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# Molecular and conventional bacteriological techniques for identification of some bacterial pathogens associated with swollen head syndrome in broilers

**A Thesis**

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# List of abbreviations

| | |
|---|---|
| ***SHS*** | Swollen head syndrome |
| ***AMC*** | Amoxycillin/Clavulanic acid |
| ***APEC*** | Avian pathogenic *Escherichia coli* |
| ***ATM*** | Aztreonam |
| ***CAZ*** | Ceftazidime |
| ***CIP*** | Ciprofloxacin |
| ***CLSI*** | Clinical laboratory standardized index |
| ***CN*** | Gentamycin |
| ***CR*** | Congo Red |
| ***CRO*** | Ceftriaxone |
| ***CT*** | Colistin sulphate |
| ***CTX*** | Cefotaxime |
| ***DNA*** | Deoxy Nucleic Acid. |
| ***DO*** | Doxycycline |
| ***DW*** | Distilled Water |
| ***E. coli*** | *Escherichia Coli* |
| ***ExPEC*** | Extra intestinal pathogenic *E.coli* |
| ***FEP*** | Cefepime |
| ***FOX*** | Cefoxitin |
| ***G*** | Grams |
| ***GLU*** | Glucose. |
| ***$H_2S$*** | Hydrogen Sulfide. |
| ***HA*** | Haemagglutination |
| ***HCL*** | Hydrochloric acid. |
| ***IND*** | Indole. |
| ***INT.*** | Integron |
| ***MDR*** | Multiple Drug Resistant |
| ***MR*** | Methyl Red |
| ***Mg*** | Milligrame. |
| ***No.*** | Number |
| ***PBS*** | Phosphate Bffered Saline |
| ***PCR*** | Polymerase Chain Reaction. |
| ***PD*** | Pullorum disease |
| ***Spp*** | Species |
| ***SXT*** | Sulphamethoxazole/Trimethoprime |
| ***TSI*** | Triple Sugar Iron |
| ***VP*** | Voges Proskaeur |
| **AR** | Antimicrobial resistance |

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# Summery

Swollen head syndrome is considered to be an important avian disease in various countries. This syndrome has caused considerable losses in the avian industry because it is responsible for mortality of 3to 4% of the birds and for reduction of 2 to 3 % at the egg production. In the present study, the prevalence of swollen head syndrome was studied in 500 broiler chickens, of which 100 were suffering from swollen head syndrome with an incidence of 200%. Identification of the causative bacterial agents was conducted focusing on *E. coli*, *pseudomonas*, *klebsiella* and *Salmonellae* isolates. The bacteriological examination revealed that out of 100 samples, 92 bacterial isolates were recovered (92%), of which 72 samples (72%) had single bacterial isolates while 20 samples (20%) had mixed two bacterial isolates. Among the recovered isolates, *E. coli* was the most prevalent isolate (n=80; 71.4%) followed by *Pseudomonas* (n=24; 21.4%), *Salmonella* spp. (n=4; 3.6%) and *Klebsiella* species (n=4; 3.6%). Antibiogram of *E. coli* isolates showed high sensitivity against fosfomycine while they were highly resistant to the other antimicrobials. *Pseudomonas* isolates showed a high sensitivity against aztreonam while they were highly resistant to the other antimicrobials. Also, *Klebsiella* isolates showed a high sensitivity against fosfomycine while they were highly resistant to the other antimicrobials. Meanwhile, *Salmonella* isolates showed high sensitivity to aztreonam while they were highly resistant to the other antimicrobials. All bacterial isolates in this study (*E. coli*, *Pseudomonas*, *Klebsiella* and *Salmonellae* isolates) showed MDR for three or more antimicrobials of different categories. PCR was applied on 7 MDR *E. coli* isolates to detect 5 resistance-associated genes (*qnr*A (0%), *qnr*B (0%), *bla*TEM (100%), *bla*SHV (28.6%) and *Tet*A(A) (100%)), Also 2 virulence-associated

genes (*iss* (100%) and CFAI (0%)) and pathotyping genes (*chu*A (100%) and *Tsp*E4C2 (57.14%)). PCR was applied on 4 MDR *Pseudomonas* isolates to detect 5 resistance-associated genes (*qnr*A (0%), *qnr*B (0%), *bla*TEM (100%), *bla*SHV(0%) and *Tet*A(A) (100%)), 5 virulence-associated genes (*mex*R (100%), *arr* (50%), *tox*A (100%), *phz*M (0%) and *ecf*X (100%)). PCR was applied on 2 MDR *klebsiella* isolates to detect 5 resistance-associated genes (*qnr*A (0%), *qnr*B (0%), *bla*TEM (100%), *bla*SHV (50%) and *Tet*A(A) (100%)), 3 virulence-associated genes (*iut*A (100%), *fim*H and *rmp*A were 0%). PCR was applied on 2 MDR *salmonella* isolates to detect 5 resistance-associated genes (*qnr*A and *qnr*B were 0%, *bla*TEM (100%), *bla*SHV and *Tet*A (A) (100%)), 5 virulence-associated genes (*pef*A (0%), *hil*A (100%), *omp*A (100%), *fim*H (0%) and *adr*A (100%)).

In conclusion, the data of the present study showed that new serovars of Salmonella were recovered from poultry. These *Salmonella* serovars were found to harbor many virulence encoding genes. These serovars expressed variable degrees of resistance to antibiotics and this requires regular monitoring of the isolated *Salmonella* for their antimicrobial susceptibility especially that of zoonotic importance.