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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