

**TITLE:** EVIDENCE THAT MOST OF THE ISOLATED *HAEMOPHILUS PARASUIS* SEROVARS ARE ABSENT IN COMMERCIAL VACCINE COMPOSITION IN BRAZIL

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**ABSTRACT:**

Glässer's disease (GD) is an important infection disease of swine caused by *Haemophilus parasuis* (*Hps*), which is characterized by pneumonia, fibrinous polyserositis, polyarthritis and meningitis resulting in substantial production losses and increased costs with antibiotic use. This pathogen is in a long time classified in fifteen serovars; amongst which SV 1, 5, 10, 12, 13 and 14 are considered highly virulent; SV 2, 4, 8 and 15 are moderately virulent and SV 3, 6, 7, 9 and 11 are of low virulence, however, a high number of isolates are non-typeable (NT) in regards to the reference strains. Vaccination is the major practice used to prevent the *Hps* infection worldwide, but in many countries the available vaccines do not induce acceptable protection against the field strains, mainly because the serovars present in them are different of those isolated from the farms. So, the identification of the serovars of *Hps* involved in a GD outbreak is crucial for designing a rational vaccination program. In this study, 460 field strains of *Hps* isolated from systemic or respiratory sites of swine from ten different states of Brazil were typable using the combination of a multiplex polymerase chain reaction (mPCR) technique and a modified hemagglutination indirect (IHAm) test. In Brazil, the field strains belonging to the serovar 4, NT and serovar 1, were the most prevalent comprising more than half of the isolates, followed by serovars 14, 5, 5/12, 15, 12, 2 and 13. Dependence between serovar and virulence as well as in regard to serovar and site of isolation were observed. NT isolates were mainly related to respiratory samples, while the serovars 4, 5 and 14 were associated to systemic outbreaks. When the serovars were grouped by their virulence, a sudden rise of the highly virulent isolates was observed from 2013 onwards in comparison with the low virulent and NT *Hps* isolates. Most of the isolates were from samples collected in MG (33.8%) and SC (27.6%) and, in these two states, we observed the circulation of strains belonging to all serovars found in Brazil. Our results shown that the vaccines commercially available in Brazil do not include the most prevalent *Hps* serovars related with the GD in our country.

**Keywords:** swine, polyserositis, typing, serovars, occurrence, vaccine

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