GENETIC AND ANTIGENIC STUDIES ON *HAEMOPHILUS PARASUIS*

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Haemophilus parasuis, an organism dependent upon nicotinamide adenine dinucleotide (NAD) or V-factor for *in-vitro* growth, is the causative agent of porcine polyserositis and arthritis (Glässer's disease) (Nicolet, 1992). The principal lesions associated with this disease are fibrinous or serofibrinous meningitis, serositis, pleuritis, pericarditis, peritonitis and arthritis that can occur in various combinations or occasionally singly (Nicolet, 1992).

A total of 41 isolates of *H. parasuis* obtained from Australian pigs were serotyped by the Kielstein-Rapp-Gabrielson scheme (Kielstein and Rapp-Gabrielson, 1992). The isolates were assigned to the following serovars: serovar 1 (1 isolate); serovar 2 (3 isolates); serovar 4 (5 isolates); serovar 5 (13 isolates); serovar 9 (2 isolates); serovar 12 (1 isolate) and serovar 13 (7 isolates). Of the remaining nine isolates, four cross-reacted with serovars 7 and 10 while five could not be assigned to a serovar. Two different serovars (5 and 13) were detected in one herd. The only two isolates obtained from clinically normal pigs (from the same herd) were serovar 9. The common serovars were isolated from pigs with pneumonia as well as from pigs with clinical signs indicative of Glässer's disease. The serological heterogeneity amongst Australian isolates of *H. parasuis* has important implications for the use of vaccines to control Glässer's disease. Inactivated vaccines are effective only against those serovars present in the vaccine. As it has been established that eight different serovars of *H. parasuis* exist in Australia, therefore the choice of vaccine strains is clearly a major issue.

The genetic diversity among 40 of the Australian isolates and eight reference strains from overseas was assessed by the use of multi-locus enzyme electrophoresis. Thirty-four electrophoretic types (ET) were recognised with a mean genetic diversity per locus of 0.405. One ET was separated by a considerable distance from the rest of the isolates, suggesting that this organism may belong in a different species. The remaining 33 ET formed two divisions (A and B) which were quite distinct from each other as the genetic distance between the divisions was 0.506. Within Division A, five subgroups (I to V) were recognised. All 12 Australian serovar 5 isolates, plus the only two reference strain for this serovar, were included in Division A. The only other serovars present in Division A were Australian isolates of serovars 4 and 13. Within Division B, the four subgroups (I to IV) recognised contained a diverse range of serovars - Australian isolates of serovars 1, 2, 9 and 13 as well as the reference strains for serovars 1, 3, 4, 8 and 9.

These results support the suggestion of other studies based on DNA hybridisation that serovar 5 isolates of *H. parasuis* form a subspecies (Moruzumi *et al.*, 1986). However, the results also suggest that it is not just serovar 5 isolates that form this subspecies - Australian isolates of serovars 4 and 13 were also in the same genetic subdivision.

It has been suggested that serovar 5 isolates are predominantly associated with outbreaks of septicaemia or polyserositis (Nicolet, 1992). Further work is needed to determine if there is any link between pathogenicity and the genetic subdivisions that have been recognised in *H. parasuis*.

References

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