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Research Paper

Genomic Analysis Reveals Strong Signatures of Selection in Guangxi Three-Yellow Chicken in China.

Liao Y, Sun J, Huang Y, Wei F, Mo G, Zellmer L and Liao DJ.

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ABSTRACT: Much like other indigenous domesticated animals, Guangxi Three-yellow chickens (GX-TYC) in China have experienced strong selective pressure, and show specific phenotypic changes in physiology, morphology and behavior. To identify genomic footprints or selection signatures left by artificial selection during domestication of GX-TYC, the whole genomes of 12 GX-TYC hens were sequenced to executed selective sweep analyses and gene functional enrichment analysis (Gene Ontology and Kyoto Encyclopedia of Genes and Genome pathways). A total of 10.13 million single nucleotide polymorphisms and 842,236 insertion/deletion polymorphisms (Indels) were found. Forty-six windows showed a Z score of heterozygosity (ZHp) lower than -5, which potentially were considered to be positively selected regions. Gene annotation identified 55 genes in these regions. Selection signatures were found mainly on the SSC5, SSC8, SSC23 and SSCZ. GO and KEGG analyses revealed that these genes were related to growth, immune responses as well as carbohydrate, lipid and amino acid metabolisms. In addition, two genes, fructose-1,6-bisphosphatase 1 and fructose-1,6-bisphosphatase 2 were enriched into four signaling pathways, three of which are involved in carbohydrate metabolism and insulin signaling. SHC3, FANCC and PTCH1, in combination with FB1 and FBP2, were clustered together in a region of chromosome Z, and thus might have been selected together. The results have uncovered some genetic footprints of chicken domestication, providing not only an important resource for further improvements of fowl breeding, but also a useful framework for future studies on the genetics of domestic chickens as well as on the phenotypic variations and certain diseases of chickens.
Key words: Chicken; Selective sweeps; Single nucleotide polymorphism; Whole genome resequencing

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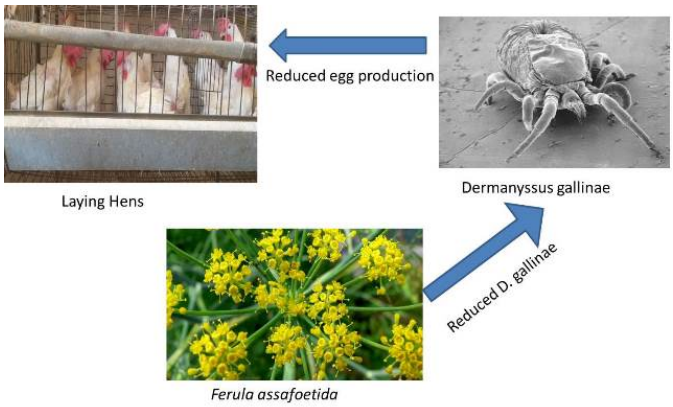

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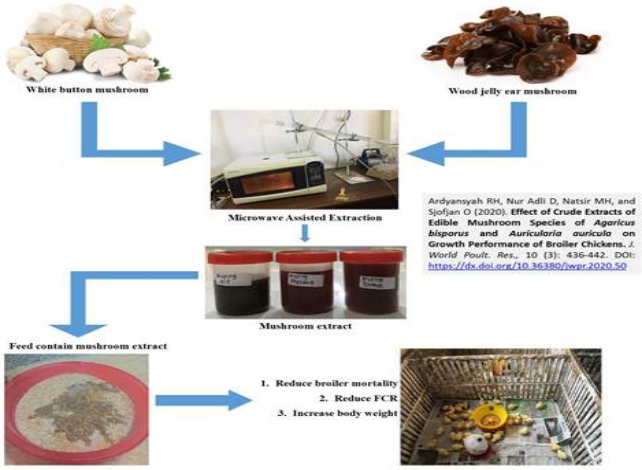

