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INRA – ISU symposium, March 19-21, 2007

# Current QTL (fine) mapping programs in French pig populations

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# Content

- Primary QTL mapping programs

=> New populations, new traits

- Use of a grand-daughter design to map QTL in French pig populations
- Mapping meat quality QTL in Duroc x Large White F2 pigs
- Mapping feed consumption and behavior QTL

- Fine mapping of QTL

=> Identifying causative polymorphisms for QTL of particular interest

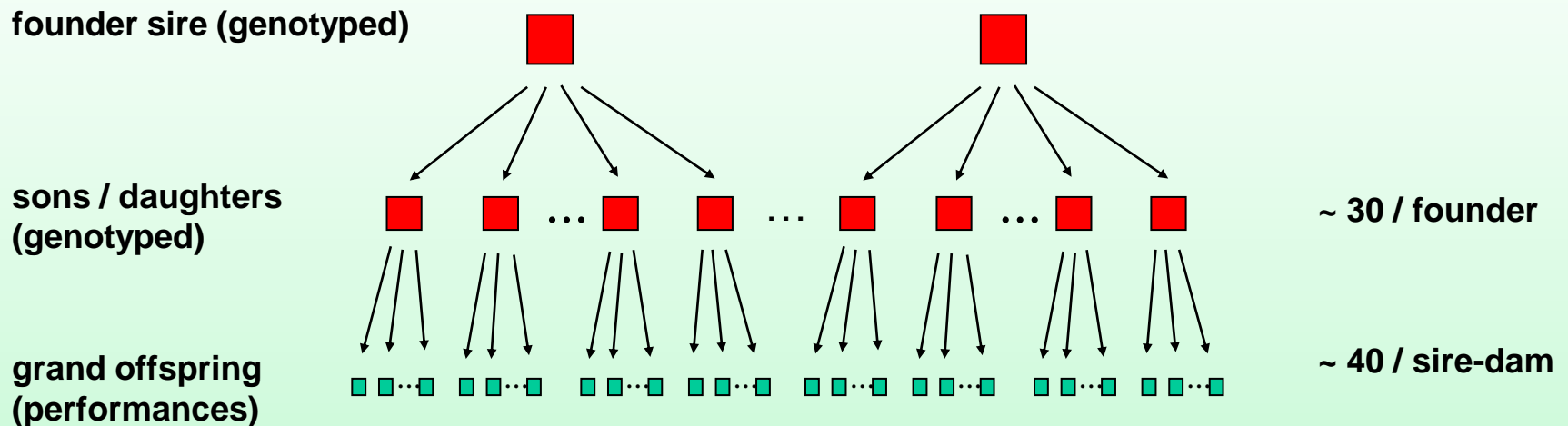
- Fine mapping of growth and body composition QTL in Meishan x Large White crosses
- (Fine) mapping of QTL for hereditary cutaneous melanoma in pigs
- BIOMARK and DELISUS projects

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- Primary QTL mapping programs
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# Use of a grand-sire design for QTL mapping in France (1/2)

In French Large White and Landrace populations (Tribout et al)



- Use of the national central database
- Use of a DNA bank for AI boars

# Use of a grand-sire design for QTL mapping in France (2/2)

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- **8 grand-sire families**
- **traits investigated**
  - growth, carcass and meat quality traits ( selection herds & central test station)
  - reproduction traits : litter size at birth (selection & multiplication herds)
- **Results (Tribout et al, 2006; 2007)**
  - Age at 100 kg and ADG : 1 QTL found on SSC4
  - Backfat thickness: 3 QTL found on SSC2, 3 and 17
  - Number of stillbirths: 3 QTL found on SSC6, 11 and 14
  - Number born alive : 3 QTL found on SSC7, 16 and 18

# Mapping meat quality QTL in Duroc x Large White F2 pigs

- **Duroc x Large White F2 pigs**
  - ~ 500 pigs – 6 large families
  - Initial objectives : mapping a major gene for IMF detected using segregation analysis + QTL mapping for meat quality traits, growth and carcass traits
  - IMF and fatty acid composition (FAC) analysed so far
- **Results (Sanchez et al, 2007)**
  - 3 QTL for IMF on SSC 1, 13 and 15
  - Several QTL for FAC (SSC 1, 7, 10, 11, 13, 14,...)

