

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

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#### ▶ To cite this version:

Jean Pierre Bidanel. Current QTL (fine) mapping programs in French pig populations. INRA - ISU Symposium, Mar 2007, Paris, France. hal-03364906

#### HAL Id: hal-03364906 https://hal.inrae.fr/hal-03364906

Submitted on 5 Oct 2021

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#### INRA – ISU symposium, March 19-21, 2007

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

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- 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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#### 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)

- 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

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Mapping meat quality QTL in Duroc x Large White F2 pigs

- Duroc x Large White F2 pigs
  - $\sim 500$  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,...)

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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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## Recombinant backcross progeny test (RBCPT) Chromosomal regions investigated





# Fine mapping of QTL on SSC7 using RBCPT





INRA – ISU Symposium 19-21/3/2007 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)

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(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

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#### Mapping results



	<u> </u>	Trait	SSC	Position (cM)	Nearest Marker	Test Statistics	$\mathbf{P}^{\mathbf{a}}$
Development	PAB	РАВ	12	95.60	SWC23	106.23	***b
		LT	2	17.90	SW2623	64.17	*
:	LT		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	***b
•	NI	<	14	98.00	SW2515	81.62	**C
		NL	3	42.00	SW487	81.62	*
Establishment			7	49.00	LRA1	82.28	*
Lotablionment	NMA	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	***p
•			17	44.80	SW2441	111.02	***p
¥	CI	CI	1	85.00	SW1020	93.88	*
•			6	108.50	S0299	88.96	*
		<	13	71.00	SW520	98.45	**
Evolution			17	52.80	SW1920	86.15	*
	ULC	ULC	2	25.90	SWR783	87.03	*
			4	4.00	S0227	98.08	** <sup>C</sup>
			7	73.00	S0102	86.76	*
	<b>N</b>		8	60.00	SW1070	84.97	*
			10	42.00	S0351	126.34	***
			12	95.60	SWC23	94.995	***
			14	34.00	SW1321	94.03	**
			18	19.00	SW787	85.79	*
		MET	9	67.00	SW2571	81.97	*
	N MET		17	35.80	SW2441	85.12	*

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## 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

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# Investigating linkage disequilibrium in pigs: the DELISUS project

#### Objectives :

- Investigate linkage disequilibrium in pig pipulations
- 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





- 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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# Acknowledgements

- Labs / people involved
- (1) SGQA : J.P. Bidanel, H. Gilbert, C. Larzul, M.P. Sanchez, T. Tribout
- (2) LGC : D. Milan, J. Riquet, N. Iannuccelli, A. Robic
- (3) LREG : S. Vincent-Naulleau, E. Bourneuf, P. Chardon, C. Rogel-Gaillard
- (4) Experimental units of GEPA, Bourges, Le Rheu

## Projects funded by:

- National Research Agency
- European Union (SABRE)
- Ministry of Agriculture
- National league against cancer
- Genopole Toulouse
- INRA Department of Animal Genetics

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