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**CARACTERIZAÇÃO MOLECULAR DOS PRINCIPAIS FATORES DE
VIRULÊNCIA E GENÓTIPOS DE *Clostridium perfringens* ISOLADOS DE
FRANGOS COM ENTERITE NECRÓTICA**

Tese apresentada ao Programa de Pós-Graduação em Microbiologia do Instituto de Ciências Biomédicas da Universidade de São Paulo, para obtenção do Título de Doutor em Ciências.

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RESUMO

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Clostridium perfringens é a bactéria responsável pela enterite necrótica (EN), que afeta a produção avícola mundial. Esta bactéria se caracteriza pela produção de diversas toxinas que causam lesões no intestino provocando elevada mortalidade, e perdas econômicas pela queda na produtividade. Este estudo avaliou os principais fatores de virulência, a susceptibilidade aos antimicrobianos e a diversidade genética de *C. perfringens* isolados de frangos com EN. Foram obtidos 22 isolados de nove das 94 amostras analisadas. Todos, menos um isolado, possuíram um ou dois genes *nanI* (95%) e *nanJ* (81%) que codificam a produção de neuraminidases, e (19/22), mostraram atividade de neuraminidase em hemácias de frango. Nenhum isolado abrigou o gene *nanH*. A atividade hemaglutinante foi observada em poucos isolados (26%). Todos os isolados foram positivos para o gene *plc* (toxina α), sendo classificados como tipo A. Sete isolados (31,8%) abrigaram o gene *tpeL* que codifica a toxina TpeL, sendo este o primeiro relato da presença desta toxina no Brasil associado a quadros de EN em frangos. Isolados *tpeL*⁺ mostraram efeito citotóxico característico da ação da toxina TpeL. Alguns isolados mostraram capacidade de aderir e invadir as células epiteliais testadas. A maioria dos isolados foi resistente à sulfaquinoxalina (100%), cefalexina (95%), eritromicina (95%), bacitracina (50%), com valores de CIM₉₀ variando entre 32 μ g/mL a \geq 512 μ g/mL. Cefoxitina, amoxicilina, enrofloxacina, amoxicilina-ácido clavulânico, penicilina-estreptomicina, cloranfenicol e metronidazol se mostraram ativos contra os *C. perfringens* avaliados. Pela técnica de AP-PCR e empregando o coeficiente UN1, todos os isolados foram agrupados em sete clusters, apresentando-se como um grupo heterogêneo.

Palavras-chave: Enterite necrótica. Frangos. *Clostridium perfringens*. Fatores de virulência. Toxina TpeL. Susceptibilidade aos antimicrobianos. Diversidade genética.

ABSTRACT

LLANCO, L. A. A. **Molecular characterization of the virulence factors and genotypes of *Clostridium perfringens* isolated from chickens with necrotic enteritis.** 2013. 109 p. Ph. D. thesis (Microbiology) – Instituto de Ciências Biomédicas, Universidade de São Paulo, São Paulo, 2013.

Clostridium perfringens cause necrotic enteritis (EN) affecting the poultry production worldwide. This bacterium produces various toxins and causes lesions in the intestine producing high mortality and economic loss due to the low productivity. In this study, the major virulence factors, antimicrobial susceptibility and genetic diversity of *C. perfringens* isolated from chickens with EN were evaluated. 22 isolates were obtained from nine out of 94 intestinal samples analyzed. All the isolates with exception of one harbored one or two genes *nanI* (95 %) and *nanJ* (81%) codifying the neuraminidase production, and 19/22 showed neuraminidase activity on chicken's erythrocytes. No isolates harbored the gene *nanH*. Haemagglutination was observed in 26% of the isolates. All isolates were positive for the gene *plc* (α toxin) being classified as type A. Seven isolates (31.8%) harbored *tpeL* gene that encodes the toxin TpeL, and this appear to be the first report of the presence of this toxin associated to chickens with EN in Brazil. Isolates *tpeL*⁺ showed characteristic cytotoxic effect. Some isolates showed the ability of adhere to and invade to epithelial cells. Most of the isolates were resistant to sulphaquinoxaline (100%), cephalexin (95%), erythromycin (95%), bacitracin (50%) with MIC₉₀ values ranging from 32 μ g /mL to \geq 512 μ g /mL. Cefoxitin, amoxicillin, enrofloxacin, amoxicillin-clavulanic acid, penicillin-streptomycin, chloramphenicol, and metronidazole showed activity against *C. perfringens*. By AP-PCR and by using the coefficient UN1, isolates were grouped into seven clusters, showing to be a heterogeneous group.

