Turkey Cellulitis: descriptive epidemiology and molecular characterization of potential etiological agents

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Introduction

Turkey cellulitis is a major disease across all geographic regions of the US. In 2008 it was ranked among the top five disease concerns by the turkey industry. Cellulitis affects primarily heavy market-age birds and is more common in males than females. Dead birds usually show accumulation of gelatinous fluid under the skin (Fig.1 arrow), specially along the thighs (inguinal area) and breast. "Bubbly tails" and fluid filled blisters associated with root-broken feathers are also commonly seen. Currently, the agent associated with the development of cellulitis in turkeys is unknown, with clostridia being the main suspect.

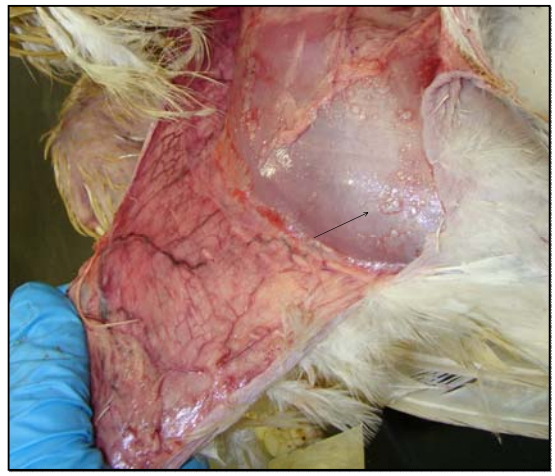
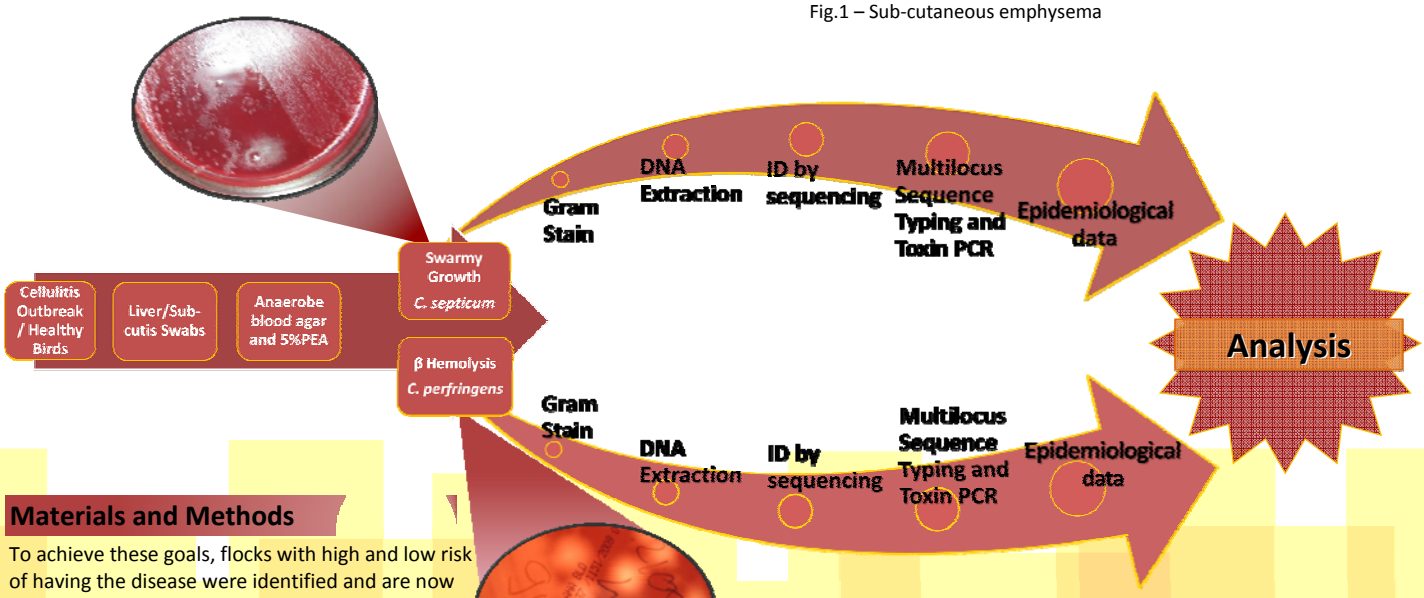


Fig.1 – Sub-cutaneous emphysema

Objectives

This study aims to (1) characterize the descriptive epidemiology of turkey cellulitis, including evaluation of the time, place, and host characteristics of this disease in turkeys and (2) identity of the molecular characteristics of clostridia associated with turkey cellulitis.



Materials and Methods

To achieve these goals, flocks with high and low risk of having the disease were identified and are now being monitored. Live and dead birds with clinical signs and/or lesions characteristic of cellulitis are submitted weekly to the University of Minnesota Veterinary Laboratory for testing. In the absence of clinical signs and lesions, randomly selected birds at the ages of 6, 8, 16 and 20 weeks are sent for diagnostic testing. Samples collected from each bird includes: liver and sub-cutis swabs, litter, and stool. Samples are cultured and isolation of *Clostridium* sp. is attempted. Isolates are further characterized by sequencing of the 16s rRNA gene, allowing the identification to the species level. *Clostridium perfringens* and *Clostridium septicum* isolates are further characterized for the presence of toxin genes using a multiplex PCR and by multilocus sequence typing (MLST) to infer relatedness. Quantitative real-time assays are used to define the number of *C. perfringens* and *C. septicum* in fecal and litter samples. The first samples from the turkey flocks involved in this study were received in November of 2008.

Relevant Results

This is an ongoing study. We have cultured samples form 94 healthy birds and 23 birds from cellulitis outbreaks. *Clostridium septicum* was isolated from 89% of the birds obtained from cellulitis outbreaks, whereas *C. perfringens* was isolated from 11% of these birds. No clostridia was isolated from samples obtained from healthy birds. *Clostridium septicum* was detected in higher levels in litter samples compared to *C. perfringens*.

Conclusions

Our preliminary data indicates that *C. septicum* is consistently isolated from turkey affected by cellulitis. We are currently generating data on toxin typing and MLST to evaluate relatedness of *C. septicum* isolates recovered from affected flocks. The presence of high levels of *C. septicum* but not *C. perfringens* in the litter samples tested suggests that environmental contamination may play an important role in the pathogenesis of turkey cellulitis.

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