

# Characterization of *netB* positive *Clostridium perfringens* Type A Recovered from Necrotic Enteritis in Commercial Broiler Flocks

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## ABSTRACT

Necrotic enteritis (NE) is a significant GI tract disease in chickens, predominantly caused by type A strains of *Clostridium perfringens*. This condition presents a substantial financial burden on the farmers, jeopardizing flock health and productivity. Recent research highlights the crucial role of the *netB* toxin, as a primary pathogenic factor in the development of NE. Present study details an outbreak of NE recorded in a commercial broiler flock raised in deep litter system. Dead birds were presented for necropsy with a history of sudden heavy mortality. Significant pathological features in the intestines and viscera of the affected birds were suggestive of NE. Microbiological evaluation including cultural examination and molecular characterization targeting 16s rRNA sequences revealed presence of *C. perfringens*. Toxinotyping of the isolate under study revealed that the predominant toxin produced was alpha toxin and that it belongs to *C. perfringens* type A. The isolate was also found to produce *netB* toxin. Heavy mortality recorded in the present investigation may be attributed to *netB* gene.

**Keywords:**  $\alpha$  toxin, *Clostridium perfringens*, Necrotic enteritis, *NetB* toxin, Toxinotyping.

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## INTRODUCTION

*Clostridium perfringens* is the primary instigating factor in the development of Necrotic enteritis (NE), first documented in Australia in 1930 (Parish, 1961). Thereafter, NE was recorded sporadically across the globe (Timbermont *et al.*, 2011). *C. perfringens* is an anaerobic, spore forming Gram positive bacterium and is a constituent of normal flora in GIT of poultry, cattle, sheep and goat (Hatheway, 1990; Ficken, and Wages, 1997). NE in chicken leads to substantial financial setback to the poultry industry by reducing feed efficiency and growth rate. NE affects the broilers in the age group of 2 to 6 weeks and layers of 3-6 months, and is mostly observed either in clinical or subclinical form (Skinner *et al.*, 2010). Clinical form of NE occurs as an outbreak with clinical signs like depression, ruffled feathers, and diarrhea with high mortality. Subclinical NE is usually manifested as impaired growth rate and inefficient feed utilization. Peracute form has also been described where the affected birds succumb in few hours, and mortality rising upto 50%. Sudden feed changes, poor hygiene, stress, mucosal damage caused by parasites like *Coccidia* spp., and other immunosuppressive diseases often predispose chickens to NE (Shojadoost *et al.*, 2012; Moore, 2016). Chronic intestinal damage caused by necrotic enteritis, combined with coccidial infections, can impair gut absorption, reduce body weights and lower feed efficiency, leading to inadequate returns.

*C. perfringens* produces variety of toxins that contributes to its virulence. Four different toxins produced by *C. perfringens* are alpha, beta, iota and epsilon. Based on the toxins produced, *C. perfringens* is subdivided into five biotypes, type A secretes alpha toxin, type B secretes alpha,

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beta and epsilon toxins, type C secretes alpha and beta toxins, type D secretes alpha and epsilon toxins, and type E secretes alpha and iota toxins (Schlegel *et al.*, 2012). Of the four toxins, alpha is appraised as the crucial element responsible for heavy mortality that occur during NE. Keyburn *et al.* (2010) found a novel virulence factor, *NetB* (Necrotic enteritis B-like toxin) in a *C. perfringens* mutant unable to produce  $\alpha$ -toxin, yet still causing NE. *NetB* gene encodes a pore-forming toxin and is located on a plasmid of size 85 Kbp. Current investigation reports an outbreak of NE in a commercial broiler flock caused by type A strains of *C. perfringens*.

## MATERIALS AND METHODS

### Clinical History and Necropsy

History revealed that a commercial broiler farm in Andhra Pradesh with a capacity of 40,000 birds experienced heavy mortality during May, 2024 in one of its broiler stocks aged 4-6 weeks. The birds were raised in deep litter system. Over a period of 15 days, the affected stock showed a mortality percentage of 7.08% (620/ 8750). A total of thirty birds were presented for postmortem examination. Before death, the affected birds exhibited clinical signs like ruffled feathers, decreased appetite, severe depression, reluctance to move, diarrhea, dehydration and progressing debility. Necropsy was performed, and samples, including intestinal scrapings and liver tissue, were aseptically collected for microbiological evaluation. Additionally, the tissues were subjected to histopathological examination.