Keywords: Necrotic enteritis. Chicken. *Clostridium perfringens*. Virulence factors. Toxin TpeL. Antimicrobial susceptibility. Genetic diversity.

INTRODUÇÃO

Dentre os microrganismos anaeróbios que colonizam o trato intestinal do homem e animais, destaca-se o gênero *Clostridium*, composto por pelo menos 150 espécies (GARRITY et al., 2007; SAVAGE, 1986). Estas bactérias anaeróbias, esporuladas e fermentadoras de diversos compostos orgânicos, participam ativamente da degradação final de alguns nutrientes no ecossistema gastrointestinal, assim como, do processo de renovação da biomassa, quando habitam solos e esgotos, cumprindo um importante papel ecológico (GONG et al., 2008; SONGER, 1996).

Apesar da maioria das bactérias deste gênero *Clostridium* ser comensal, aproximadamente 10% possui elevada patogenicidade, recorrente da produção de potentes toxinas. Este gênero bacteriano abriga espécies que produzem aproximadamente 20% de todas as toxinas bacterianas conhecidas (POPPOF; VOUBET, 2013).

Dentre as espécies do gênero *Clostridium*, a mais frequentemente isolada de casos de enterites, abscessos, e toxemias, entre outros, é *C. perfringens*. Este microrganismo é o principal responsável pela gangrena gasosa, por intoxicações alimentares, e diarréias associadas ao uso de antibióticos em humanos (ROOD et al., 1997). Também, esta bactéria tem sido isolada de doenças inflamatórias crônicas, como colite ulcerativa e doença de Crohn, sendo também proposta por alguns autores a sua participação no desenvolvimento de câncer de cólon (PRUTEANU et al., 2011; PRUTEANU; SHANAHAN, 2013).

Clostridium perfringens também desenvolve processos infecciosos em animais, produzindo a enterite necrótica (EN) em aves. Esta doença causa morte súbita quando se apresenta na forma aguda, e baixo rendimento produtivo na forma subclínica, assim como também, produz grandes perdas econômicas em países exportadores de carne de aves, principalmente frangos (VAN IMMERSEEL et al., 2009).

Esta espécie bacteriana é capaz de produzir mais de quinze toxinas, que constituem seus principais fatores de virulência. Dessas toxinas somente quatro, consideradas letais: α , β , ϵ e ι , servem para classificar essa espécie em

cinco toxinotipos: A, B, C, D, e E, os quais estão relacionados às doenças de importância na medicina humana e veterinária (PETIT; GIBERT; POPOFF, 1999; SONGER, 1996).

A toxina α é o fator de virulência de *C. perfringens* mais estudada, devido a seu rápido efeito letal em animais de experimentação, à ampla distribuição de seus receptores e substratos na superfície de células eucarióticas, e à sua relação com doenças severas (GOÑI; MONTES; ALONSO, 2012; SONGER, 1996; TITBALL; NAYLOR; BASAK, 1999). O gene *plc* codifica a produção desta toxina, que está localizada muito próxima da origem de replicação no genoma dos *C. perfringens* sequenciados, e é considerado um fator de virulência de origem cromossomal (MYERS et al., 2006; SHIMIZU et al., 2001; SHIMIZU et al., 2002a).

Na EN se observa a degradação das células eucarióticas intestinais, e este processo é produzido pela toxina α , considerada uma fosfolipase tipo C. Estudos têm mostrado que, a inativação da toxina α diminui a severidade das lesões, sugerindo-se a participação de outros fatores no desenvolvimento deste processo infeccioso (KEYBURN et al., 2006; THOMPSON et al., 2006).

Estudos realizados por Keyburn et al. (2008), relataram a presença de uma nova toxina denominada NetB a qual é de origem plasmidial e apresenta uma atividade de formação de poros na membrana de células eucarióticas. Essa toxina NetB é a última descrita em *C. perfringens*, e também, é sugerida a sua participação nas lesões iniciais da EN. Recentemente, Lepp et al. (2010), analisando a origem plasmidial do gene *netB*, identificaram três loci de patogenicidade: locus 1, locus 2 e locus 3. Os loci 1 e 3 são de origem plasmidial, sendo que o gene *netB* se encontra localizado no locus 1. O locus 2 é considerado de origem cromossomal que ao lado do locus 3 (plasmidial) carregam genes relacionados ao metabolismo bacteriano e produção de adesinas, entre outros. Também, estes autores relataram que esses três loci eram observados somente em cepas patogênicas e não em cepas comensais.

