Characterization of Avian Pathogenic Escherichia coli Associated with Complicated Chronic Respiratory Disease

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Abstract

Among other factors, infectious diseases are the real threat to the poultry development. Of the various infectious microorganisms Escherichia coli and Mycoplasma are of prime importance. These microorganisms persist for reasonably long periods in the flocks and there by lead to high economic losses through mortality, loss of weight and production. E. coli cannot readily infect the air sacs unless they are previously invaded by Mycoplasma gallisepticum alone or in combination of either infectious bronchitis or Newcastle disease virus. The present research was therefore designed to study the susceptibility of Mycoplasma infected birds towards E. coli as the average mortality rates observed in the occurrence of CRD as an individual disease was 8 per cent, whereas E. coli combined outbreaks recorded 15 per cent. In the present study, a total of 255 clinical specimens which included choanal swabs (244) from live and trachea (11) from dead birds affected with Mycoplasmosis were processed. Out of total 68 (12.15%) E. coli isolates recovered, 31 (45.58%) were associated with Mycoplasmosis and were recovered from choanal swabs. Recovered E. coli isolates subjected to AST by using different antibiotics like ampicillin (AMP), oxytetracycline (O), tylosine (TL), erythromycin (E), enrofloxacin (EX), norfloxac (NX) and gentamicin (GEN). Multiple drug resistance was observed in all isolates of E. coli. Conventional characterization of E. coli isolates revealed, 12 (41.37%) isolates haemolytic, 26 (83.87%) invasive E. coli and 7 (22.58%) isolates positive for haemagglutination, respectively. In cvi gene PCR, 6 (19.32%) isolates yielded an amplification product of ~1181 bp. Out of 20 isolates tested which are resistant to ampicillin, 3 (15%) and 17 (85%) isolates yielded a product of ~403 bp in blaTEM gene specific PCR using chromosomal and plasmid DNA, respectively. Plasmid profiling of the Escherichia coli isolates detected four different sizes of plasmids (~700 bp, ~1100bp, ~1650bp and >12kbp) with presence of >12kbp plasmid in all the isolates. The plasmids were distributed at random in the isolated E. coli strains. Correlation of presence of blaTEM gene and plasmid profile was observed with resistance to ampicillin seen in AST.

Keywords
Cultural isolation and identification, E. coli, Antibiotic sensitivity test, Congo red binding assay, Haemolysis assay, Haemagglutination test, PCR, Plasmid profiling.

Introduction

Complicated chronic respiratory disease is an infectious disease of birds causing serious economic losses to the poultry industry. CRD is usually caused by Escherichia coli in association with poultry Mycoplasmosis (Nagalakshmi et al., 2013 and Kamble, 2014).
Cultural isolation and identification of Escherichia coli associated with Mycoplasmosis is of crucial importance since it provides useful information on epidemiology of the disease and facilitates tracing the origins of pathogen. Severe airsacculitis characterized by appearance of large masses of caseous exudate in the air sacs and egg peritonitis were observed in combined infection with E. coli, whereas uncomplicated CRD affected birds showed milder airsacculitis (Sivaseelan and Balasubramaniam, 2013).

Now a day, the molecular techniques include various types of PCR assays targeting different virulence genes are widely employed for detection of pathogenic Escherichia coli and plasmid profiling for to know the gene involved in antibiotic resistance among Escherichia coli. Inspite of being such an important disease; there is no such work carried out on this aspect of complicated chronic respiratory disease. Therefore, present investigation was designed for characterization of Escherichia coli associated with poultry Mycoplasmosis which can help in prevention and control of disease and thereby reducing the economic losses.

Materials and Methods

Materials

Clinical specimens: Choanal swabs and tracheal tissue

Culture media: MacConkey agar and Eosin methylene blue agar (HiMedia) used for isolation of E. coli, Congo red agar prepared by Trypticase soy agar supplemented with 0.003% Congo red dye and 0.15% bile salt was used for determination of invasive E. coli while blood agar was used for haemolysis assay.

