:1)
  - QTL evenly distributed

SUMMARY

- 43 QTL with CIM *vs* 11 QTL with Single Marker
- Plant crop: 18 QTL
  - 8 for TPH; 4 for TCH; 5 for POL; 1 for Fiber
  - Most QTL on SP80-4966 (high sugar)
  - Segregation: 15 (1:1), 2 (1:2:1) e 1 (3:1)
- Ratoon crop: 23 QTL
  - 6 for TPH; 4 for TCH; 7 for POL; 6 for fiber
  - Segregation: 18 (1:1), 3 (1:2:1), 1 (3:1) e 1 (1:1:1:1)
  - QTL evenly distributed

SUMMARY

- 43 QTL with CIM *vs* 11 QTL with Single Marker
- Plant crop: 18 QTL
  - 8 for TPH; 4 for TCH; 5 for POL; 1 for Fiber
  - Most QTL on SP80-4966 (high sugar)
  - Segregation: 15 (1:1), 2 (1:2:1) e 1 (3:1)
- Ratoon crop: 23 QTL
  - 6 for TPH; 4 for TCH; 7 for POL; 6 for fiber
  - Segregation: 18 (1:1), 3 (1:2:1), 1 (3:1) e 1 (1:1:1:1)
  - QTL evenly distributed

Genetic Architecture

Multipoint approach

- It is very important to have good maps, since we need to use all information available (multipoint QTL probabilities)

Usefull information

1. QTL number
2. Positions
3. Effects (most additive), segregation and linkage phases
4. Evidence of QTL $\times$ Ratoon interaction
5. Since we are using EST-based markers, the odds of finding QTL are higher

Genetic Architecture

Multipoint approach

- It is very important to have good maps, since we need to use all information available (multipoint QTL probabilities)

Usefull information

1. QTL number
2. Positions
3. Effects (most additive), segregation and linkage phases
4. Evidence of QTL $\times$ Ratoon interaction
5. Since we are using EST-based markers, the odds of finding QTL are higher

Genetic Architecture

Multipoint approach

- It is very important to have good maps, since we need to use all information available (multipoint QTL probabilities)

Usefull information

1. QTL number
2. Positions
3. Effects (most additive), segregation and linkage phases
4. Evidence of QTL $\times$ Ratoon interaction
5. Since we are using EST-based markers, the odds of finding QTL are higher

Genetic Architecture

Multipoint approach

- It is very important to have good maps, since we need to use all information available (multipoint QTL probabilities)

Usefull information

1. QTL number
2. Positions
3. Effects (most additive), segregation and linkage phases
4. Evidence of QTL $\times$ Ratoon interaction
5. Since we are using EST-based markers, the odds of finding QTL are higher

Genetic Architecture

Multipoint approach

- It is very important to have good maps, since we need to use all information available (multipoint QTL probabilities)

Usefull information

1. QTL number
2. Positions
3. Effects (most additive), segregation and linkage phases
4. Evidence of QTL $\times$ Ratoon interaction
5. Since we are using EST-based markers, the odds of finding QTL are higher

Genetic Architecture

Multipoint approach

- It is very important to have good maps, since we need to use all information available (multipoint QTL probabilities)

Usefull information

1. QTL number
2. Positions
3. Effects (most additive), segregation and linkage phases
4. Evidence of QTL $\times$ Ratoon interaction
5. Since we are using EST-based markers, the odds of finding QTL are higher

Genetic Archictecture

We need to go further

1. Still using models for dyploids
2. Need to deal with polyploids, all segregation patterns, SNPs, etc
3. Models for multiple traits, ratoons, environments and populations
4. Estimate the breeding values for MAS
5. Hopefully this will be usefull as a framework for eQTL mapping and Association Mapping
6. A software will be released in the future

Genetic Archictecture

We need to go further

1. Still using models for dyploids
2. Need to deal with polyploids, all segregation patterns, SNPs, etc
3. Models for multiple traits, ratoons, environments and populations
4. Estimate the breeding values for MAS
5. Hopefully this will be usefull as a framework for eQTL mapping and Association Mapping
6. A software will be released in the future

Genetic Archictecture

We need to go further

1. Still using models for dyploids
2. Need to deal with polyploids, all segregation patterns, SNPs, etc
3. Models for multiple traits, ratoons, environments and populations
4. Estimate the breeding values for MAS
5. Hopefully this will be usefull as a framework for eQTL mapping and Association Mapping
6. A software will be released in the future

