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Short Communications

# PASTEURELLOSIS TO MANNHEIMIOSIS: TAXANOMIC CHANGES

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## SUMMARY

**Pasteurellosis is a disease of ruminants that have been recognized for long but there has been extensive reclassification of the aetiologic agent. *Pasteurella haemolytica* is the agent of pasteurellosis. Recent advances have renamed the organism to *Mannheimia haemolytica* conversely changing the disease name to Mannheimiosis. The bacterium has 17 serovars presently but serovars 3, 4, 10 and 15 retained the name *Pasteurella* which is predominantly associated with septicaemia while the rest are now known as *Mannheimia*. In Nigeria, serotypes A1, 2, 6, 7, 8, 9, 10, 11 and T10 has been reported. Therefore, pasteurellosis may well be called mannheimiosis.**

**KEYWORDS:** Pasteurellosis, Mannheimiosis, *Pasteurella haemolytica, Mannheimia haemolytica*

## INTRODUCTION

Pasteurellosis is an infection that causes considerable economic loss to the cattle and sheep industries (Frank, 1989; Gilmour and Gilmour, 1989) with climatic and animal management factors being involved in the pathogenesis of the disease (Gilmour and Gilmour, 1989; Brogden et al., 1998).

The disease is caused by Pasteurella haemolytica now known as Mannheimia haemolytica which is a heterogenous bacterial pathogen. The heterogeneity of this bacterium is evident from the fact that historically, there have been two biotypes recognized- biotype A consisting of isolates that ferment L-arabinose and biotype T consisting of isolates that ferment trehalose (Smith, 1959); together they are represented by 1-17 P. haemolytica serovars (Gilmour and Gilmour, 1989; Younan and Wallmann, 1989). In addition, about 10% of isolates are untypable (UT) (Gilmour and Gilmour, 1989). Furthermore, extensive epidemiological studies of M. haemolytica strains using molecular typing techniques have shown some significant level of heterogeneity even within strains of the same serovars isolated from various hosts and also from different geographical areas (Davies et al., 1997).

P. haemolytica undergoes a niche change from commensal to pathogenic under condition of stress, making the control of the expression of its virulence factors of significant interest (Highlander, 2001).

## TAXONOMY AND HISTORICAL BACKGROUND OF PASTEURELLA HAEMOLYTICA

Pasteurella haemolytica is a weakly haemolytic, gram-negative coccobacillus with the following complete taxonomy: Superkingdom-Bacteria; Phylum-Proteobacteria; Class-Gammaproteobacteria; Order-Pasteurellales; Family-Pasteurellaceae; Genus-Pasteurella (www.ncbi.nlm.nih.gov/taxonomy).

The bacterium has been a subject of extensive reclassification in the past; first called Bacterium bipolare multocidum by Theodore Kitt in 1885. The genus name Pasteurella was first suggested by Italian Count Trevisan to commemorate Louis Pasteur's work with the causative agent of fowl cholera in turkeys (Mutters et al. 1989). It was renamed Pasteurella haemolytica in 1932 by Newsome and Cross and classified into two biotypes A and T, based on its ability to ferment arabinose and trehalose respectively, though other biovariats have been revealed (Kilian and Fredenriksen, 1981; Bisgaard and Mutters). There are 13 A serotypes and 4 T serotypes identified (Younan and Fodor, 1995), the latter being reclassified as Pasteurella trehalosi in 1990 (Bingham et al., 1990). Nine years later, studies based on DNA-DNA hybridization and 16SrRNA sequencing led to renaming previous A serotypes (A1, A2, A5, A6, A7, A8, A9, A12, A13, A14, A16 and A17) as Mannheimia haemolytica while the remaining A11 serotype became M. glucosida (Angen et al., 1999). Studies of genomic DNA or ribosomal RNA have revealed lack of homologies acceptable for inclusion of some organisms at the genus or species level (Dewhirst et al., 1992). The name Mannheimia was given in tribute to Walter Mannheim, a German biologist whose research has improved the understanding of the taxonomy of the Pasteurellaceae family (Angen et al., 1999).