Reference strain: Escherichia coli (ATCC® 25922™)


Methods

Collection of material

Success in recovery of E. coli after culturing specimens depends on careful collection of suitable specimens, proper transportation and accurate processing of clinical sample. In present study specimens were collected aseptically and placed in sterile leak-proof containers of appropriate size (OIE, 2008). The specimens were packed in stout polystyrene foam containers and transported with care as early as possible.

A total of 255 samples which included, choanal swabs (244) from live birds and trachea (11) from dead birds, suspected for CCRD formed the material for investigation in the present study (Table 1).

Isolation and identification of E. coli

Isolation of E. coli was carried out on MacConkey agar and Eosin methylene blue agar using suitable incubation conditions. Inoculated agar plates were incubated at 37°C temperature for 24 hrs. The isolates suggestive of Escherichia coli were stained with Gram’s staining and after observation as Gram negative bacilli, the isolates were further subjected to conventional bacteriological procedures as per Quinn et al., (2002) for confirmation as Escherichia coli. The identification of field isolates of
Escherichia coli was done on the basis of various biochemical tests like Indole, Methyl red, Voges proskauer, Nitrate, Citrate, Urease, TSI, Oxidase, Catalase and Motility test.

**Antibiotic sensitivity test of Escherichia coli**

All isolates of *E. coli* were subjected to *In vitro* antibiotic sensitivity test by disc diffusion method described by Bauer et al., (1966) using suitable commercial available antibiotic discs viz., Oxytetracycline, Ampicillin, Tylosine, Erythromycin, Norfloxacin, Enrofloxacin and Gentamicin (Hi Media).

**Conventional characterization of *E. coli* isolates**

All isolates of *E. coli* were characterized conventionally by using congo red binding assay, haemolysis assay and haemagglutination test for to detect virulence properties of the *E. coli*.

**Molecular characterization of *E. coli* isolates**

Molecular characterization of *E. coli* isolates was carried out by PCR of *cvl* gene described by Ewers et al., (2005) and bla<sub>TEM</sub> gene described by Bali et al., (2010) and plasmid profiling. Plasmid DNA and Chromosomal DNA extraction was carried out as per the protocol described by Sambrook and Russell (2008).

**Results and Discussion**

In cultural isolation from 255 specimens the isolation of *Escherichia coli* was successful from 68 (26.66%) specimens while remaining 187 (73.33%) specimens were proved to be negative for *E. coli*. Out of 68 *E. coli* isolates recovered, 31 (45.58%) isolates were associated with Mycoplasmosis. All *E. coli* isolates were recovered from choanal swabs (Table 2). All 31 field isolates were identified and confirmed as *E. coli* based on results of conventional identification methods (Plate 1, 2, 3, 4, 5, 6, 7, 8 and 9).

All 31 *E. coli* isolates associated with CCRD were tested for susceptibility to seven suitable antibiotics by disc diffusion method. The results of antibiotic susceptibility test indicated maximum resistance of *E. coli* isolates to ampicillin and oxytetracycline (64.51%) followed by tylosine (61.29%) and erythromycin (45.16%). The least resistance was observed to enrofloxacin (38.70%) and norfloxacin (22.58%), whereas all the isolates were sensitive to gentamicin (100%) (Plate 10).

Conventional characterization of 31 *E. coli* isolates revealed 26 (83.87%), 12 (41.37%) and 7 (22.58%) were invasive (Plate 11), haemolytic and positive for haemagglutination test (Plate 12), respectively. Molecular characterization of *E. coli* isolates showed that 6 (19.32%) isolates amplify a product of ~1181bp specific for *cvl* gene (Plate 13).

Out of 20 isolates showed resistant to ampicillin, 3 (15%) and 17 (85%) isolates yielded a product of ~403 bp in bla<sub>TEM</sub> gene specific PCR using chromosomal and plasmid DNA respectively (Plate 14).

