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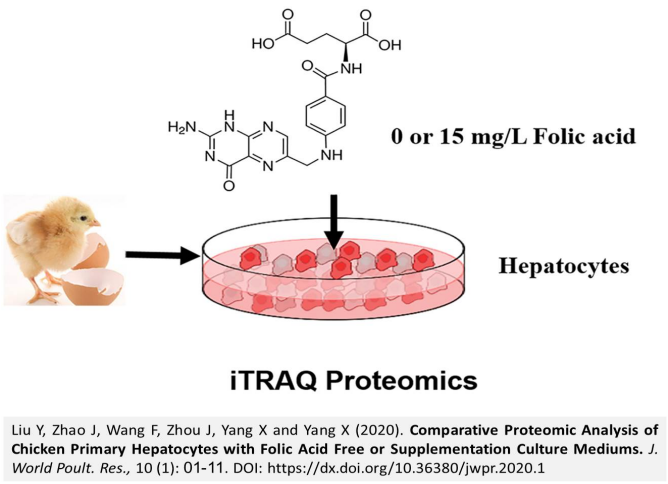

Liu Y, Zhao J, Wang F, Zhou J, Yang X and Yang X (2020). **Comparative Proteomic Analysis of Chicken Primary Hepatocytes with Folic Acid Free or Supplementation Culture Mediums.** *J. World Poult. Res.*, 10 (1): 01-11. DOI: https://dx.doi.org/10.36380/jwpr.2020.1

Research Paper

Comparative Proteomic Analysis of Chicken Primary Hepatocytes with Folic Acid Free or Supplementation Culture Mediums.

Liu Y, Zhao J, Wang F, Zhou J, Yang X and Yang X.

J. World Poult. Res. 10(1): 01-11, 2020; pii: S2322455X2000001-10

DOI: https://dx.doi.org/10.36380/jwpr.2020.1

ABSTRACT: Folic acid had been reported to develop much metabolic regulation function in animals and human beings due to its roles in one carbon metabolism. The current study was conducted to explore folic acid regulation function in primary chicken hepatocytes via supplement and deprivation culture models based on proteomic analysis. Results have shown that folic acid supplement significantly increased intracellular folic acid, 5-Me-THF and SAM contents when compared with folic acid free group ($P < 0.05$). Whereas, there was no difference about genome 5mC levels and DNMTs mRNA expression between these two groups. Proteomic analysis found 85 differential expressed proteins with 35 down and 50 up regulation. COG and KEGG pathway analysis revealed that amino acid metabolism, carbohydrate metabolism and antioxidant function were affected by folic acid. Posttranslational modification, protein turnover, chaperones and transcription were gathered by COG analysis in relative high proportion. PRMT7 and ARID4B which were associated with histone methylation were up-regulated in the folic acid supplement group, suggesting that folic acid was likely to take part in metabolism regulation of hepatocytes via histone methylation manner in the study. In conclusion, proteomic analysis found 85 differential expressed proteins in hepatocytes with folic acid free and supplementation medium. Folic acid might be involved in amino acid and carbohydrate metabolism and oxidation resistance by its epigenetic modifications functions. Our study also provided fundamental differential protein profiles mediated by folic acid, which can facilitate the understanding of folic acid regulation function in hepatic metabolism.
Key words: Folic acid, Histone methylation, Primary chicken hepatocytes, Proteomics

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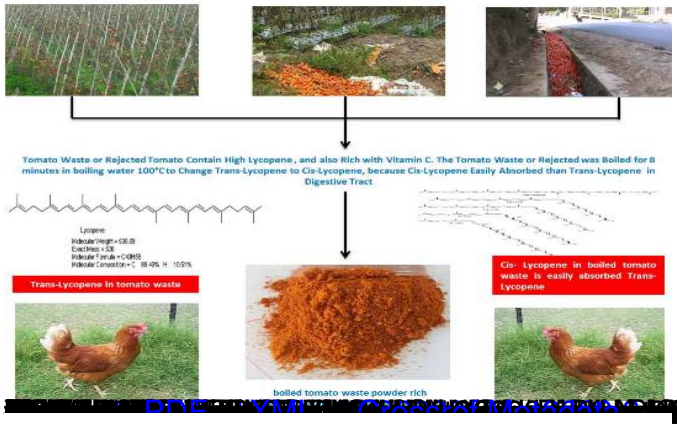
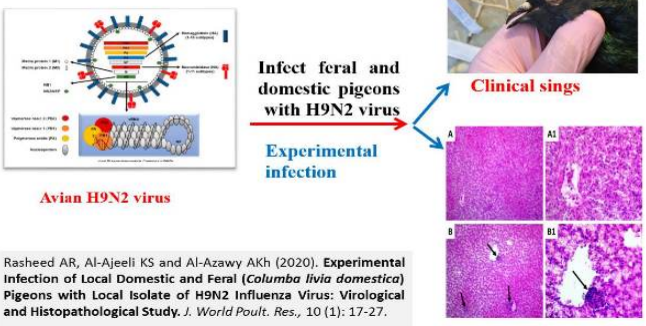


