

SELECTING FOR INCREASED OR DECREASED RESISTANCE TO *SALMONELLA* CARRIER STATE IN FOWLS.

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Introduction

In France as in other countries, *Salmonella* remains a major cause of human disease related to food consumption. In one third of cases, the serotype responsible for human food poisoning is *Salmonella enteritidis* (4). Poultry products are the main source of human *Salmonella* infections, mostly because chickens may be asymptomatic carriers (*i.e.* remain contaminated by *Salmonella* for several weeks without showing any symptom that could help to their detection). Both caecal and ovarian *Salmonella* carrier-states may be involved in human contamination. While the latter may result in vertical transmission of *Salmonella* and in yolk contamination, the former is responsible for a horizontal transmission of the bacteria and for human disease through contamination of the egg shell at the oviposition and of the carcass during evisceration. In both cases, the existence of asymptomatic carriers dramatically complicates the prophylaxis of this disease.

Food safety could potentially benefit from an increase in the genetic resistance of fowls to the *Salmonella* carrier-state (*i.e.* a better ability of animals to clear *Salmonella*), which can be measured by the persistency of the bacterial infection after inoculation. To address this question, experimental models of infection were defined in chicks (5) and adult hens (11). Using these models, the heritability of resistance was estimated at 0.20 in young birds (3) and more than 0.35 in laying hens (1). These results show that the *Salmonella* carrier-state is partly genetically controlled and strongly suggested that selection for increased resistance to *Salmonella* colonisation and excretion could be efficient and reduce the risk of foodborne *Salmonella* infection. A selection experiment has therefore been realized for four generations to test the feasibility of such a genetic improvement and obtain genetic models that should be very helpful in understanding the mechanisms of resistance. The goal of this work is to present the first results of this experiment, which are both responses to selection and estimated genetic parameters.

Material and methods

The base population consisted of 79 animals sampled from a layer-type line. A divergent selection on resistance was carried out. Moreover, from the second generation on, breeders from adult and young lines were distinguished *i.e.* two resistant and two susceptible lines have been selected. Chicks were inoculated at one week of age and resistance assessed five weeks later by caecal contamination as in (5). According to the rate of clearance, *Salmonella* was either present in almost all

animals or in a small proportion of them. In the former case, resistance was assessed by the level of contamination and coded in a quantitative trait by the logarithm of the number of c.f.u. per caeca and, in the latter, as an all-or-none trait (*i.e.* presence or absence of *Salmonella*). In adult laying hens, contamination of caeca, spleen, liver and ovary was assessed, as described in (11), and a total of five traits were thus considered, *i.e.* presence/absence of *Salmonella* in each of these four organs as well as presence/absence of the bacteria in either spleen, liver or caeca. The latter was coded "1" if at least one organ was found positive and "0" in the other cases. Selection for or against chicken resistance was performed on the mean genetic value (EBV) for both traits.

As inoculated animals could no more be kept for reproduction, sib-selection has been performed. A total of 3817 animals were measured, among which 1408 at the adult age and 2409 at the younger age. In the latter, resistance could be measured as an all-or-non trait in 690 animals and in a quantitative trait in 1719 chicks. Genetic parameters were estimated using REML and VCE software (10) in one hand, Gibbs Sampling in the other one.

Results

For the lines selected on chicken resistance, no significant difference in level of contamination could be observed. At the opposite, a significant difference (of about 10% in incidence) was observed when presence or absence of *Salmonella* was considered. Clear and significant differences were observed between the lines selected in a divergent way on resistance to the adult carrier-state: percentages of contaminations differed by about 20% for liver, spleen and caeca.

For all traits, significant heritabilities were observed. All of them were higher than 0.20. The ability of chicks to clear *Salmonella* (*i.e.* presence/absence of *Salmonella*) appeared to be genetically independent of the level of contamination. A major and unexpected result was the estimated negative genetic relationships between adult and chick resistance.

Discussion

Indeed, the large and unpredictable variations in *Salmonella* clearance do not facilitate selection at a younger age, especially as level of contamination and presence/absence of *Salmonella* are uncorrelated. One solution could be to slaughter a representative sample of animals at regular intervals in order to find out the relevant *post inoculation* interval at which animals should

be slaughtered and resistance be assessed as an all-or-none trait with an optimal contamination rate (of about 50%), as suggested by Duchet-Suchaux (personal communication). But such a strategy would complicate the organization very much. It was therefore decided to slaughter animals at a given interval and use all available information. In addition to sib-selection and a technical problem at the third generation, this feature probably explains why no difference in level of contamination could be observed yet in spite of favourable heritability coefficients.

Adult selection seems to be, at least until now, more efficient. Further generations should allow us to confirm this result. More importantly, estimated genetic correlations between presence/absence of *Salmonella* in different organs appeared to be positive and of average value, which is favourable for selection : for example increasing resistance to spleen contamination should also result in a decreased ovary contamination. This result is also in favour of considering the global contamination of animal, since it is more precisely assessed and combines several traits, all of which are positively correlated.

All these results confirm that selection for reduced carrier state is possible. It stresses the importance of a precise definition of the trait, *i.e.* of the *Salmonella* strain, the dose to inoculate, the organ to be tested, the interval *post inoculation* and so on, as the genetic control may be strongly dependant of those conditions. In a longer term, it will be very interesting to compare these lines in different conditions or after contamination with different bacterial strains.

Though promising these results may seem, selection for increased resistance would be very difficult to implement since experimental infections, which are both very expensive and time consuming, are required. Identifying the underlying genes could make it possible to alleviate the need of such measures. Indeed, the effects on resistance to *Salmonella* carrier-state of several genes were already demonstrated or suggested (2, 6, 7, 8, 9). Such an experiment can also be used to test their interest in commercial stocks.

Conclusion

This study confirmed that resistance at both ages and in all organs exhibited a genetic background which may profitably be used as an additional mean of prevention of human food poisoning. It also emphasized the importance of the choice of the selection criteria.

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