Genetic Archictecture

We need to go further

1. Still using models for dyploids
2. Need to deal with polyploids, all segregation patterns, SNPs, etc
3. Models for multiple traits, ratoons, environments and populations
4. Estimate the breeding values for MAS
5. Hopefully this will be usefull as a framework for eQTL mapping and Association Mapping
6. A software will be released in the future

Genetic Archictecture

We need to go further

1. Still using models for dyploids
2. Need to deal with polyploids, all segregation patterns, SNPs, etc
3. Models for multiple traits, ratoons, environments and populations
4. Estimate the breeding values for MAS
5. Hopefully this will be usefull as a framework for eQTL mapping and Association Mapping
6. A software will be released in the future

Genetic Archictecture

We need to go further

1. Still using models for dyploids
2. Need to deal with polyploids, all segregation patterns, SNPs, etc
3. Models for multiple traits, ratoons, environments and populations
4. Estimate the breeding values for MAS
5. Hopefully this will be usefull as a framework for eQTL mapping and Association Mapping
6. A software will be released in the future

PEOPLE

- Dr. Anete Pereira de Souza, UNICAMP
  - Estela Costa, Tallis R Rodrigues, Andréia N Mezza, Laura H M Teixeira, Thiago G Marconi
- Dr. Antonio Augusto Franco Garcia, ESALQ/USP
  - Gabriel R. A. Margarido (OneMap, MIM models, multivariate models)
  - Marcelo Mollinari (Multipoint approach for polyploids, OneMap, multivariate models)
  - Maria M. Pastina (QTL and linkage maps in sugarcane, QTL×E)
  - Rodrigo Gazaffi (PhD thesis, March 2009 - new model for outcrossing species)
- Dr. Karine M. Oliveira (UNICAMP/CTC*), Dr. Luciana R. Pinto (UNICAMP/IAC*), Dr. Eugênio C. Ulian (CTC*, Monsanto), Dr. José A. Bressiani (CTC*, Canavialis), Dr. Rubens L. C. Braga (CTC), Dr. Sabrina M. Chabregas (CTC), Dr. Maria C. Falco (CTC), Dr. William L. Burnquist (CTC)

PEOPLE

- Dr. Anete Pereira de Souza, UNICAMP
  - Estela Costa, Tallis R Rodrigues, Andréia N Mezza, Laura H M Teixeira, Thiago G Marconi
- Dr. Antonio Augusto Franco Garcia, ESALQ/USP
  - Gabriel R. A. Margarido (OneMap, MIM models, multivariate models)
  - Marcelo Mollinari (Multipoint approach for polyploids, OneMap, multivariate models)
  - Maria M. Pastina (QTL and linkage maps in sugarcane, QTL×E)
  - Rodrigo Gazaffi (PhD thesis, March 2009 - new model for outcrossing species)
- Dr. Karine M. Oliveira (UNICAMP/CTC*), Dr. Luciana R. Pinto (UNICAMP/IAC*), Dr. Eugênio C. Ulian (CTC*, Monsanto), Dr. José A. Bressiani (CTC*, Canavialis), Dr. Rubens L. C. Braga (CTC), Dr. Sabrina M. Chabregas (CTC), Dr. Maria C. Falco (CTC), Dr. William L. Burnquist (CTC)

PEOPLE

- Dr. Anete Pereira de Souza, UNICAMP
  - Estela Costa, Tallis R Rodrigues, Andréia N Mezza, Laura H M Teixeira, Thiago G Marconi
- Dr. Antonio Augusto Franco Garcia, ESALQ/USP
  - Gabriel R. A. Margarido (OneMap, MIM models, multivariate models)
  - Marcelo Mollinari (Multipoint approach for polyploids, OneMap, multivariate models)
  - Maria M. Pastina (QTL and linkage maps in sugarcane, QTL×E)
  - Rodrigo Gazaffi (PhD thesis, March 2009 - new model for outcrossing species)
- Dr. Karine M. Oliveira (UNICAMP/CTC*), Dr. Luciana R. Pinto (UNICAMP/IAC*), Dr. Eugênio C. Ulian (CTC*, Monsanto), Dr. José A. Bressiani (CTC*, Canavialis), Dr. Rubens L. C. Braga (CTC), Dr. Sabrina M. Chabregas (CTC), Dr. Maria C. Falco (CTC), Dr. William L. Burnquist (CTC)