### Bacteriological Examination

Intestinal scrapings suspended in sterile normal saline were heated in water bath at 80 °C for 20 min. The treated samples were inoculated into thioglycolate broth and incubated in an anaerobic jar with gas generating packs at 37° C for 18-24 h. Broth culture was subsequently spread onto Perfringens agar base (Tryptose Sulphite Cycloserine -TSC) supplemented with 5% egg yolk and incubated in an anaerobic jar with gas generating packs at 37° C for 24 h. The identity of *C. perfringens* was confirmed based on lecithinase activity and haemolysis pattern on TSC agar and 5% blood agar, respectively, Gram staining and lactose fermentation.

### Isolation of DNA and PCR

Boiling and snap-chilling method was used to isolate DNA. Briefly, 2 mL of overnight *C. perfringens* culture was spinned at 10,400 g for 10 min. PBS was added to the pellet and spinned once again at the same speed for 10 min. The pellet obtained was then solubilized in 200 µL of nuclease free water and boiled at 100 °C for 10 min, immediately followed by snap chilling for 6-7 min. The lysate was spinned for 10 min at 10,400 g and the supernatant was transferred into fresh tubes and preserved at -20 °C.

The extracted DNA was used to identify *C. perfringens* using primers targeting 16s rRNA gene producing a predicted amplicon of 481 bp (Tonooka *et al.*, 2005). PCR was performed in 10 µL reaction mixture, 2X master mix (M/s ProMega) and 10 pmol of each primer. DNA amplicons were electrophoresed on 1% agarose gel with ethidium bromide and visualized using UV light.

### Toxinotyping of *C. perfringens*

*C. perfringens* toxinotyping was accomplished by multiplex PCR to identify the presence of genes encoding alpha, beta, iota and epsilon toxins using previously described primers (Van Asten *et al.*, 2009). Additionally, a separate PCR was

conducted to detect *netB* gene using primers reported in previous study (Keyburn *et al.*, 2010).

## RESULTS AND DISCUSSION

*Clostridium perfringens* is a major pathogen affecting livestock, poultry and humans, causing a range of enteric infections and fatal intoxications in various animal species (Markey *et al.*, 2013). Necrotic enteritis in poultry is a significant disease caused by *C. perfringens*. In this study, we isolated *C. perfringens* from a four to six week old broiler flock exhibiting symptoms consistent with necrotic enteritis. Previous studies have also reported the occurrence of this condition in both broiler (Mwangi *et al.*, 2013; Thomas *et al.*, 2014) and layer (Kurkure *et al.*, 2017) flocks.

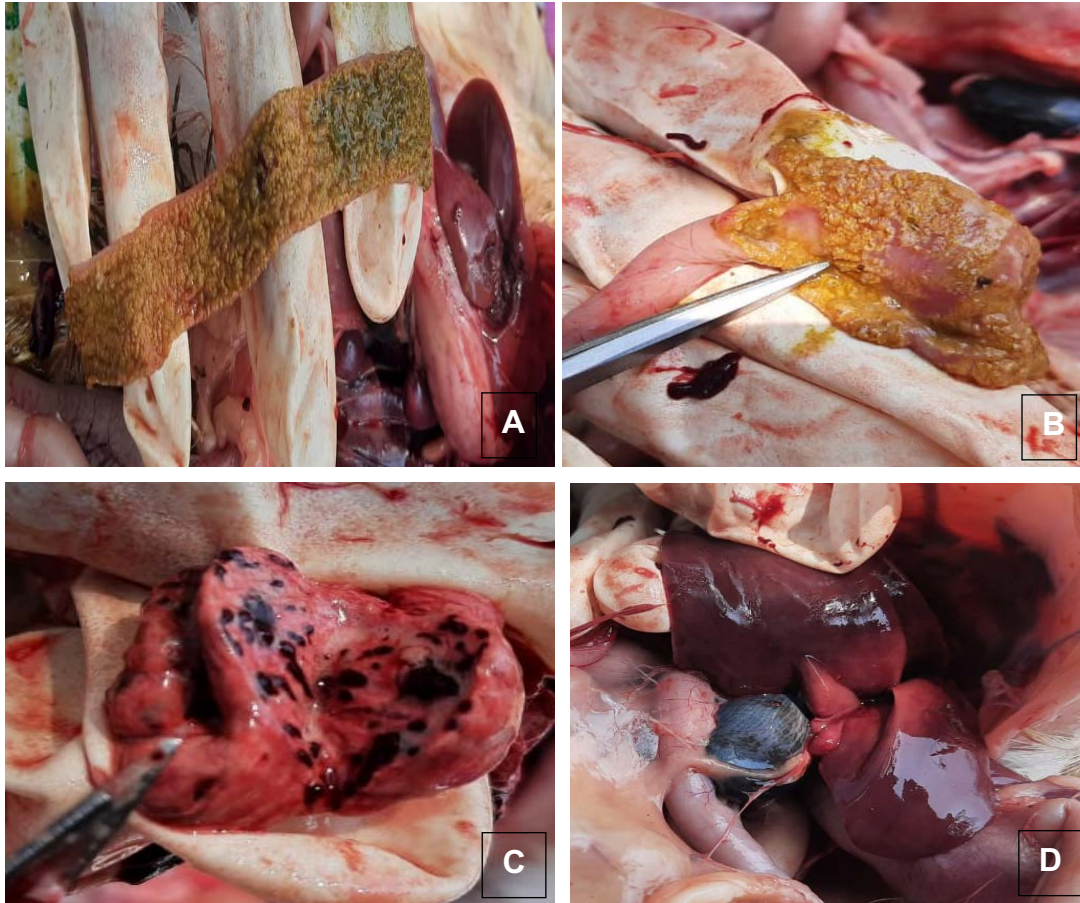
Clinical examination of the affected flock exhibited symptoms such as diarrhoea, anorexia, listlessness and ruffled feathers. Necropsy revealed predominant lesions in the GI tract. Intestines were thick, dark with bluish discoloration. Mucosal surfaces resembled turkish towel like appearance with blackish discoloration, consistent with findings of Park *et al.* (2015). Other changes observed were echymotic haemorrhages in lungs, necrotic foci and congestion in liver and mild swelling and congestion in kidneys (Fig. 1).