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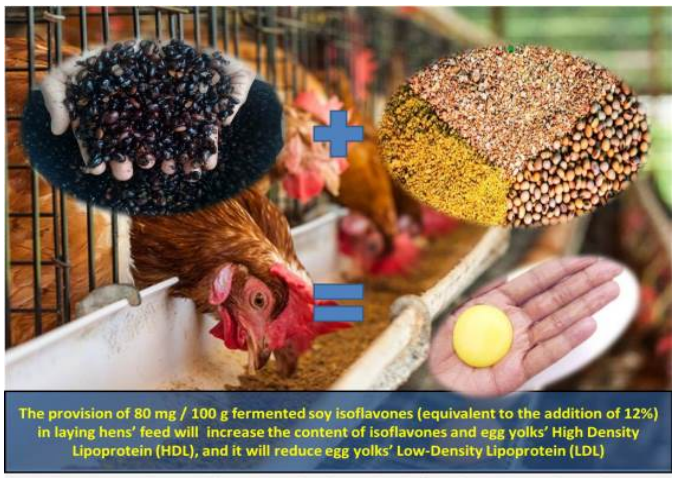

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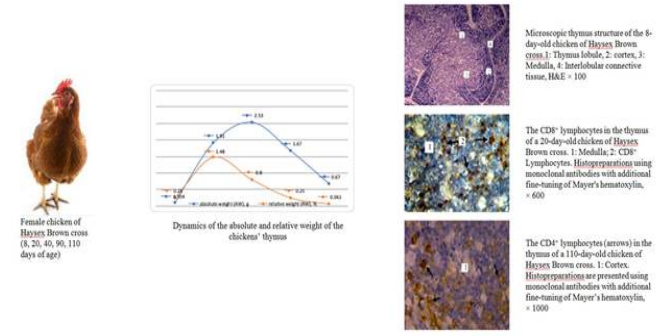

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Production Performances of Indonesian Native Rooster (*Gallus gallus domesticus*) Supplemented with Germinated Mung Bean Sprouts and Acidifiers in the Diet

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Table 1. Nutrient compositions of research treatments

Nutrient composition	A0K0 (control)	A0K1	A1K0	A1K1	A2K0	A2K1	A3K0	A3K1
Energy (kcal/kg)	2809	2818	2802	2807	2800	2800	2798	2795
Crude protein (%)	17.20	17.00	17.00	17.00	17.00	17.00	17.00	17.00
Crude fats (%)	3.20	3.10	3.10	3.00	3.10	2.90	3.10	2.90
Crude fiber (%)	4.40	4.40	4.40	4.40	4.30	4.40	4.30	4.40
Ca (%)	0.90	0.90	0.90	8.00	0.80	0.80	0.70	0.70
P (%)	0.50	0.40	0.40	0.40	0.40	0.40	0.40	0.40

Description: A0K0 (control) = 0% mung bean sprout and 0% acidifiers; A0K1 = 1.0% mung bean sprout and 0% acidifiers; A1K0 = 0% mung bean sprout and 0.4% acidifiers; A1K1 = 1.0% mung bean sprout and 0.4% acidifiers; A2K0 = 0% mung bean sprout and 0.8% acidifiers; A2K1 = 1.0% mung bean sprout and 0.8% acidifiers; A3K0 = 0% mung bean sprout and 1.2% acidifiers; A3K1 = 1.0% mung bean sprout and 1.2% acidifiers.

Table 2. Daily feed consumption and feed conversion of the research data

Treatments	Daily intake (g/head)	FCR
A0K0 (Control)	91.75 ± 4.69	1.16 ± 0.06
A0K1	87.56 ± 3.46	1.23 ± 0.13
A1K0	94.11 ± 2.47	1.17 ± 0.11
A1K1	91.49 ± 6.65	1.17 ± 0.15
A2K0	94.14 ± 1.37	1.22 ± 0.03
A2K1	92.85 ± 0.92	1.22 ± 0.03
A3K0	93.06 ± 0.82	1.15 ± 0.10
A3K1	91.94 ± 1.11	1.14 ± 0.06

Table 3. Bodyweight and average daily gain of the research data

Treatments	Bodyweight (g)	Average daily gain (g/day)
A0K0 (control)	2.380 ± 228.11	170 ± 65.28
A0K1	2.137 ± 136.52	275 ± 54.79
A1K0	2.425 ± 294.07	260 ± 65.19
A1K1	2.348 ± 138.12	284 ± 115.68
A2K0	2.315 ± 97.34	228 ± 12.12
A2K1	2.281 ± 32.59	259 ± 45.13
A3K0	2.446 ± 198.14	219 ± 26.08
A3K1	2.434 ± 155.28	305 ± 54.93