Out of 31 *E. coli*, 16 (51.61%) possessed ~700 bp plasmid, 17 (54.83%) had ~1100 bp plasmid, 6 (19.35%) had ~1650 bp plasmid, while the presence of >12kbp plasmid observed in all the isolates. All the isolates displayed different numbers of plasmids as shown in (Plate 15).
### Table 1: Details of specimens used for investigation

<table>
<thead>
<tr>
<th>No.</th>
<th>Source</th>
<th>Type of bird</th>
<th>Specimen</th>
<th>No. of Samples</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Anand (Gujarat)</td>
<td>Breeders</td>
<td>Choanal swabs</td>
<td>50</td>
<td>50</td>
</tr>
<tr>
<td>2.</td>
<td>Bangalore (Karnataka)</td>
<td>Breeders</td>
<td>Choanal swabs</td>
<td>45</td>
<td>45</td>
</tr>
<tr>
<td>3.</td>
<td>Vijayawada (Andhra Pradesh)</td>
<td>Layers</td>
<td>Choanal swabs</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>4.</td>
<td>Aurangabad (Maharashtra)</td>
<td>Breeders</td>
<td>Trachea</td>
<td>11</td>
<td>11</td>
</tr>
<tr>
<td>5.</td>
<td>Hyderabad (Andhra Pradesh)</td>
<td>Layers</td>
<td>Choanal swabs</td>
<td>19</td>
<td>40</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Trachea</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Breeders</td>
<td>Choanal swabs</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td>6.</td>
<td>Pune (Maharashtra)</td>
<td>Breeders</td>
<td>Choanal swabs</td>
<td>23</td>
<td>70</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Layers</td>
<td>Choanal swabs</td>
<td>47</td>
<td></td>
</tr>
<tr>
<td>7.</td>
<td>Palghar (Maharashtra)</td>
<td>Broilers</td>
<td>Choanal swabs</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td>8.</td>
<td>Pen (Maharashtra)</td>
<td>Broiler</td>
<td>Choanal swabs</td>
<td>14</td>
<td>14</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Grand Total</td>
<td></td>
<td></td>
<td>244</td>
<td>255</td>
</tr>
</tbody>
</table>

### Table 2: Results of isolation of *E. coli* from clinical specimens

<table>
<thead>
<tr>
<th>Sr. No.</th>
<th>Sources</th>
<th>Specimens</th>
<th>No. of Samples</th>
<th>No. of <em>E. coli</em> isolates recovered</th>
<th>No. of <em>E. coli</em> isolates associated with CRD</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Anand (Gujarat)</td>
<td>Choanal swab</td>
<td>50</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td>2.</td>
<td>Bangalore (Karnataka)</td>
<td></td>
<td>45</td>
<td>20</td>
<td>13</td>
</tr>
<tr>
<td>3.</td>
<td>Vijayawada (Andhra Pradesh)</td>
<td></td>
<td>10</td>
<td>01</td>
<td>01</td>
</tr>
<tr>
<td>4.</td>
<td>Aurangabad (Maharashtra)</td>
<td>Trachea</td>
<td>11</td>
<td>11</td>
<td>00</td>
</tr>
<tr>
<td>5.</td>
<td>Hyderabad (Andhra Pradesh)</td>
<td>Choanal swab</td>
<td>40</td>
<td>10</td>
<td>00</td>
</tr>
<tr>
<td>6.</td>
<td>Pune (Maharashtra)</td>
<td></td>
<td>70</td>
<td>07</td>
<td>00</td>
</tr>
<tr>
<td>7.</td>
<td>Palghar (Maharashtra)</td>
<td></td>
<td>15</td>
<td>03</td>
<td>00</td>
</tr>
<tr>
<td>8.</td>
<td>Pen (Maharashtra)</td>
<td>Choanal swab</td>
<td>14</td>
<td>02</td>
<td>02</td>
</tr>
<tr>
<td></td>
<td>Total</td>
<td></td>
<td>244</td>
<td>57</td>
<td>31</td>
</tr>
<tr>
<td></td>
<td>Grand total</td>
<td>Choanal swab</td>
<td>255</td>
<td>68</td>
<td>31</td>
</tr>
</tbody>
</table>
Plate 1. E. coli on MacConkey agar