Coccidial oocysts were identified in the intestinal scrapings collected during necropsy. Impression smears of these scrapings, stained with Leishman's stain, revealed numerous thick bacilli (Fig. 2). Histopathological examination showed thickening of the serosal and mucosal layers, leukocytic infiltration, villous disruption, and haemorrhages in the lamina propria and submucosa (Fig. 3). Coccidial infection damages the intestinal lining, compromising its integrity and increasing permeability, which facilitates rise in the population of *C. perfringens* and establishment of infection (Shojadoost *et al.*, 2012). The outbreak occurred in May, coinciding with high environmental temperatures and humidity levels. In the present investigation, disease incidence was recorded in birds raised under a deep litter system that might have contributed to coccidial infections due to accumulation of moisture and organic material in the litter. Although *C. perfringens* is a commensal in the GIT of poultry, animals and humans, an increase in the bacterial counts was recorded in the present study, as evidenced by the abundant bacilli in the impression smears of intestinal scrapings. This aligns with the findings of McDevitt *et al.* (2006), who reported an increase in the population of *C. perfringens* from approximately 10<sup>4</sup> CFU in healthy birds to 10<sup>7</sup>-10<sup>9</sup> CFU in chicken with NE.

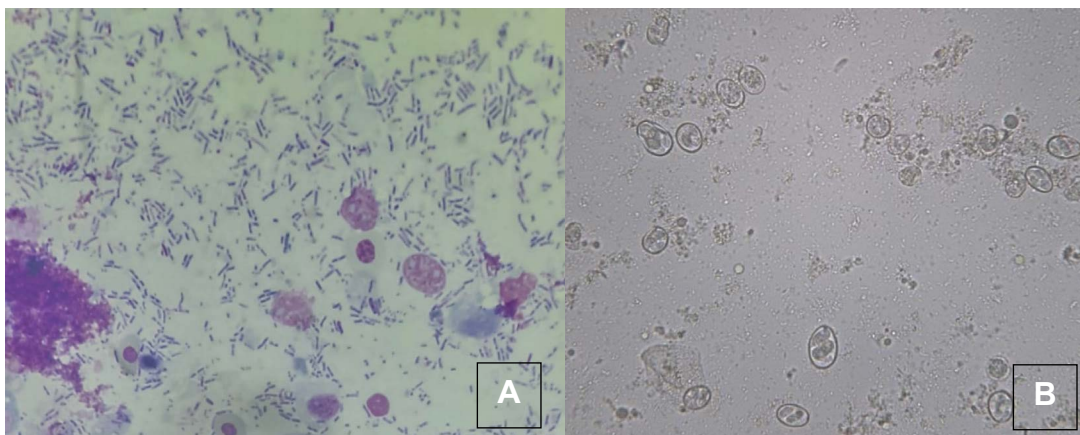
Microscopically, the gastrointestinal tract exhibited thickening of the serosal and mucosal layers, along with villous disruption in the submucosal layers and lamina propria-specific lesions of necrotic enteritis (Kurkure *et al.*, 2017). Bacterial culture findings showing black colonies with opalescence on Perfringens agar base and partial haemolysis in 5% sheep blood agar were in accordance with Alsaab *et al.*, (2021).

