

TITLE: Genes associated with virulence in *Trueperella pyogenes* infections in domestic animals

AUTHORS: RISSETI R, M.¹; DE PAULA, C.L.¹; LISTONI, F.J.P.¹; COLHADO, B.S.¹; PORTILHO, F.V.R.¹; ZASTEMPOWSKA, E.²; TWARUZEK, M.²; LASSA, H.²; RIBEIRO, M.G.¹

INSTITUTION: ¹FACULDADE DE MEDICINA VETERINÁRIA E ZOOTECNIA, UNIVERSIDADE ESTADUAL PAULISTA-UNESP, BOTUCATU, SP, BRAZIL; ²INSTITUTE OF EXPERIMENTAL BIOLOGY, FACULTY OF NATURAL SCIENCE, KAZIMIERZ WIELKI UNIVERSITY, BYDGOSZCZ, POLAND.

ABSTRACT:

Trueperella pyogenes is an opportunistic pathogen that causes diverse infections in animals. Pathogenicity of this microorganism is attributed to various mechanisms, including development of pyogranulomatous reactions. The variety of virulence factors expressed by *T. pyogenes* could explain the ability of the pathogen to colonize and infect various cells and tissues, causing great diversity of pyogenic infections in domestic animals. To date, pyolysin, a potent cytolysin associated with tissue damage, is considered the major virulence factor of the pathogen. The genes that encode the exotoxin pyolysin (*plo*) and other putative factors that promote adhesion of pathogen to host cells, including fimbriae (*fimA*, *fimC*, *fimE*, *fimG*), neuraminidases (*nanH*, *nanP*), and collagen-binding protein (*cbpA*) have been associated with virulence. In this context, the genes *plo*, *fimA*, *fimC*, *fimE*, *fimG*, *nanH*, *nanP*, and *cbpA* were investigated in 36 *T. pyogenes* strains recovered from cattle, sheep, goats, dogs, equines, and a pig, isolated from abscesses, reproductive tract diseases, pneumonia, lymphadenitis and encephalitis. The most common genes harbored by the isolates were: *plo* (36/36=100.0%), *fimA* (35/36=97.2%), *nanP* (28/36=77.8%), *fimE* (27/36=75.0%), *nanH* (24/36=66.7%), and *fimC* (23/36=63.9%), whereas *cbpA* (2/36=5.6%) and *fimG* (2/36=5.6%) were uncommon. The most frequent genotypes were *plo/fimA/fimE/fimC/nanH/nanP* (9/36=25.0%), *plo/fimA/fimE/nanH/nanP* (7/36=19.4%), and *plo/fimA/fimE/fimC/nanP* (5/36=13.9%). No association was observed between the presence of genes versus clinical signs or host species. Besides the great variation of frequency among the selected genes investigated in *T. pyogenes*, genes encoding virulence markers of pathogen detected from reproductive pyogenic infections in equines and abscesses in dogs were described here for the first time. Investigations of virulence factor profiles of *T. pyogenes* from animal origin could contribute to the understanding of the molecular epidemiology, pathogenicity, and public health threats posed by animal-to-human transmission of this pathogen.

KEYWORDS: *Trueperella (Arcanobacterium) pyogenes*, pathogenicity, virulence factors, livestock, companion animals