# Mapping feed consumption and behaviour QTL

(Piétrain x Large White) x Large White BC pigs (Gilbert et al)

- 16 families x 48 pigs
- Focused on feed consumption and behaviour traits (measured using ACEMO electronic feeders), but growth and carcass traits also investigated
- Part of SABRE integrated European project
- Animals genotyped in 2007
- Analyses in 2007-2008

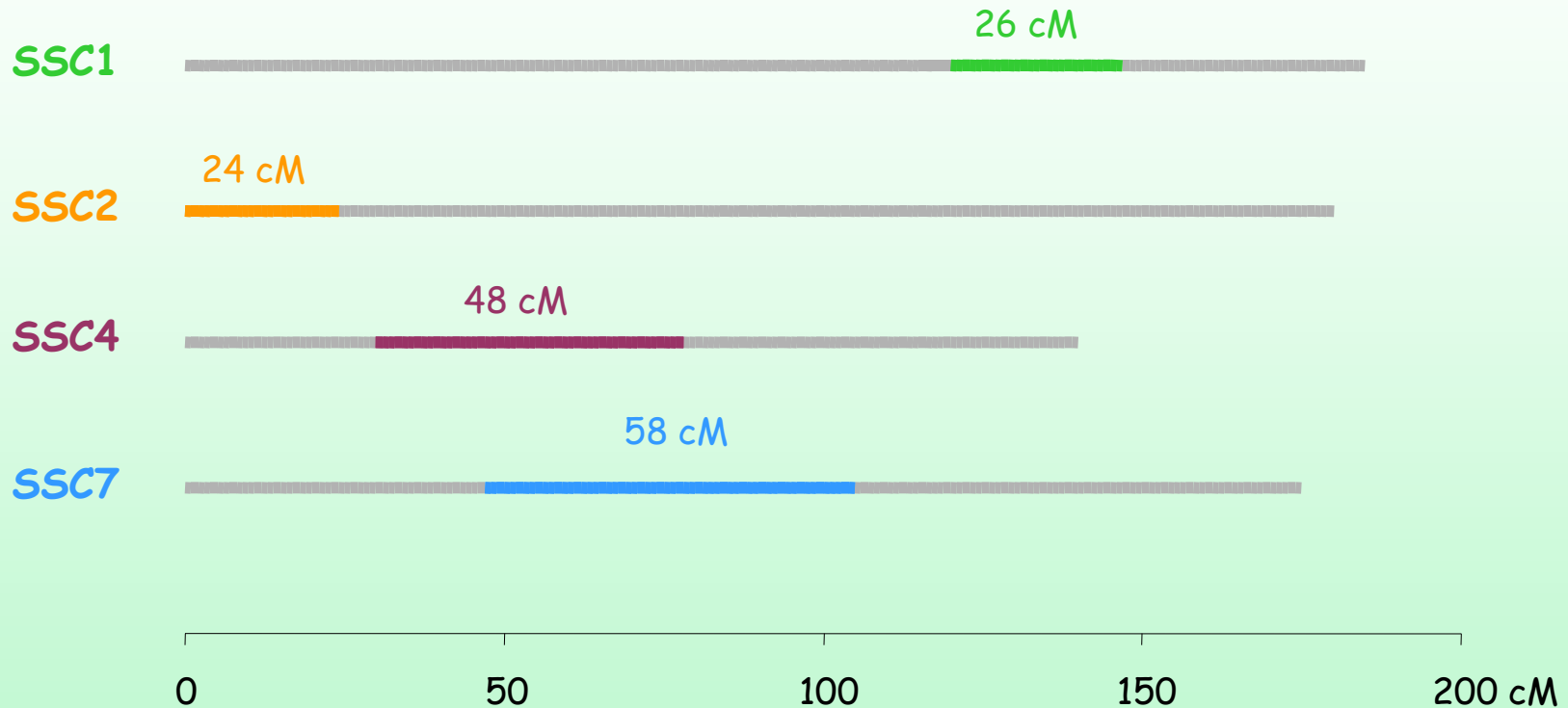


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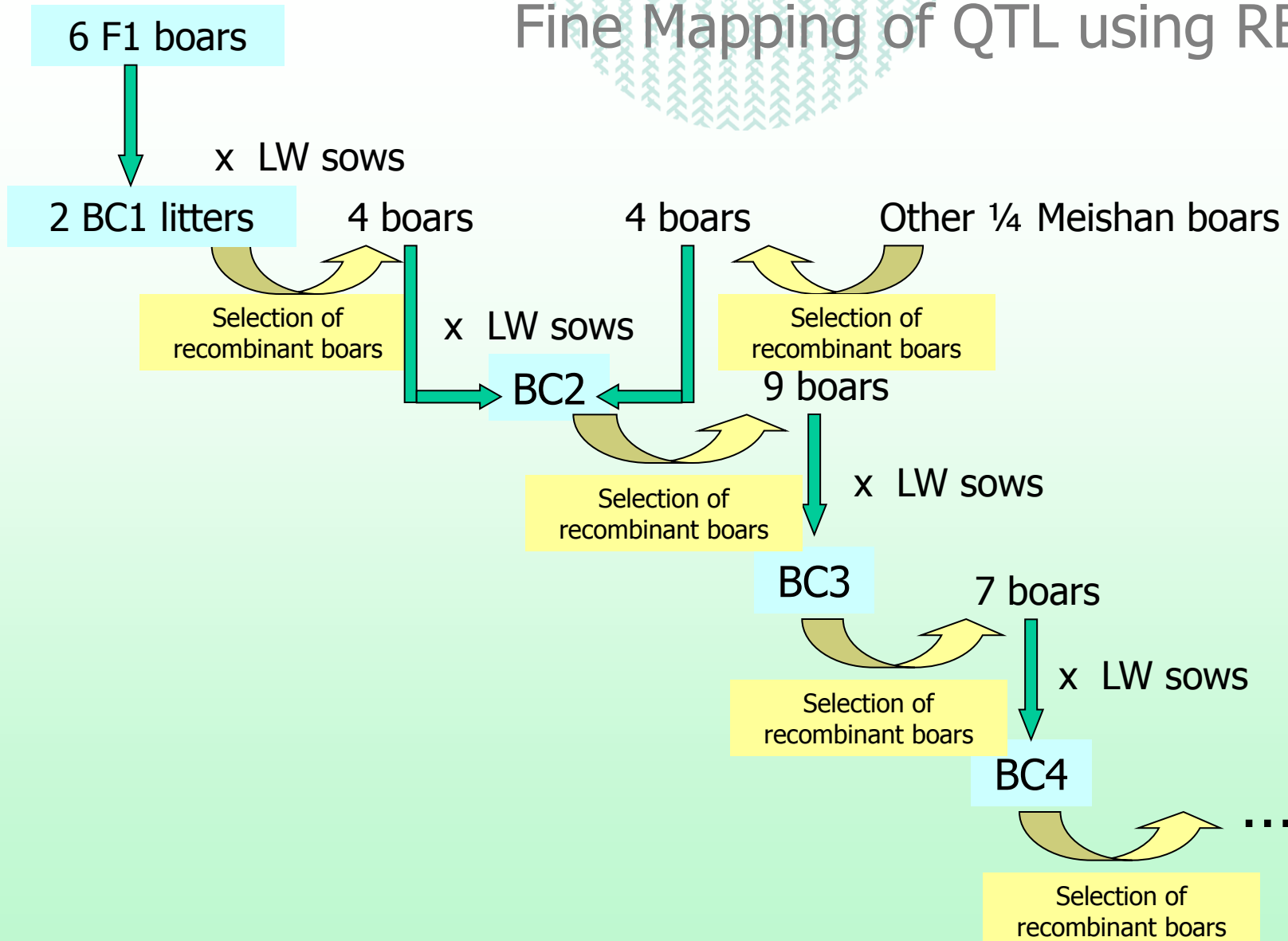
- Primary QTL mapping programs
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# Recombinant backcross progeny test (RBCPT)

