

S51 **Insight in the genetic diversity of wild and domestic Gallus**

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A set of 54 wild birds from the 4 junglefowl species (*Gallus gallus*, *Gallus sonneratii*, *Gallus lafayetii* and *Gallus varius*) sampled across countries and zoological gardens has been genotyped with the chicken 57K Illumina chip. Data from other genotyping projects were pooled to gather a total of 703 chickens, representing experimental lines, local breeds, village chickens and commercial lines. Genotypes (757 birds) were analysed using principal component analysis, clustering methods, and neighbor-joining tree based on euclidian distances. The results showed a decreasing calling rate for *G. sonneratii*, *G. lafayetii* and *G. varius*, consistent with the phylogenetic relationships between *Gallus* species, and the construction of the SNP panel, informative for commercial chickens. These 3 species were clearly separated from all the *G. gallus*, either domestic or wild. One H'Mong chicken from Vietnam was intermingled in the group of wild *Gallus*, which is consistent with previous evidence of introgression of wild *G. gallus* into H'Mong chickens. Apart from this case, wild and domestic *Gallus* clustered in different groups. Clustering of domestic chickens was consistent with their known selection history; two sire broiler lines from different breeders were intermingled, suggesting that a shared reference population could be relevant for genomic selection. Deep sequencing of 18 wild *Gallus* and 18 domestic chickens is scheduled to search for introgressions between wild and domestic birds.

S52 **Genetic variations and regional Genetic contributions in Chicken populations from Europe, Asia and Africa**

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Genetic variations of 113 chicken populations from Africa, Asia, and Europe were studied using 29 microsatellite markers. These populations included three wild chicken populations (RJF) and nine commercial purebred lines for comparison. Allele frequencies, mean number of alleles, heterozygosity, and Wright's fixation indices were estimated to investigate the extent of genetic variability between and within chicken populations from different geographical regions. Phylogenetic network and the degrees of relatedness between chicken populations were judged from molecular data by estimating marker-estimated kinship. Ranking of regional chicken subpopulations were evaluated by computing their contribution to the optimal core set and sequential safe set analyses. High heterozygosity and lower genetic differentiation (FST) were observed in RJF, African and Asian chickens relative to European and Commercial breeds. Higher populations kinship coefficients were corresponded to lower genetic diversity. Asian chicken populations contributed most, followed by African chickens and European breeds contributing least in a core set analysis. Although European breeds have lower genetic contribution to the sequential safe set, yet many populations are required from Europe to the total genetic diversity contribution as they have higher range of genetic differentiation. Attention should be drawn to conservation of some European chicken breeds in maintaining the entire genetic diversity threshold.