Identification of a New QTL For Resistance to *Salmonella* Carrier-State

F. Calenge[*], A. Vignal[†], K. Fève[‡], P. Velge[§] and C. Beaumont[*]

Introduction

Chicken's ability to carry *Salmonella* without displaying disease symptoms, i.e. *Salmonella* carrier-state, leads to an invisible propagation of *Salmonella* in poultry stocks and contributes to human infections through the consumption of contaminated meat or eggs. Using chicken lines more resistant to carrier-state could improve both animal health and food safety. Previous studies identified several QTL for resistance to carrier-state (Tilquin, P., Barrow, P.A., Marly, J. et al. 2005; Calenge, F., Lecerf, F., Demars, J. et al. 2009). Nevertheless, the genetic maps used were incomplete due to a lack of known markers on a great portion of the genome. In order to be more exhaustive and to improve both power and precision of QTL detection, we performed a new genome scan using SNP markers typed on a higher number of animals.

Material and methods

Animals. A first F2 progeny of 185 animals (progeny 1) was derived from the experimental inbred White Leghorn lines N and 6_1 (USDA Avian Disease and Oncology Laboratory, East Lansing, MI) and has been studied previously (Tilquin, P., Barrow, P.A., Marly, J. et al. 2005; Calenge, F., Lecerf, F., Demars, J. et al. 2009). A second, independent $Nx6_1$ F2 progeny of 193 animals was produced in 2007 (progeny 2): 18 F0 males and 20 F0 females were used to produce the F1 progeny, and 6 F1 males and 18 F1 females (3 females per male) were used to produce the 185 F2 animals.

***Salmonella* Enteritidis challenges.** Both progenies were challenged independently using the same protocol of experimental infection. As described by Duchet-Suchaux, M., Léchopier P., Marly, J. et al. (1995) and used in the previous QTL anaysis (Tilquin, P., Barrow, P.A., Marly, J. et al. , 2005), animals were orally infected at one week of age with 5×10^4 bacteria of the same phage type 4 strain 1009 of *S.* Enteritidis. The numbers of colonies forming units (c.f.u.) in caeca were counted five weeks post inoculation. Analyses were achieved after transformation into logarithms of c.f.u.

[*] INRA UR83 Unité de Recherches Avicoles, 37380 Nouzilly, France
[†] INRA Laboratoire de Génétique Cellulaire, Castanet-Tolosan, France
[‡] INRA Laboratoire de Génétique Cellulaire, Castanet-Tolosan, France
[§] INRA UR1282 Infectiologie Animale et Santé Publique, 37380 Nouzilly, France

SNP typing. SNP markers were first tested on F1 males in order to choose a set of informative, segregating SNP. A set of 480 SNP markers was chosen to type the 378 F2 animals. Genotypes were produced using the Illumina GoldenGate technology. Genetic maps were constructed using the CRI-MAP software.

Statistical analyses. The GridQTL software (http://www.gridqtl.org.uk/) was used to detect QTL, using the F2 analysis option, with the progeny as a fixed effect when both progenies were used. QTL were identified in either each progeny independently or in both progenies merged for a common analysis. For each QTL detected, a significance probability threshold at the chromosome level was calculated by permutation analysis. The percentage of phenotypic variation explained by QTL was calculated as a percentage of the difference between the residual sum of squares (RSS) of the reduced model and the full model, divided by the full model RSS.

Results and discussion

Using this new SNP marker set, the genome coverage was much improved compared to previous studies. Chromosomes 1 to 28 were covered (see figure 1), while in the previous genome wide analysis, only 19 chromosomes were covered with more than one marker (Tilquin, P., Barrow, P.A., Marly, J. et al. 2005). This improved coverage led to the identification of a new QTL for resistance to *Salmonella* carrier-state on chromosome 14. This chromosome was not included in previous genetic maps. Furthermore, the use of both progenies in a common analysis greatly improved the power and the precision of QTL detection (Table1, Figure 1). The F-value associated with QTL analysis is much higher when analyzing both progenies together, raising from 6.20 with progeny 2 to 13.51 with joined progenies. Intriguingly, the dominance effect of the QTL is much higher than its additive effect. To our knowledge this is the first report of a QTL or candidate gene related to *Salmonella* resistance on chromosome 14.

Table 1: parameters associated with the QTL identified on chromosome 14. F 5%/ 1%: significance thresholds at 5%/ 1% of F value according to chromosome-wide permutation analysis. a/d: additivity/ dominance. R^2: percentage of phenotypic variation explained by the QTL.

Progeny	Position (cM)	F	LOD	F 5%	F 1%	a	d	R^2
1	80	8.54	3.54	5.66	8.24	-0.106	0.901	8,62
2	72	6.20	2.61	5.43	6.78	-0.166	0.924	6,13
1+2	74	13.51	5.67	5,18	7,81	-0.136	0.940	6,77

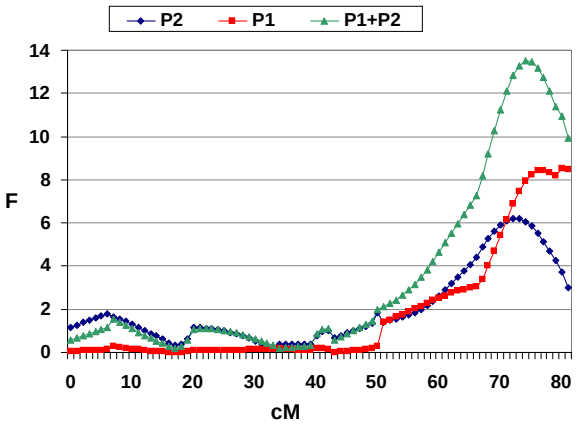

Figure 1. F-curves showing a QTL for *Salmonella* carrier-state resistance on chromosome 14 after F2 GridQTL analysis. P1: progeny 1; P2: progeny 2.

Conclusion

The use of SNP markers allowed a more complete genome scan, which led to the identification of a new QTL for resistance to *Salmonella* carrier-state on chromosome 14. In addition, the use of a larger progeny led to a clear improvement of QTL detection power and accuracy on this chromosome. The interest of this QTL for selection purpose should be tested on commercial chicken lines, as was done previously for other QTL for carrier-state resistance (Calenge, F. Lecerf, F., Demars, J. et al. 2009).

Acknowledgement

The second F2 Nx6 progeny could be produced thanks to the European project EADGENE (European Animal Disease Genomics Network of Excellence for Animal Health and Food Safety) and SNP genotyping was funded by the European project SABRE (sustainable animal breeding).

References

Calenge, F. Lecerf, F., Demars, J. et al (2009). *Animal Genetics*, 40:590-597.

Duchet-Suchaux, M., Léchopier, P., Marly, J. et al (1995). *Avian Diseases* **39:**796-803.

Tilquin, P., Barrow, P.A., Marly, J. *et al.* (2005). *Genetic Selection Evolution*, 37:539-561.