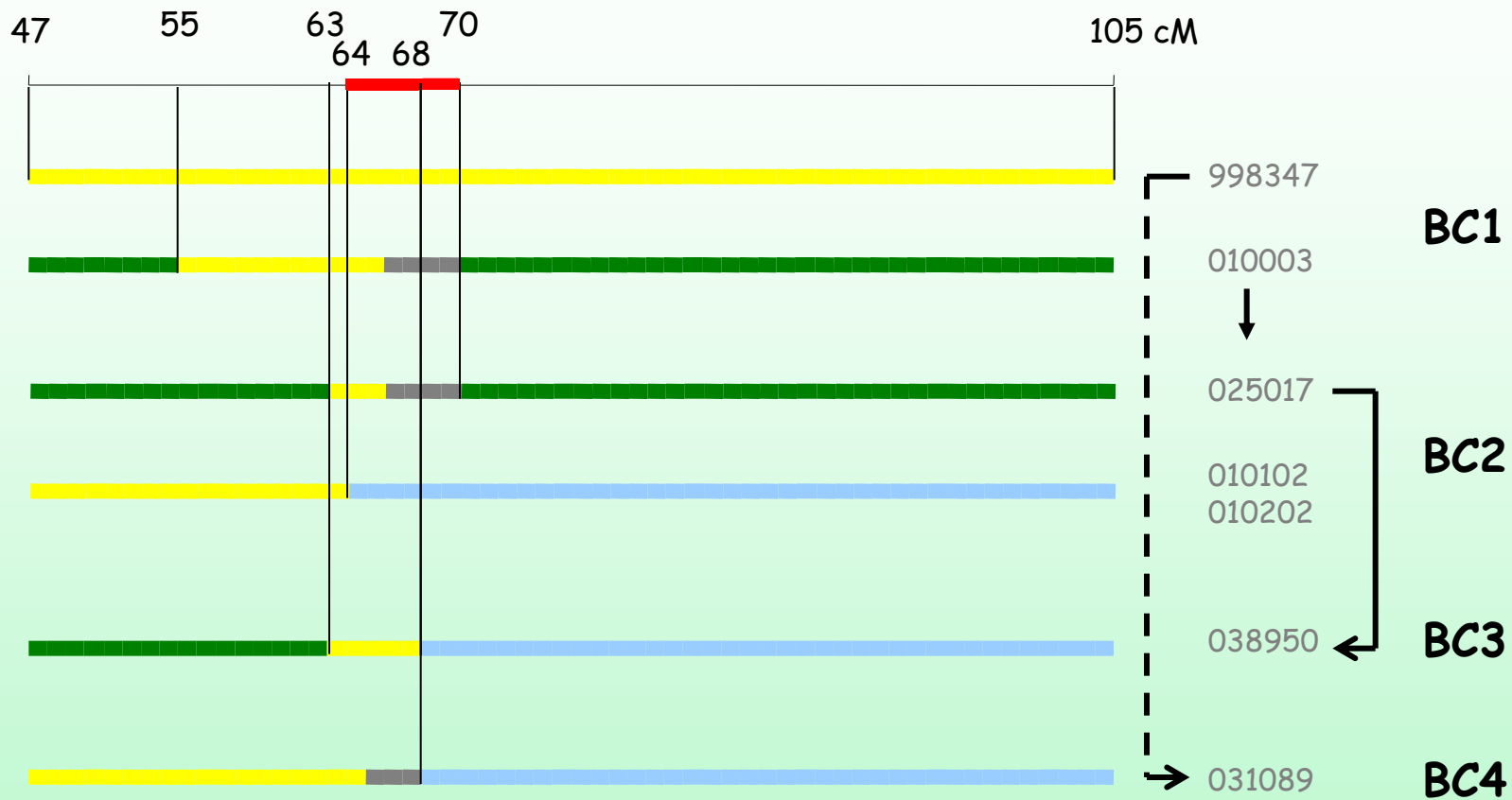
## Chromosomal regions investigated



# Fine Mapping of QTL using RBCPT



# Fine mapping of QTL on SSC7 using RBCPT



# Fine mapping of QTL on SSC7 using RBCPT

## Current localization of growth/carcass QTL

SSC1 : 1 to 5 cM

SSC2 : IGF2 (low effect) + second QTL

SSC4 : 2 QTL ~10 cM

SSC7 : ~ 6 cM interval