Experimental Infection of Local Domestic and Feral (Columba livia domestica) Pigeons with Local Isolate of H9N2 Influenza Virus: Virological and Histopathological Study



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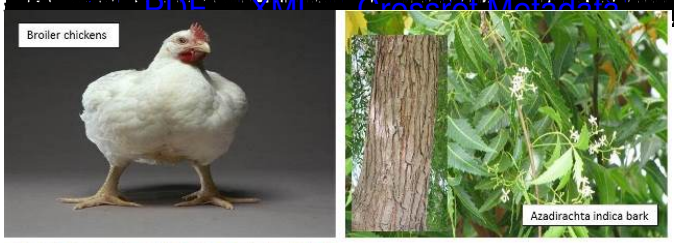

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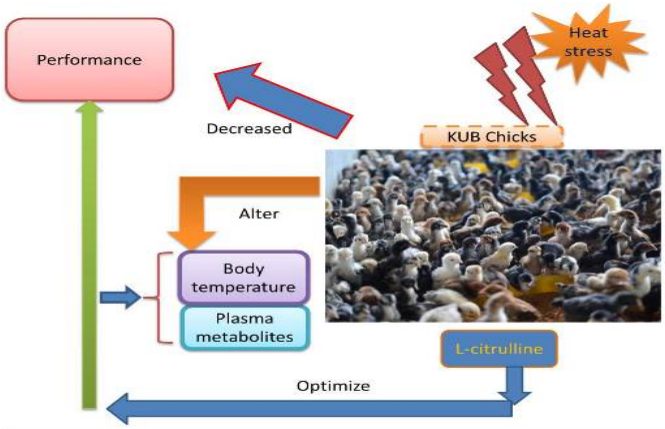

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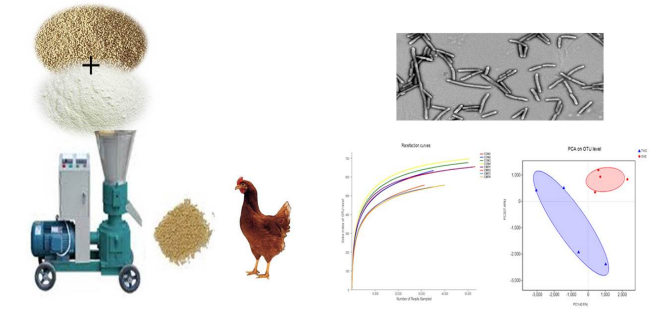

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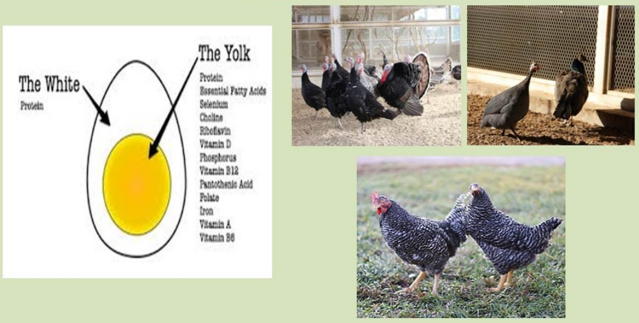

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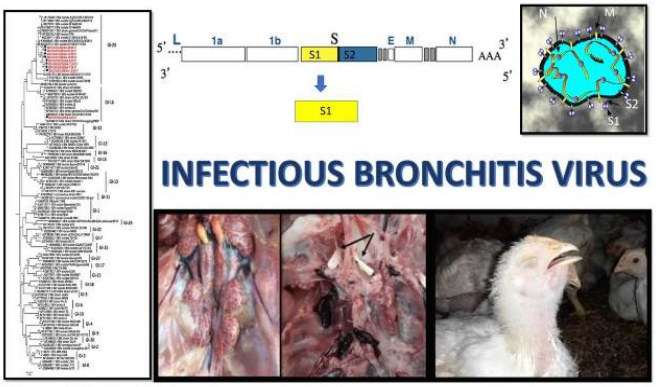