Estudos têm mostrado que a prevalência do gene *netB* em *C. perfringens* de diferentes origens, é baixa, e frequentemente observado em isolados bacterianos de animais saudáveis do que em doentes (ABILDGAARD et al., 2010; CHALMERS et al., 2008a; MARTIN; SMYTH, 2009). Isto sugere que, a presença da toxina NetB não seja suficiente para iniciar o processo

infeccioso. Por outro lado, Coursodon et al. (2010), avaliando a produção da toxina α no intestino de frangos inoculados com *C. perfringens* (*plc* mutantes) questionou o experimento realizado por Keyburn et al. (2008), uma vez que estes autores não utilizaram animais livres de germes, e esta toxina poderia ser produzida por *C. perfringens* residentes no intestino aviário.

Amimoto et al. (2007) relataram a presença da toxina TpeL a qual foi classificada como pertencente a Família das Grandes Citotoxinas Clostridiais (LCT): junto às toxinas A e B de *C. difficile*, toxina letal de *C. sporogenes*, e toxina alfa de *C. novyi*. Esta família de toxinas se constitui importante fator de virulência envolvida em doenças entéricas de interesse médico veterinário (AKTORIES et al., 2012; BUSCH; AKTORIES, 2000).

Também, sabe se que, a atividade desta toxina TpeL tem atividade glicosilante nas proteínas Rho-Ras GTPases, modifica a estrutura da actina e afeta a fisiologia das células epiteliais, particularmente, das células Vero (rim de macaco verde) (CARTER; ROOD; LYRAS, 2012; DJOUDER et al., 2000; NAGAHAMA et al., 2011). Assim, Chalmers et al. (2008a) e Coursodon et al. (2012), ressaltaram a importância dessa toxina no agravamento das lesões, aumentando a mortalidade por EN em animais de experimentação.

O processo de adesão ao epitélio intestinal se constitui a etapa mais importante na colonização bacteriana, a qual pode ser mediada por estruturas fimbriais e não fimbriais (PARKER; SPERANDIO, 2009). Em *C. perfringens* o processo de adesão tem sido demonstrado pela capacidade de produzir biofilmes, e essa capacidade é favorecida pela presença de pili tipo IV e pela produção de sialidases (BORASTON; FICKO-BLEAN; HEALEY, 2007; VARGA; THERIT; MELVILLE, 2008; WALTERS; STIREWALT; MELVILLE, 1999). Vidal et al. (2009b) e McClane (2010), relataram que o processo de adesão realizado por *C. perfringens* serviria como um regulador positivo para a produção de neuraminidases e toxinas.

A EN é considerada um processo infeccioso que causa aproximadamente U\$ 2 bilhões de dólares por ano, no mundo todo, e é causada pelas toxinas produzidas por *C. perfringens*, adicionado da ausência de vacinas efetivas para o controle da EN; assim, maiores estudos são necessários para minimizar os fatores que participam dessa doença. Alguns antimicrobianos vêm sendo muito utilizados como promotores de crescimento

de aves, trazendo como consequência o surgimento de bactérias resistentes a múltiplas drogas antimicrobianas, dificultando o tratamento de vários processos infecciosos de interesse na medicina veterinária (VAN IMMERSEEL et al., 2009). A presença de cepas bacterianas multirresistentes constitui-se um sério risco para saúde humana, uma vez que esses animais são utilizados na alimentação do homem (KATHER; MARKS; FOLEY, 2006; SCHENTAG; GUILLILAND; PALADINO, 2001; SONGER, 1996).

Estudos de susceptibilidade aos antimicrobianos de *C. perfringens* são pouco observados na literatura, principalmente, avaliando-se comparativamente os perfis de resistência entre localidades e granjas de criação avícola (MARTEL et al., 2004; VAN IMMERSEEL et al., 2004). Drogas como penicilinas, bacitracina e ionóforos vêm sendo utilizados como promotores de crescimento em aves, assim como para o tratamento e prevenção da EN em vários países como Índia, Argentina e Brasil. Entretanto, os Estados Unidos, Canadá e países Europeus, o uso de antimicrobianos como promotores de crescimento está totalmente proibido.

CONCLUSÕES

Os resultados obtidos neste estudo permitem concluir que:

1. Os *C. perfringens* isolados foram classificados como tipo A (*plc+*), sendo que alguns deles abrigaram também o gene *tpeL*;
2. A maioria dos isolados apresentou característica citotóxica, adesiva e invasiva;
3. Os isolados mostraram perfil similar de resistência para alguns antimicrobianos; e
4. Os *C. perfringens* avaliados neste estudo foram agrupados em clusters estreitamente relacionados apesar de apresentarem características fenotípicas e genotípicas heterogêneas.

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