## Additional work on :

Intramuscular fat content (SSC7)

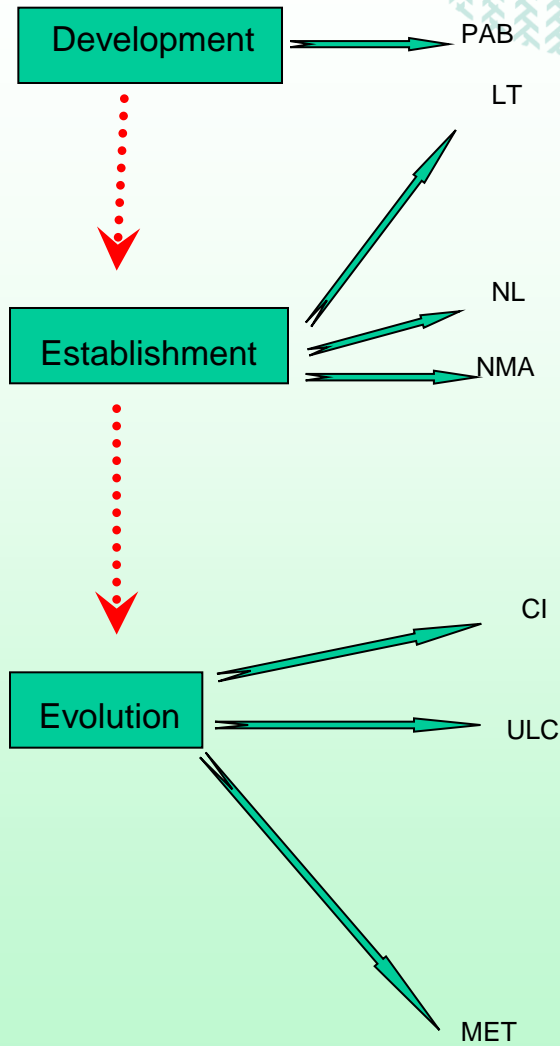
Boar taint (SSC7)

# (Fine) mapping of QTL for hereditary cutaneous melanoma in pigs

- Use of a pig line spontaneously developing melanoma
- Backcross program with colored (Duroc) pigs
- Clinical and histological characterization of the tumor
  - Genetic characterization of predisposition