Microbiological investigations aligned with the clinical findings and confirmed the presence of *C. perfringens* in birds suspected for NE. TSC agar supplemented with egg yolk emulsion showed black colonies with a surrounding zone of opalescence. Gram staining of the colonies showed Gram positive straight bacilli (Fig. 4). Culturing on 5% sheep blood agar produced grey round, smooth colonies exhibiting partial haemolysis.

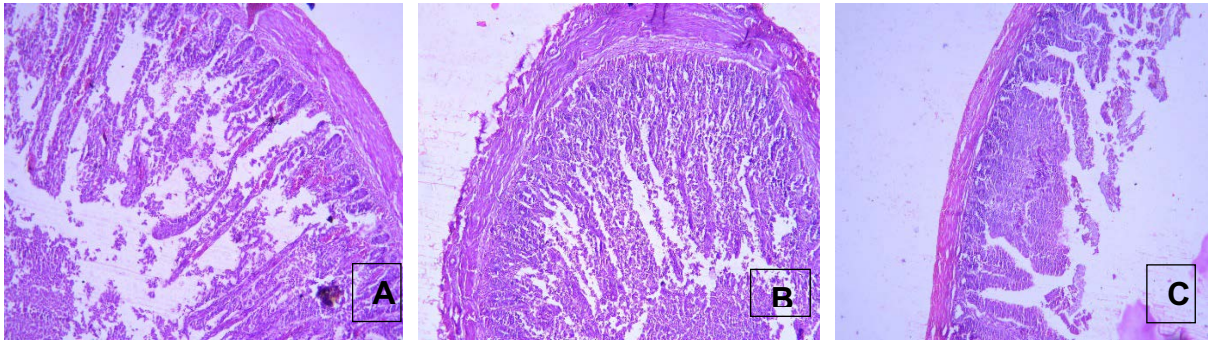
Molecular characterization established based on 16s rRNA amplified the required DNA product of 481 bp confirming the presence of *C. perfringens* in the samples collected from affected birds. Multiplex PCR for *C. perfringens* toxinotyping detected only the  $\alpha$ -toxin (*cpa*), while all other toxins (*cpb*, *etx* and *iap*) were absent. Notably, this isolate was also positive for *netB* toxin gene (Fig. 5).



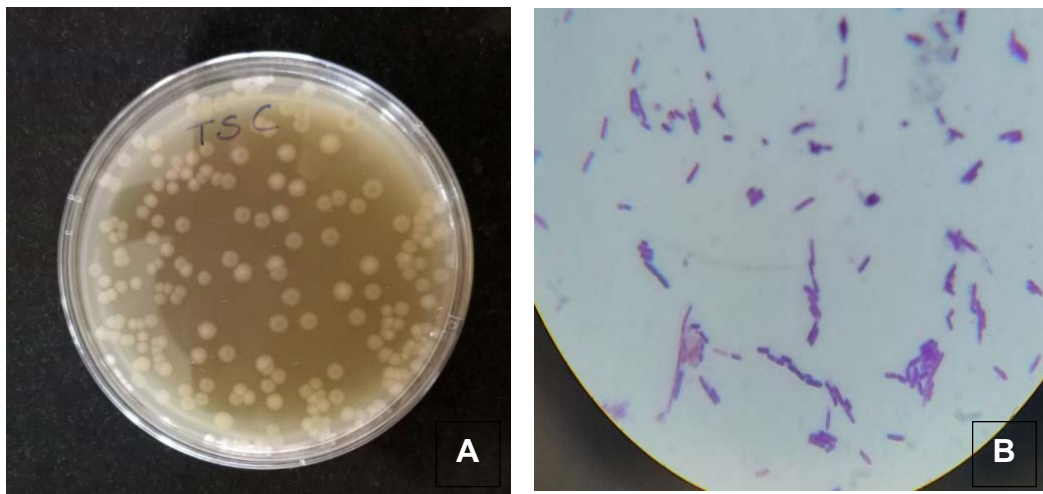
**Fig.1: A & B** Turkish towel like appearance of intestines with blackish discoloration. **C.** Echymotic haemorrhages on lungs. **D.** Necrotic foci and congestion in liver