Although P. haemolytica is now classified as three distinct species- M. haemolytica, M. glucosida and P. trehalosi, for the purpose of identification and serotyping they are still treated as one species (Odugbo et al., 2003). In addition to isolates which fall into one of the above serotypes, approximately 10% of disease isolates from ruminants is untypable (Quirie et al., 1986). The taxonomy of Pasteurellaceae is not well settled and is under continuous revision. The taxonomy has involved mainly phenotypic characterization, including the determination of polyamine patterns (Olsen et al., 2004). A few thorough studies have also been carried out at the genotypic level. Whole genome DNADNA hybridizations were carried out some time ago on Pasteurellaceae (Mutters et al., 1984) and genetic relatedness was investigated by DNArRNA hybridization (De Ley et al., 1990).

## DISTRIBUTION AND DISEASE ASSOCIATION OF MANNHEIMIA (PASTEURELLA) HAEMOLYTICA

Pasteurella species are common commensals on mucous membranes of most domestic animals in all climatic zones (Biberstein, 1979). Most ruminants are asymptomatic carriers of P. haemolytica or P. trehalosi and they frequently carry strains of P. multocida as well. The majority of isolates from cattle have been P. haemolytica, although P. trehalosi strains have been sporadically isolated from cases of bovine abortion and pneumonia (Ward, 1990).

Serotypes A1 and A2 are prevailing all over the world (Zacchinon et al, 2005). A1 and A2 are both able to colonize the upper respiratory tract of cattle and sheep but they are often species-specific (Zacchinon et al, 2005). So, healthy cattle frequently carry serotype A2 in their upper respiratory tract but following a stress or a co-infection, A1 quickly takes the place of A2 as the main serotype (Frank and Smith, 1983), probably by horizontal transfer from ill animals (Highlander, 2001). Serotype A1 was most frequently associated with bronchopneumonia with serotype A2 involved in fewer cases and other serotypes reported sporadically (Frank, 1989). Both P. haemolytica and P. trehalosi have been associated with disease in sheep with serotype A2 most frequently isolated from cases of pneumonia and mastitis, and serotypes T3, T4, T10 and T15 more commonly associated with septicaemia (Smith, 1959; Gilmour and Gilmour, 1989). P. trehalosi strains the majority of which were serotypes T3 accounted for 45% of 186 Pasteurella cultured from clinically healthy domestic pack goats and were the only types isolated in some flocks (Ward and Frank, unpublished data). Pasteurellosis in goats was reported to be associated with serotypes 2, 5, 6, 7, 8 and 11 (Fodor et al., 1989; Viera et al., 1993).

Recent surveys have shown that serotypes A6 is increasingly prevalent in the United Kingdom (Donachie, 1998) and the USA (Al-Ghamdi et al., 2000) with about 30% of strains serotyped. Nevertheless, based on lipopolysaccharide profiles and outer membrane proteins within serotype, it has been concluded that, apart from the nature of their capsules, serotypes A1 and A6 are extremely similar (Davies and Donachie, 1996; Morton et al., 1996). In Nigeria, serotypes A2 and A12 was reported from chickens (Antiabong et al., 2005) while eight serptypes (A1, 2,6,7,8,9,11, and T10) were recovered from pneumonia in five states of northern Nigeria (Odugbo et al., 2003).

## CONCLUSION

Pasteurella (Mannheimia) haemolytica continues to be an inscrutable organism. The organism has undergone major reclassification and is still under revision. The bulk of the former P. haemolytica (12 out of 17 serovars) is now known as M. haemolytica. Therefore, pasteurellosis may well be called mannheimiosis. The capabilities to identify by serotypes, the strains of Pasteruella haemolytica of aetiologic significance to small ruminants are crucuial in studies of the disease and in the development of an effective bacterin. The genome sequence of Mannheimia haemolytica was recently completed and published (Gioia et al., 2006). This will help in our understanding of its virulence and pathogenesis for development of better control/preventive strategies.

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