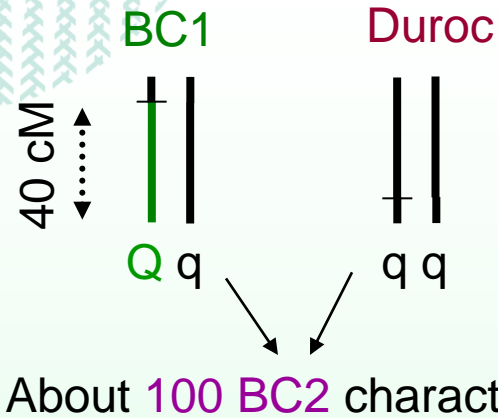
# Mapping results



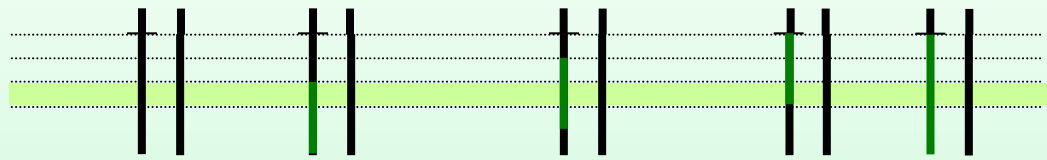
Trait	SSC	Position (cM)	Nearest Marker	Test Statistics	P <sup>a</sup>
PAB	12	95.60	SWC23	106.23	*** <sup>b</sup>
LT	2	17.90	SW2623	64.17	*
	4	84.00	SW1996	78.13	**
	6	140.50	SW322	65.05	*
	8	22.00	SW905	73.94	*
	9	42.00	SW911	77.29	**
	13	81.00	SW398	93.24	*** <sup>b</sup>
	14	98.00	SW2515	81.62	** <sup>c</sup>
NL	3	42.00	SW487	81.62	*
	7	49.00	LRA1	82.28	*
NMA	1	78.00	SW962	92.29	** <sup>c</sup>
	2	21.90	SWR783	87.89	*
	6	17.50	SW2406	82.48	*
	7	4.00	S0025	92.68	**
	10	54.00	SWC19	87.05	*
	16	45.30	SW1454	103.93	*** <sup>b</sup>
	17	44.80	SW2441	111.02	*** <sup>b</sup>
CI	1	85.00	SW1020	93.88	*
	6	108.50	S0299	88.96	*
	13	71.00	SW520	98.45	**
	17	52.80	SW1920	86.15	*
ULC	2	25.90	SWR783	87.03	*
	4	4.00	S0227	98.08	** <sup>c</sup>
	7	73.00	S0102	86.76	*
	8	60.00	SW1070	84.97	*
	10	42.00	S0351	126.34	*** <sup>b</sup>
	12	95.60	SWC23	94.995	** <sup>c</sup>
	14	34.00	SW1321	94.03	** <sup>c</sup>
	18	19.00	SW787	85.79	*
MET	9	67.00	SW2571	81.97	*
	17	35.80	SW2441	85.12	*

# Fine mapping program

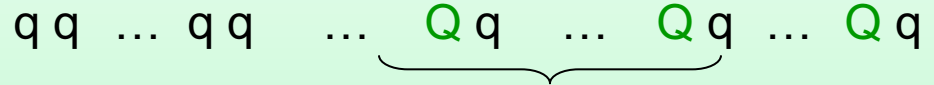
- > 3 QTL Virulence of melanoma
- Region interacting with MC1R
- Variability between F1 families
- Fine mapping of SSC1 region 75 cM



Marker info



Phenotype info  
Ill/not ill



Sélection of 1 or 2 males developing M

100 BC3, new markers

... up to < 2cM



# Large scale QTL mapping : the BIOMARK project

- ❑ “A thorough evaluation of several QTL segregating in commercial pig lines for fine QTL mapping and the setting up of MAS”
- ❑ Objectives :
  - Use of data from as many well-characterized (for the QTL investigated) families from a maximum number of different pig populations for the fine mapping of 6 QTL regions
  - Confirm QTL effects in commercial pig populations
- ❑ Methods
  - Investigated haplotype diversity and effects in ~ 5000 animals
  - Production of new families from commercial populations
    - 15 sire families with progenies of ~100 pigs
    - Measured for a large number of traits
    - Design also used to test known genes / markers polymorphisms

# Investigating linkage disequilibrium in pigs: the DELISUS project

## □ Objectives :

- Investigate linkage disequilibrium in pig populations
- Association studies for a large number of traits (growth, carcass, meat quality, immunology)

## □ Methods

- Sample small families 1 sire/3 dams/3 offspring in several pig populations
- Set of >10,000 markers

# Conclusion

- ❑ Interest of different QTL mapping programs to identify chromosomal regions of interest
- ❑ Fine mapping have been successful to reduce mapping interval, but not yet to identify causative mutations
- ❑ Increased efficiency expected from new technologies (SNP) and large scale analyses of various populations
- ❑ Some applications have been developed (selection of BC MS x LW boars, synthetic MS x LW populations)
- ❑ Development of larger MAS programs in the near future

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