Plate 2. E. coli on Eosin methylene blue medium

Plate 3. E. coli in Gram stained Smear
Plate 4 *E. coli* showing Indole positive reaction

Plate 5 *E. coli* showing MR positive reaction

Plate 6 *E. coli* showing VP negative reaction
Plate 7 *E. coli* showing citrate negative reaction

Plate 8 *E. coli* showing urease negative reaction

Plate 9 *E. coli* showing oxidase negative reaction
Plate 10 E. coli showing catalase positive reaction

Plate 11 E. coli showing TSI negative reaction

Plate 12 Antibiogram of Escherichia coli isolates showing multi drug resistance
Plate.13 Invasive and non invasive E. coli on Congo red agar medium

Plate.14 Haemagglutination test of E. coli field isolates

<table>
<thead>
<tr>
<th>Dilutions</th>
<th>1:1</th>
<th>1:2</th>
<th>1:4</th>
<th>1:16</th>
<th>1:32</th>
<th>1:64</th>
<th>RBC control</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Positive control</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Plate. 15 PCR of \textit{cvi} gene of \textit{E. coli} isolates

100 bp standard DNA ladder, Lane-2 to Lane-6: positive \textit{E. coli} isolates, Lane-7: Positive control and Lane-8: Negative control

Plate. 16 PCR of \textit{bla}_{TEM} gene of \textit{E. coli} isolates

(Lane-1: 100 bp standard DNA ladder, Lane-2 to Lane-6: positive \textit{E. coli} isolates, Lane-7: Positive control and Lane-8: Negative control)
In the present investigation, isolation of *Escherichia coli* was successful only from 31 (45.58%) isolates. Several researchers (Radwan *et al.*, 2014, Ramasamy *et al.*, 2008, Syuhada *et al.*, 2013 and Fatma *et al.*, 2008) throughout the world have reported isolation of *Escherichia coli* from different clinical specimens with varying degrees of success (17% to 60%). Since number of factors are likely to influence the successful isolation of *Escherichia coli* from clinical specimens; especially the availability of appropriate material at the appropriate stage of the disease, season of sample collection, transportation conditions and processing time.

All 31 *E. coli* isolates associated with CCRD were tested for susceptibility to seven suitable antibiotics by disc diffusion method. The *E. coli* isolates in the present study showed multi drug resistance towards six out of seven antibiotics used. The source of the resistance may be assumed from the poultry feeds consumed, since antibiotics are used as feed additives to improve feed efficiency and weight gain. Many antibiotics are also used in feed and water to control the diseases. Indiscriminate use of antibiotics has provided selective pressure for the emergence of drug resistance resulting in a larger proportion of *E. coli* resistance as reported by (Atere *et al.*, 2015).

In the present study, conventional characterization of *E. coli* isolates was carried out using Congo Red (CR) binding assay, haemolytic activity and haemagglutination test. The results of present study showed that, out of 31 *E. coli* isolates, 26 (83.87%) were CR positive. The similar findings for Congo red binding activity were observed by (Aziz *et al.*, 1995 and Seifi *et al.*, 2015) in the range of (82.6% to 88.75%) CR positive *E. coli* strains, respectively.

