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Crossbreeding parameters of general immune response traits in White Leghorn chickens

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Abstract

Crossbreeding parameters of immune response traits were estimated from a set of well characterized crossbred populations derived from three chicken lines selected over 12 generations for three different general immune response traits and their F1, F2 and backcrosses. The three traits investigated were the selection criteria from each of the lines, i.e. antibody response to the Newcastle disease virus vaccine 3 weeks after vaccination (ND3), cell-mediated immune response (response to phytohemagglutinin, PHA) and phagocytic activity measured as carbon clearance (CC). Crossbreeding parameters included direct and maternal additive line effects, direct and maternal heterosis as well as direct epistatic recombination loss. They were estimated as linear combinations of genetic group effects estimated using animal model methodology. Significant line differences were obtained for ND3 and, to a lesser extent, CC. They were mainly due to direct effects, maternal effects being significant for none of the 3 traits. Significantly negative direct heterosis effects were also observed for ND3 and CC, but not for PHA. Maternal heterosis effects were not estimated for CC. They were non significant for PHA, and negative and significant (-0.78 ± 0.24**) for ND3. The significant favourable recombination gain estimated for ND3 (3.21 ± 0.88***) indicates that epistatic interactions could be important for this trait.

The present work shows that it was worthwhile to complete second generation crosses to be able to assess to what extent immunity gained by selection is maintained in advanced crossbred generations, and to compare the transmission of immune traits implicated in different aspects of immunity.

Keywords: Selection; Immune response; Chicken; Crossbreeding

1. Introduction

Since it would be hardly feasible to select for resistance against all major pathogens that farm animals may encounter, selecting for general immune response can be a good alternate way to enhance disease resistance (Kjaer, 2007; Mallard et al., 1998; Wilkie and Mallard, 1999) and

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complement vaccination. Yet, immune response pathways are extremely complex so that a large number of different immune response traits can be considered. Several of them have been selected successfully in poultry (e.g. see review by Pinard-van der Laan et al., 1998), raising the question of their combination in crosses between selected lines for building up some complementary immunity. If successful, this crossing approach might be paralleled in intensive poultry production by taking advantage of the two-step crossbreeding design (F1 and F2) used to produce most commercial chickens (Fulton, 2004). The knowledge of crossbreeding parameters for immune response traits, however, is still very limited for most farm animals and poultry in particular, despite early exploratory reviews (Gavora and Spencer, 1983; Warner et al., 1987).

A three-line selection experiment for increased general immune response in the chicken was started in 1994 at INRA, and was focused on three different in vivo immunity-related traits: antibody response, phagocytic activity and T cell-mediated activity. This was done in order to select for one of the components of the immune system in each line, so that both innate and acquired immunity would be implicated in the experiment.

The responses after 12 discrete generations of single-trait within-line selection were significant for all three traits, which were found to be independent (Pinard-van der Laan et al., 1998). This rare set of well characterized lines was a good experimental population to evaluate how genetic variation would be passed on to crossbred generations, in a case-study on transmission of immune response in poultry.

The aim of the present work was to estimate crossbreeding parameters of immune response traits from the INRA lines selected on immune response in order to estimate to what extent immunity gained by selection may be maintained in advanced crossbred generations. For that purpose, average direct additive effects, average maternal effects, direct and maternal heterosis, and recombination loss were estimated.

2. Materials and methods

2.1. Selected lines

A detailed description of the selection experiment was given by Pinard-van der Laan (2002). Briefly, the parental lines were developed by 12 generations of selection in a population derived from a cross between an experimental White Leghorn line segregating for the sex-linked dwarf (*dw*) gene and a commercial Babcock® White Leghorn line. Three immunity-related traits were measured on all birds at each generation, but each line was under selection for one of them only: high antibody response to Newcastle disease virus (HB1 vaccine) 3 weeks after vaccination (ND3) in L1 (ND3-L) at six weeks of age, high cell-mediated immune response using the wing web response to phytohemagglutinin at 9 weeks of age in L2 (PHA-L), high phagocytic activity measured as clearance of carbon at 12 weeks of age in L3 (CC-L), and random selection in L4 (Control). Every year, all birds were hatched in a single batch, and 15 males and 30 females out of 100 candidates per sex and line were chosen for breeding, by within-family mass selection based on individual phenotypic performance. Mating was at random, but full and half-sib matings were prohibited.

2.2. Crossbreeding design

All genetic groups (L1 to L24) produced for this study are listed in Table 1, and the first three columns of this table summarize the design of the experiment. In 2005, 15 males and 30 females from each line (L1 to L4), which were the parents of generation 10 (G10), were also used (1 sire/2 dams) to produce F1 crossbreds by reciprocal crosses between the three selected lines and a contemporary replicate of the control line (L10), with 200 animals per genetic group. F1 individuals from the crosses between L1 (ND3-L) and L2 (PHA-L) as well as purebred breeders of the G10 from these two lines were used to obtain 200 reciprocal F2 (from 15 sires and 30 dams), and 400 BC (from 8 sires and 14 dams per BC type). Two hundred contemporary unselected birds were also produced as a replicate of the control line (L24) at generation 11. F2 and BC generations were not produced for L3, the line selected for carbon clearance due to the unexpected lack of variation of the response in all the F1 progeny groups (Minozzi et al., 2006), possibly because of differences in the ink which was used at that time. A total of 24 genetic groups were produced. The pedigree file contained 10,862 animals, starting with the first 2 generations of random matings before selection started, followed by 12 generations of selection and ending with the first and second generation crosses. Pedigree information of the last five generations of pure line selection was used to estimate the crossbreeding parameters with a mixed linear animal model.

2.3. Flock management

After hatching, all chicks were housed in a three-tier battery of collective cages until the end of the experiment. Each cage housed about 13 animals of the same sex and randomly selected from each progeny group. Artificial light was 16 h/d. The birds were fed a layer diet (2.685 ME/kg and 175 g/kg crude protein) *ad libitum*, with free access to water. Birds were vaccinated against Marek's disease, infectious bronchitis, Gumboro disease, Newcastle disease, avian encephalomyelitis and for avian infectious Rhinotracheitis or Swollen Head Syndrome (SHS) before the start of the experimental immunizations.

2.4. Traits

Antibody response to Newcastle disease vaccine (HB1 vaccine) was measured three weeks after eye drop vaccination, at 6 weeks of age. The measure was based on a hemagglutination