

# Cellulitis - Gangrenous Dermatitis of Turkeys (GDT)

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A survey of turkey industry veterinarian in 2006 lists turkey cellulitis as the second largest issue facing the industry. The disease runs an acute course with quick onset with escalating mortality. Flocks on endemic farms break with the disease approximately 5-8 weeks prior to processing. During this time the toms are valued at \$10 to \$17 a bird. Mortality typically ranges from 1-3% a week. The excess mortality due to cellulitis is valued at approximately \$12,000 for a flock size of 10,000 toms placed. The excess mortality reduces the grower's income by \$2,000 for every 10,000 toms placed. During the course of the disease it approximately costs \$3,000 in antibiotics to treat a flock of 10,000 to control mortality. The excess mortality also costs the company approximately \$4,000 per 10,000 birds in lost pounds. The total Cellulitis related losses can be as high as \$20,000 for every 10,000 toms. A severe case of cellulitis can be an economic devastation to the grower and the company that owns the birds. Therefore effective control and treatment procedures need to be investigated

Gangrenous dermatitis of turkeys (GDT) is similar in its presentation to gangrenous dermatitis in broilers (GD); symptoms of the disease include swelling of the tailhead, accumulation of gelatinous fluid in the abdomen, breast or inner thighs, severe necrosis of the subcutaneous tissues and sometimes swelling and accumulation of serosanguinous fluid in the subcutis of the wings (2). The involvement of *Clostridium perfringens* in these diseases has been established by several researchers (2,3).

*C. perfringens* is a spore-forming, Gram-positive anaerobe and is ubiquitous in the poultry production environment. Typically classified into five toxin types based on the production of a combination of four major toxins ( $\alpha$ ,  $\beta$ ,  $\epsilon$  and  $\iota$ ), type A strains generally produce the most  $\alpha$ -toxin and are the most widespread (8). Also recognized as the causative agent of gas gangrene, *C. perfringens* type A has the ability to produce many minor toxins and enzymes in addition to  $\alpha$ -toxin that act synergistically to produce the pathology observed (1).

As anaerobic cellulitis continues to become more prevalent in commercial poultry production it is increasingly important to better understand the microorganisms involved. Of these organisms, *Clostridium perfringens* is typically one of the most ubiquitous. In addition to high litter populations, the bacteria are frequently found in the intestines of poultry as well as other warm blooded animals and are capable of producing an array of extra-cellular enzymes that degrade host tissues. At Agtech Products, Inc., we study the genetic diversity of *C. perfringens* and *Clostridium septicum* isolates recovered from turkeys experiencing anaerobic cellulitis. The results of this work suggest a substantial degree of genetic diversity among the isolates tested. Interestingly, isolates from producers in different states did not cluster independently indicating a rather homogeneous population overall.

The results of this work indicate a substantial degree of genetic variability within isolates of *C. perfringens* harvested from tissues affected with anaerobic cellulitis. Thirty-two unique families were identified among the 196 isolates examined. Eighteen of these were comprised of more than three isolates. Although high levels of diversity within this species have been established previously (4,5,7) this work shows a substantial degree of genetic diversity even within isolates associated with a specific disease condition. It was especially interesting that isolates from different states clustered together, but that overall the diversity remained high. One of the mechanisms proposed to explain such great genomic variability is frequent recombination events (6). Certain virulence factors can exist in variable genomic locations (6) possibly creating many different genetic fingerprints despite all of the essential genes required for a particular disease process being present. This may explain why the overall population remains rather homogeneous despite being seemingly genetically isolated. The dynamic nature of the *C. perfringens* genome also suggests an ability to adapt to a multitude of environmental situations.

Several aspects of the disease including some prevention and control measures will be discussed.

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