

# Review of: "Whole-genome sequencing revealed genetic diversity and selection of Guangxi indigenous chickens"

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This article comprehensively characterized the genome diversity and the selective signatures of indigenous chickens from Guangxi Zhuang Autonomous Region, which is adjacent to the potential chicken domesticated location. The genetic variations uncovered from those indigenous chicken breeds/populations with richness in genetic diversity expand the chicken existing SNP dataset, and genotype imputation especially concerning ancient chicken samples may benefit. Somewhat ambiguously, the authors didn't illustrate that the XYC and the GDC were separately more fat-deposited and smaller compared with SHC, when they compared these two populations with SHCs to identify the selective signals involving fat-deposition and body size. Also, the authors identified a large body of selective signals from Chromosome (Chr) Z in terms of fat-deposition and body size, and thus they claimed the selected genes of fat deposits were located on Chr 12 and Z (Fig. S6). This seems an inappropriate deduction as the huge selective signals identified on Chr Z were probably resulted from its haploid if the 27 SHCs, 17 XYCs and 10 GDCs were not all male ZZ diploid. Actually, the gender information of the samples genome-sequenced was absent in this study. Furthermore, for the selective signals related to body size identified in GDC and SHC, it will be better if the authors could illustrate their highlighted putatively selected genes were not the results of an introgression from commercial broiler chickens (BRA), as a higher proportion of BRA genetic composition could be observed in the large-body-sized SHC compared with GDC (Fig. 3C; K = 5, the best K).