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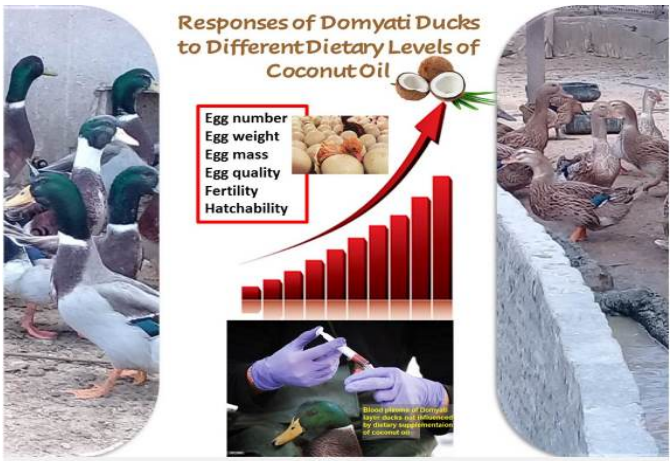

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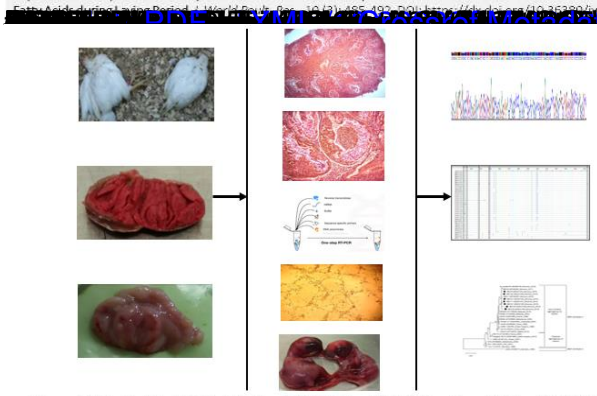

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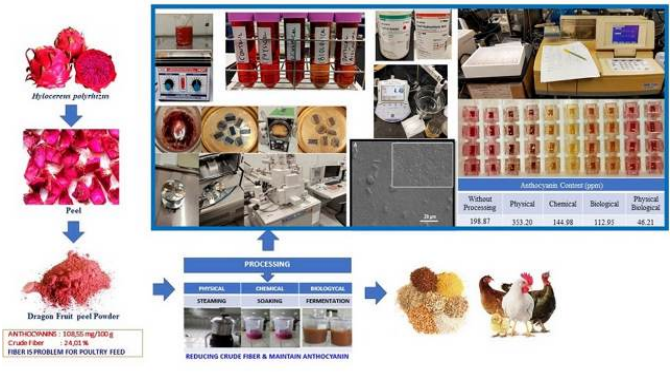

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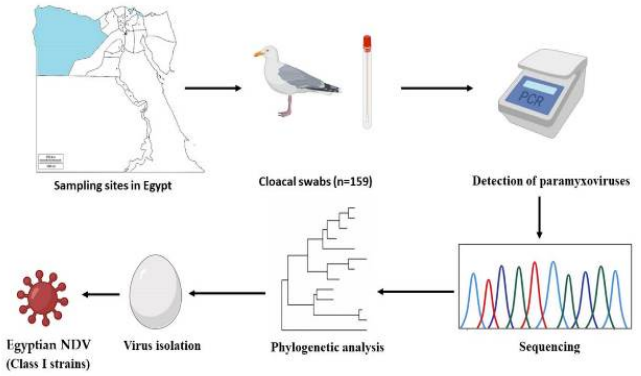

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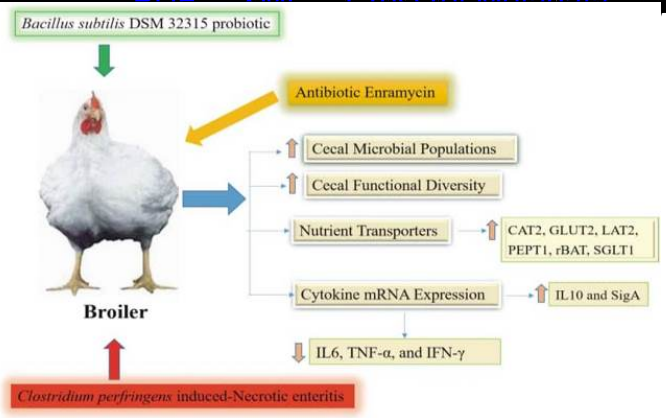

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