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Quantitative trait loci for chronic respiratory diseases and immune traits in Landrace purebred swine

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Objectives

The objective of this study was to identify the quantitative trait loci (QTL) for the lesion score of chronic respiratory disease and immune traits in the population of Landrace purebred swine.

Materials & Methods

Animals

About 1,300 Landrace purebred pigs were used.

This population had been selected over 5 generations at the Miyagi Prefecture Animal Industry Experiment Station. The selection traits were meat production (daily gain from 30 to 105kg of body weight, backfat thickness), litter size, and the lesion score of Mycoplasmal pneumonia of swine in the lung.

Trait information

The lesion score were measured from about 600 pigs after slaughter (see Fig 1.). Immune traits were measured from peripheral blood collected from about 1,300 pigs at age 7wk and at 105 kg body weight (see Table 1.). Some phenotypic values were log-transformed to approximate the normal distribution.

Markers

99 microsatellite markers covering all autosome were genotyped on their animals.
The average distance between markers on the sex averaged map was 23.75 cM.

Statistical analysis

1. The effect sex, environments and generations were estimated ; phenotypic data were corrected using these effects.
2. The IBD scores were estimated with the corrected data using MCMC method with LOKI software.
3. The variance component and LOD score were estimated using SOLAR program.

Results

Table 2 shows the LOD score and QTL position.
We detected 7 significant QTL and 10 putative QTL.
I'd like to mention 3 points in our results.

First of all, to our knowledge, we first reported QTL for the mycoplasma lesion score on Sus Scrofa Chromosome (SSC) 2 (see Fig2.) , and QTL for PA on SSC14 and 5.

Next, the QTL for White Blood Cell at 7weeks and 105kg on SSC2 were detected (see Fig2.). These QTL were detected in a region close to the QTL for white blood cell that was previously identified in pigs (Yang et al. 2008).

Finally, we detected the QTL for Cortisol level at 105kg on SSC7.This QTL was previously identified in pigs (Désautés et al. 2002) and that region harbors the corticosteroid binding globulin gene (Ousova et al. 2004). Therefore, we think the candidate gene of this QTL is CBG gene.

Other candidate genes are currently under investigation.

Conclusion

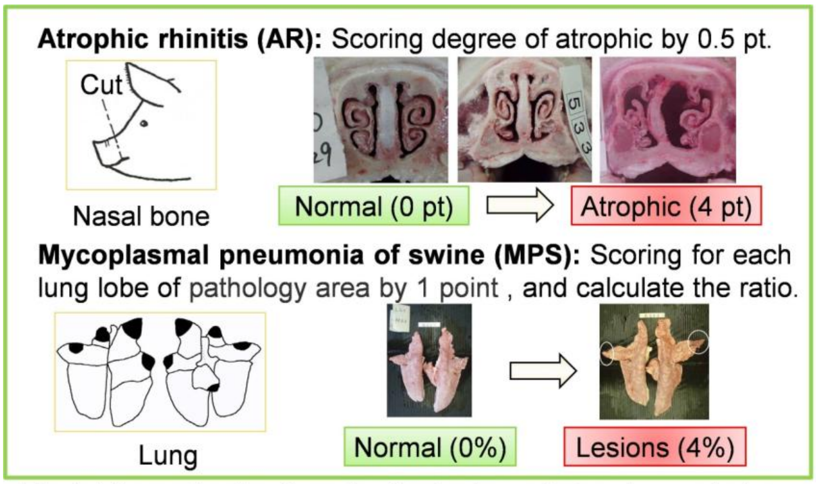
In conclusion , we detected a total of seven teen QTL for the lesion score of chronic respiratory disease and immune traits in the population of Landrace purebred swine. The results not only confirmed some of the previous reports, but also identified some novel QTL. Moreover , it is the first time that QTL for the mycoplasma lesion score and Pagocytic activity.

References

Yang, S.; Ren, J.; Yan, X.; Huang, X.; Zou, Z.; Zhang, Z.; Yang, B.; Huang, L. (2008)
Quantitative trait loci for porcine white blood cells and platelet-related traits in a White Duroc × Erhualian F2 resource population *Animal Genetics, Volume 40, Number 3, June 2009 , pp. 273-278(6)*

C. Désautés, J. P. Bidanel, D. Milan, N. Iannuccelli, Y. Amigues, F. Bourgeois, J. C. Caritez, C. Renard, C. Chevalet and P. Mormède, (2002)
Genetic linkage mapping of quantitative trait loci for behavioral and neuroendocrine stress response traits in pigs *J. Anim. Sci. 2002. 80:2276-2285*

Olga Ousova, Véronique Guyonnet-Duperat, Nathalie Iannuccelli, Jean-Pierre Bidanel, Denis Milan, Carine Genêt, Bastien Llamas, Martine Yerle, Joël Gellin, Patrick Chardon, Agnès Emptoz-Bonneton, Michel Pugeat, Pierre Mormède and Marie-Pierre Moisan
Corticosteroid Binding Globulin: A New Target for Cortisol-Driven Obesity *Molecular Endocrinology 18 (7): 1687-1696*



Atrophic rhinitis (AR): Scoring degree of atrophic by 0.5 pt.