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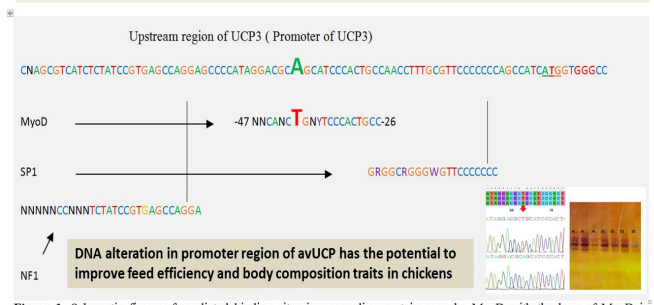

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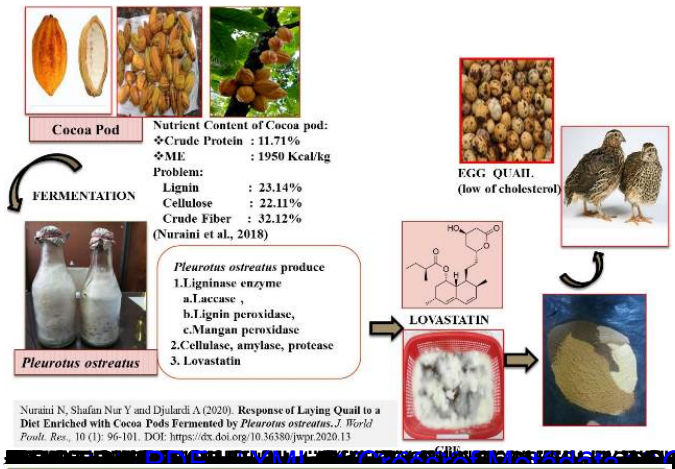
Figure 3. Schematic figure of predicted binding sites in uncoupling protein gene by MyoD with the logo of MyoD in Bioinformatics analysis. UCP3: Uncoupling protein3; SP1: Specificity Protein 1; MyoD: Myoblast determination protein; NF1: Nuclear factor 1



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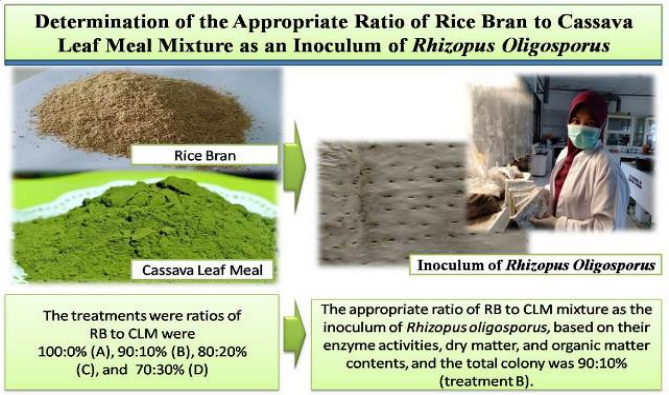

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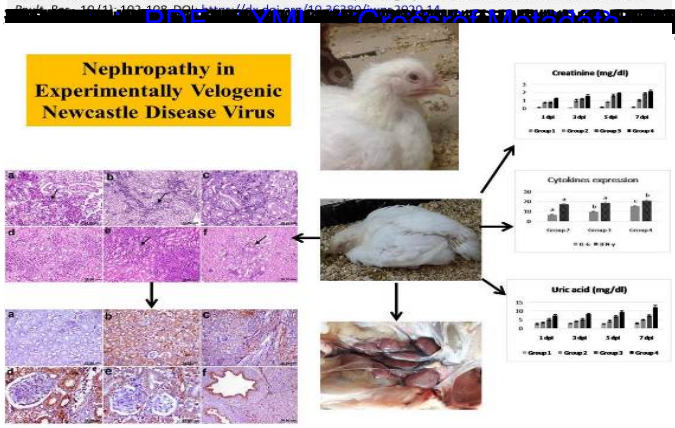

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