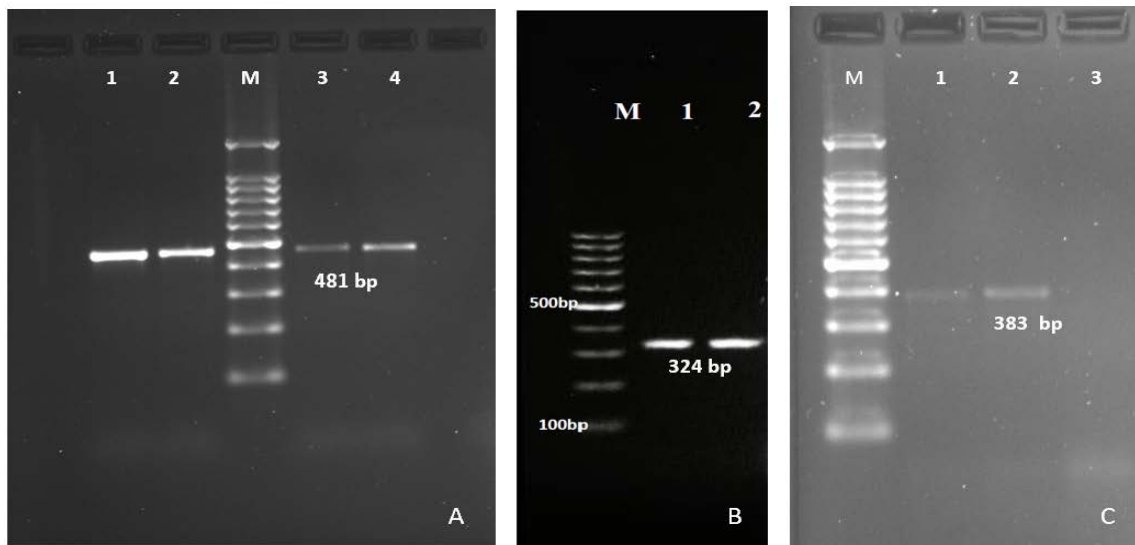
**Fig. 2: A.** Large number of *C. perfringens* bacilli in the impression smears of intestinal scrapings stained by Leishman's staining (1000X). **B.** *Eimeria* oocysts in the intestinal scrapings (400X).



**Fig. 3:** Intestine showing: A. disruption of villi and congestion, B. Thickening of serosal layer, C. Necrosis



**Fig. 4:** A. Black colonies surrounded by zone of opalescence on TSC agar, B. Gram positive straight bacilli (1000X)



**Fig. 5:** A. PCR gel pictures showing amplification of 16s rRNA gene of *C. perfringens*. B. Multiplex PCR gel pictures showing amplification of *cpa* (Alpha toxin) gene. C. PCR gel pictures showing amplification of *netB* gene of *C. perfringens*.

Type A strains of *C. Perfringens* is the frequent toxin-producing type, with alpha-toxin recognized as a critical pathogenicity determinant responsible for NE in chicken and food poisoning in humans (Timbermont *et al.*, 2011). The alpha toxin is a pore-forming toxin with phospholipase, haemolytic, dermonecrotic and lecithinase activities, produced by all *C. Perfringens* subtypes. Alpha toxin gene is a part of the larger genetic element, *i.e.* bacterial chromosome (Stiles *et al.*, 2013; Simpson *et al.*, 2018).

*NetB* gene, first identified in 2008, has been recognized as a major pathogenicity element involved in development of NE in chicken. It is plasmid encoded and functions as a pore-forming toxin that damages the intestinal epithelial cells, leading to gut tissue necrosis (Savva *et al.*, 2013). Strains of *C. perfringens* with *netB* gene have been linked to higher disease incidence and more severe forms of NE in broiler flocks. Challenge experiments have demonstrated that strains negative for *netB* induced mild or no disease, whereas, *netB* positive strains cause severe necrotic enteritis in healthy chickens. Furthermore, chicken vaccinated with recombinant *netB* toxin showed high immunogenicity against challenge with virulent *C. perfringens*, highlighting the immunogenic potential of *netB* toxin (Keyburn *et al.*, 2013).

## CONCLUSION

This investigation details the isolation and characterization of *C. perfringens* in broilers suffering from necrotic enteritis. Toxin typing identified the presence of genes encoding  $\alpha$ -toxin and *netB* toxin. Future research is warranted to clarify the specific function of *netB* toxin in the disease process and to investigate whether a synergistic interaction between  $\alpha$ -toxin and *netB* toxin contributes to heightened mortality in affected birds.

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