PEOPLE

- Dr. Anete Pereira de Souza, UNICAMP
  - Estela Costa, Tallis R Rodrigues, Andréia N Mezza, Laura H M Teixeira, Thiago G Marconi
- Dr. Antonio Augusto Franco Garcia, ESALQ/USP
  - Gabriel R. A. Margarido (OneMap, MIM models, multivariate models)
  - Marcelo Mollinari (Multipoint approach for polyploids, OneMap, multivariate models)
  - Maria M. Pastina (QTL and linkage maps in sugarcane, QTL×E)
  - Rodrigo Gazaffi (PhD thesis, March 2009 - new model for outcrossing species)
- Dr. Karine M. Oliveira (UNICAMP/CTC*), Dr. Luciana R. Pinto (UNICAMP/IAC*), Dr. Eugênio C. Ulian (CTC*, Monsanto), Dr. José A. Bressiani (CTC*, Canavialis), Dr. Rubens L. C. Braga (CTC), Dr. Sabrina M. Chabregas (CTC), Dr. Maria C. Falco (CTC), Dr. William L. Burnquist (CTC)

PEOPLE

- Dr. Anete Pereira de Souza, UNICAMP
  - Estela Costa, Tallis R Rodrigues, Andréia N Mezza, Laura H M Teixeira, Thiago G Marconi
- Dr. Antonio Augusto Franco Garcia, ESALQ/USP
  - Gabriel R. A. Margarido (OneMap, MIM models, multivariate models)
  - Marcelo Mollinari (Multipoint approach for polyploids, OneMap, multivariate models)
  - Maria M. Pastina (QTL and linkage maps in sugarcane, QTL$\times$E)
  - Rodrigo Gazaffi (PhD thesis, March 2009 - new model for outcrossing species)
- Dr. Karine M. Oliveira (UNICAMP/CTC*), Dr. Luciana R. Pinto (UNICAMP/IAC*), Dr. Eugênio C. Ulian (CTC*, Monsanto), Dr. José A. Bressiani (CTC*, Canavialis), Dr. Rubens L. C. Braga (CTC), Dr. Sabrina M. Chabregas (CTC), Dr. Maria C. Falco (CTC), Dr. William L. Burnquist (CTC)

PEOPLE

- Dr. Anete Pereira de Souza, UNICAMP
  - Estela Costa, Tallis R Rodrigues, Andréia N Mezza, Laura H M Teixeira, Thiago G Marconi
- Dr. Antonio Augusto Franco Garcia, ESALQ/USP
  - Gabriel R. A. Margarido (OneMap, MIM models, multivariate models)
  - Marcelo Mollinari (Multipoint approach for polyploids, OneMap, multivariate models)
  - Maria M. Pastina (QTL and linkage maps in sugarcane, QTL$\times$E)
  - Rodrigo Gazaffi (PhD thesis, March 2009 - new model for outcrossing species)
- Dr. Karine M. Oliveira (UNICAMP/CTC*), Dr. Luciana R. Pinto (UNICAMP/IAC*), Dr. Eugênio C. Ulian (CTC*, Monsanto), Dr. José A. Bressiani (CTC*, Canavialis), Dr. Rubens L. C. Braga (CTC), Dr. Sabrina M. Chabregas (CTC), Dr. Maria C. Falco (CTC), Dr. William L. Burnquist (CTC)

PEOPLE

- Dr. Anete Pereira de Souza, UNICAMP
  - Estela Costa, Tallis R Rodrigues, Andréia N Mezza, Laura H M Teixeira, Thiago G Marconi
- Dr. Antonio Augusto Franco Garcia, ESALQ/USP
  - Gabriel R. A. Margarido (OneMap, MIM models, multivariate models)
  - Marcelo Mollinari (Multipoint approach for polyploids, OneMap, multivariate models)
  - Maria M. Pastina (QTL and linkage maps in sugarcane, QTL$\times$E)
  - Rodrigo Gazaffi (PhD thesis, March 2009 - new model for outcrossing species)
- Dr. Karine M. Oliveira (UNICAMP/CTC*), Dr. Luciana R. Pinto (UNICAMP/IAC*), Dr. Eugênio C. Ulian (CTC*, Monsanto), Dr. José A. Bressiani (CTC*, Canavialis), Dr. Rubens L. C. Braga (CTC), Dr. Sabrina M. Chabregas (CTC), Dr. Maria C. Falco (CTC), Dr. William L. Burnquist (CTC)