Production of haemolysin is usually associated with pathogenicity of *E. coli* especially responsible for more severe forms
of infection (Johnson, 1991). The result of haemolysin production i.e., 41.37% (12/31) of present study laid between the range reported by different authors. Varying results of haemolytic activity were observed by different workers viz., higher rate of E. coli strains positive for haemolytic activity observed in 73%, 56.47%, 59%, 92.9% and 84.2% by Aziz et al., (1995), Fatma et al., (2008), Bashar et al., (2011), Al-Arfaj et al., (2015), Hassan and Bakeet (2014), respectively. Whereas very low haemolytic activity of 1.52%, 10% and 37.03% was observed by Shankar et al., (2010), Raji et al., (2003) and Ruaa et al., (2014) respectively.

The adhesion ability of an organism is assessed by determining the haemagglutination, because the erythrocyte membrane is believed to possess the homologous of the mucosal substances involved in bacterial adherence to epithelial cells (Hager et al., 2010). Haemagglutination assay in the present study demonstrated 7 (22.58%) isolates positive. The findings of present research range between the Ruaa et al., (2014) and Aziz et al., (1995) stated that 3.70% and 87.5 % of E. coli isolates were able to induce hemagglutinin respectively.

In the present study, molecular characterization of 31 E. coli isolates was carried out for detection of cvi and blaTEM gene by PCR and antibiotic resistance by plasmid profiling.

Out of 31 E. coli subjected to PCR, targeting cvi gene, 6 (19.32%) E. coli isolates were found positive for cvi gene. All cvi gene PCR positive isolates yielded an amplification product of ~1181 bp. The results of PCR of cvi correlated with results of Ewers et al., (2005) and Arabi et al., (2013) where they reported an amplification product of ~1181 bp specific for cvi gene of E. coli, respectively.

Out of 31 E. coli isolates, 20 isolates which showed resistance to ampicillin phenotypically were subjected to PCR by using chromosomal DNA and plasmid DNA for amplification of blaTEM gene. Out of 20 isolates, 3 (15%) and 17 (85%) isolates yielded a product of ~403 bp in blaTEM gene specific PCR using chromosomal and plasmid DNA, respectively. The results of PCR of blaTEM gene correlated with result of Bali et al., (2010), who reported an amplification product of ~403 bp specific for beta lactam resistant gene of E. coli. The higher percentage of blaTEM gene was observed in plasmid DNA (85%) than chromosomal DNA (15%) i.e., suggesting plasmid borne resistance to ampicillin. The results of blaTEM gene correlates with the findings of the Wang et al., (2013) and Ammar et al., (2015) detected the blaTEM gene by using plasmid DNA in 65.9% and 100% E. coli isolates, respectively and reported the resistance to beta lactam antibiotic.

In plasmid profiling of 31 E. coli isolates, four different sizes of plasmids were estimated viz., ~700 bp, ~1100 bp, ~1650 bp and >12 kbp. Nsfofor and Iroegbu (2013) reported that isolates with high multi drug resistance profile possessed multiple plasmids with large sizes in the range of 1 to 120 Kb.

In conclusion from the present research it is concluded that association of Escherichia coli with chronic respiratory disease was observed in 45.58% cases with overall incidence of 12.15% in respiratory tract infection. Escherichia coli isolates associated with chronic respiratory disease could be recovered from choanal swabs. Gentamicin was found to be most effective antibiotic followed for treatment of Escherichia coli infection in CCRD. Most of Escherichia coli isolates (83.87%) were found to be pathogenic based on Congo red binding activity and showed association in different virulence factors. All
isolates positive for cvi gene in molecular characterization of virulence were also positive for virulence factor tested phenotypically. Correlation of presence of blaTEM gene and plasmid profile was observed with resistance to ampicillin seen in AST. Further studies focussing on evaluation of PCR analysis of various suitable genes associated with the virulence and antibiotic resistance on a larger numbers of clinical isolates will produce valuable data useful in molecular epidemiology. Studies on synergistic effect of different combinations of antibiotics for effective treatment against both Mycoplasma spp. and E. coli infection are recommended.

References


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