

Genetic variation with respect to growth, sexual maturity and early egg production of Canadian layer strains

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The magnitude of genetic parameters in a breedable population provides information on the success achievable from its selection program. Two pure lines imported from Ottawa, Canada were mixed for several generations at Central Poultry Research Station, Kundasale to form the base population on which selection was to be carried out to improve growth, sexual maturity and egg production. Randomly selected dams of the parent population were mated to random sires through artificial insemination following hierarchical design. The fertile eggs laid were incubated in pedigree boxes. The resulting 300 chicks were wing banded and managed intensively in individual cages following brooding. *Ad libitum* feeding was practiced following standard feeding recommendations for breeding stocks. Weekly body weights (BWT), age at sexual maturity (ASM) and egg weights of individual birds up to 9 months of age (293 birds) were measured. Full-sib analysis was conducted using unbalanced ANOVA procedure (dams nested within sires) for BWT at different ages, ASM, and average egg weight (EWT), total egg mass (TEM) and total egg number (TEN) at 9 months of age. Additive genetic variance was determined using sire and dam variance components. Finally heritability was estimated using additive and error components of variance for each trait at different growth stages. Heritability estimates for body weight of chicks at day 7, 14, 21, 28 and 56 were 0.78, 0.79, 0.58, 0.99 and 0.64, respectively. The higher heritability estimates were mostly due to control of environmental variation in the breeder flocks. For ASM (days), EWT (g), TEM (kg), and TEN, the heritability estimates were 0.442, 0.776, 0.446, 0.304, respectively. The corresponding phenotypic variance components were 177.71, 149.54, 2.006, 1567.3, respectively. High phenotypic variance components and heritability estimates in all traits indicate that sufficient genetic variability exists in the breedable population to carry out intense selection to improve all traits considered. The sire components of variance were much higher than dam components for all traits, which indicate that more genetic gain can be achieved through relatively higher selection differentials in the sire path.

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