Mycoplasmal pneumonia of swine (MPS): Scoring for each lung lobe of pathology area by 1 point , and calculate the ratio.

Fig 1. The methods of scoring the lesions of chronic respiratory.

Table 1. Number, Means and SD for the lesion score and immune traits

Traits	Units	7wk			105kg		
		N	Mean	SD	N	Mean	SD
AR	pt		—		639	0.94	0.83
MPS	%		—		630	2.90	5.30
PA	10^6RLU	1332	4.55	3.10	1318	4.30	3.24
CAPA	OD_{413}	1321	0.37	0.19	1304	0.40	0.23
WBC	no. × 10^3/mL	1311	1.96	0.47	1304	1.87	0.35
RGL	%	1021	0.73	0.33	1060	0.82	0.58
CORT	μg/dL	700	2.50	1.55	1197	1.21	1.07
AP	titres		—		1304	68.8	83.8

AR: atrophic rhinitis score MPS Mycoplasmal pneumonia of swine score,
PA: phagocytic activity CAPA: complement alternative pathway activity
WBC: white blood cell number RGL: ratio of granular leukocyte to lymph cells
CORT: cortisol level AP: antibody production against sheep red blood cell.

Table 2 . The LOD score and QTL position.

Traits	SSC	Position†	LOD score‡	Marker range		h_p^2 §	h_q^2¶
AR	**3**	**69**	**1.57***	**SW902**	**SW2047**	**0.29**	**0.10**
	4	**8**	**1.68***		**SW489**		**0.09**
	6	**78**	**2.02***	**SW2406**	**SW1607**		**0.17**
MPS	**2**	**44**	**3.60****	**SW1650**	**SW240**	**0.23**	**0.20**
	12	**121**	**1.42***	**SWR1802**	**S0106**	**0.23**	**0.12**
PA7wk	**14**	**30**	**2.59****	**SW1125**	**SWC6**	**0.16**	**0.13**
CAPA7wk	**5**	**37**	**1.50***	**SW413**	**SW2425**	**0.10**	**0.11**
	10	**6**	**1.61***	**SW830**	**SW443**		**0.07**
WBC7wk	**2**	**70**	**2.91****	**SW240**	**SW2442**	**0.36**	**0.07**
	4	**68**	**1.59***	**S0175**	**S0214**		**0.04**
	6	**125**	**1.86***	**SW1823**	**SW353**		**0.04**
PA105	**5**	**154**	**2.22****	**S0018**	**SW995**	**0.27**	**0.07**
WBC105	**2**	**71**	**4.09****	**SW240**	**SW2442**	**0.21**	**0.09**
	3	**55**	**2.93****	**SW1443**	**SW902**		**0.06**
	16	**58**	**1.63***	**SWR2080**	**SW2517**		**0.06**
CORT105	**7**	**177**	**3.07****	**S0212**		**0.11**	**0.07**
AP	**9**	**109**	**1.95***	**S0119**	**S0295**	**0.24**	**0.06**

†Map position in Haldane cM

‡Levels of significance(chromosome level: **P=0.01,*P=0.05)

§ Polygene heritability

¶ QTL heritability

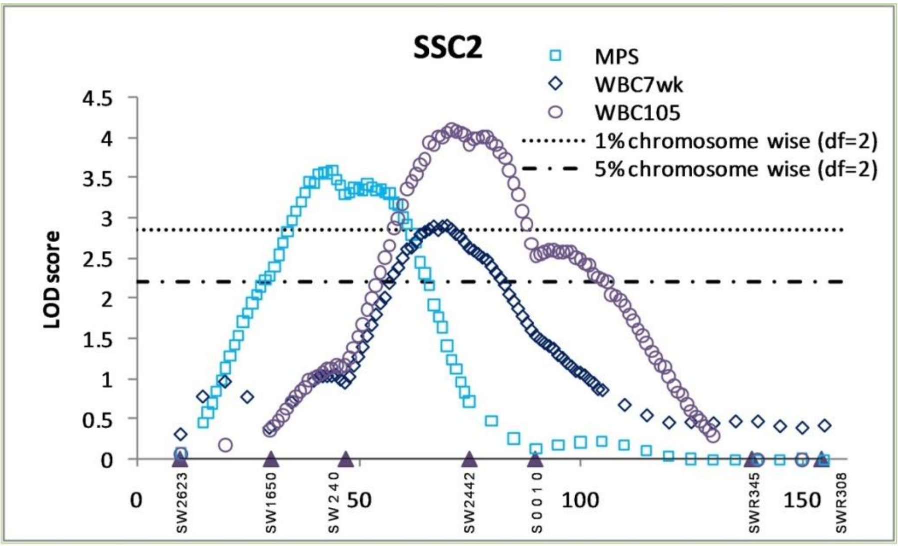


Fig 2. LOD score curves of QTL on SSC2.