

Poultry processing plant waste disposal, utilization of rendered products as protein source for livestock production

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Without the rendering industry, the accumulation of unprocessed animal; India's animal wealth is huge in terms of its population of cattle (204.5 million), buffaloes (98.59 million), poultry (800 million), sheep (64.99 million), goats (125.3 million) and pigs (14.2 million) as per world estimates 2008. Compared with the rest of the livestock sector the poultry industry in India is more scientific; it is well organized and progressing towards modernization. The Indian poultry industries success story is uniquely exceptional. The utilization and disposal of product specific waste is difficult, due to its inadequate biological stability, potentially pathogenic nature, high water content, potential for rapid auto oxidation and high level of enzymatic activity. On a global perspective, rendering provides an important service to society and the animal feeding industries by processing approximately 60 million tonnes per year of animal byproducts derived from the meat and animal production industries. During slaughter and processing, between 33 and 43 percent by weight of the live animal is removed and discarded as inedible waste. We conducted a study to detect the quality and chemical composition of poultry rendered products feather meal, offal meal, blood meal and poultry by-product meal.

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Effect of TLR6-5 gene on different economic traits along with its polymorphism, sequencing and phylogenetic analysis in swine

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The current study was proposed to see the effect of TLR6 gene on different selective economic traits (Growth+Reproductive traits) along with polymorphism, sequence and phylogenetic study of TLR6 gene in *Sus scrofa*. For it nine primers were taken. DNA was extracted from 48 animals at R.V.C., Pig farm belonging to three genetic groups namely Tamworth, Desi and T&D were subjected to SSCP. The result after analysis with SPAB was sent for sequencing at Xcleris. Sequencing result was studied with DNASTAR and further used for phylogenetic studies using BLAST and NCBI. A total of six growth traits namely body weight at 0-day, 7-day, 14-day, 28-day, 42-day and 56-day and reproductive traits namely Litter size at birth and weaning and litter weight at birth and weaning. The 5th primer with forward and reverse base sequence as 5' GTCCTCAGGTACCAAGCACA 3' and 3'TGGAAAGGCTGCTAAAGGAA5' respectively has four haplotypes namely A, B, C and D. In Desi, Tamworth and T&D, Haplotypes A, A&C and D had the highest value of 57.14%, 35.71 and 60.00 respectively. The population means were observed to be 09.378±00.7323, 10.945±00.8840 kg, 09.030±00.5850 and 81.275±6.7156, 01.178±00.086, 01.689±00.3480, 02.950±00.5387, 04.057±00.5821, 05.976±00.5881 & 06.935±00.9902 kg for litter size at birth, litter weight at birth, litter size at weaning, litter weight at weaning, body weight at birth, body weight at 7-day, body weight at 14-day, body weight at 42-day and body weight at 56-day respectively. Haplotypes for primer-5 (TLR6-5) had non-significant effect on all the traits. The nucleotide sequence alignments were carried out using alignment tools, viz., Clustal W (DNA star Inc. USA) and BLAST to reveal single base variations. With respect to TLR 6-5 gene fragment, phylogenetic studies showed the genetic distance among the different species of animals with reference sequence ICI/40627 of TLR6-5 gene fragment from which TLR6 mRNA and TLR 6, TLR 1 and TLR10 seems to have evolved. Further based on this sequence *Sus scrofa* is equidistant from other domestic animals with respect to phylogeny. These studies could be used for MAS based on disease resistance. The research coupled with further work on the same topic could be crucial for breeding, genetics as well as evolutionary studies.

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