

Letter to the editor

**IDENTIFICATION IN BIRDS OF THE *Stenotrophomonas maltophilia*
PROVINCE OF HAVANA, CUBA**

Dear editor.

In the etiology of Chronic Respiratory Syndrome (CRS) of birds, *Mycoplasma gallisepticum* is recognized as the main etiological agent, although it may be associated to a wide range of microorganisms that affect the airways, such as viruses and bacteria. Among the bacterial agents associated with this syndrome we can find glucose no-fermentative gram negative rods shape (BGNNF), highlighting in this group *Stenotrophomonas maltophilia*.

In the present study swabs from trachea, palatine fosse, lungs and air sacs of 100 animals from a poultry farm in the province of Havana with a typical SRC pattern, were processed. It was able to isolate mycoplasma from the field identified by morphological studies. *S. maltophilia* was isolated from 100% birds trachea by Gram stain and biochemical tests.

S. maltophilia is an organism with limited virulence. It has now emerged as an important opportunistic pathogen, primarily due to intrinsic multidrug resistance phenotype to multiple antimicrobials, being able of producing a wide clinical spectrum of infections such as pneumonia. Its presence has been reported after damages caused by a viral infection, or when the animal has been immunocompromised as in the case of mycoplasmosis.

This would be a possible explanation for the presence of *S. maltophilia* in birds affected with CRS. Further experiments to characterize this agent as well as its degree of pathogenicity in birds have to be carried out.

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