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Stocking density and access to open-air influences feed efficiency in a strain of slow-growing naked neck chicken.

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To limit sanitary risk and maximize the expression of genetic potential, selection of Label Rouge chickens takes place indoors while animals in production are reared with access to outdoors, at lower density and with a less energetic diet. This situation is leading to interactions between genotype and environment that can reduce the effectiveness of selection. Our study thus aimed at estimating the intensity of these interactions on feed efficiency which is an important determinant of the sector's economic profitability and environmental impact.

To do this we reared 600 related broilers (300/group) of a naked neck strain either indoors with a stocking density of 5 chicken/m² (S) or with access to outdoors from 27 days of age and with a stocking density of 3.5 chicken/m² inside and 9 chicken/m² outside (P), mimicking respectively selection and production conditions. The two batches were fed with the same diet, close to the one used in selection. Feed intake (FI), weight gain (WG) and feed conversion ratio (FCR) were recorded individually and daily from 2 weeks to slaughter thanks to an electronic feed station. FCR was first compared in P and S and the intensity of genotype by environment interaction was assessed by estimating the genetic parameters of FCR, WG and FI between 16 and 75 d in each environment.

FCR was systematically higher from 3 weeks of age in P than in S (males: 1.93 ± 0.23 in P, 1.77 ± 0.34 in S; females: 1.90 ± 0.24 in P, 1.77 ± 0.36 in S). This difference was maximal at 37 d, where FCR is 0.43 higher in P than in S and decreased thereafter. Females also had a higher FCR than males from 36 days on. The heritability was comparable between the P and S conditions with regard to FI (P: 0.28 ± 0.16 ; S: 0.26 ± 0.13) but was much higher in P for WG (P: 0.18 ± 0.15 ; S: 0.05 ± 0.05) and FCR (P: 0.42 ± 0.15 ; S: 0.13 ± 0.12). The acquisition of data over a second generation will make it possible to obtain a more precise estimation of heritabilities and genetic correlations between environments to access the genotype-environment interactions.