An Up-To-Date Review of Piglet Isosporosis: New Insights and Therapeutic Perspectives

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ABSTRACT

Piglet isosporosis caused by Isospora suis represents a considerable problem worldwide with great economic losses and veterinary importance in pig production. So the control of this parasite is a great need. However, little is known about porcine coccidiosis concerning dynamics, pathophysiology and immunology of this disease, as well as host-parasite interactions. In addition, only few studies deal with experimental modelling of this illness with parameters such as the excretion patterns and the age-related susceptibility. However, besides natural I. suis infections occurring in pig farms, there are some experimental infections described that allow investigating accurately the course of infection. Experimental infections could contribute to a more effective control of these infections. In addition, managerial practices of farrowing facilities and piglet manipulations can contribute to this purpose. So, the description of hygiene measures, the appropriate management of farrowing facilities and piglet manipulations, as well as appropriate farm-specific environment, comprising appropriate design and materials of the farrowing pen and enough room, could diminish the occurrence and transmission of this parasite. However, unfortunately there are only very few reports documenting all this subjects that are so important for the effective control of this disease.

Keywords: Apicomplexa Phylum, Apicomplexan Protozoan Parasites, Coccidia, Cystoisospora, Eimeriidae, Epizootic Disease, Isospora, Oocyst, Neonatal Porcine Coccidiosis, Sarcocystidae, Sporocyst, Zoonosis

INTRODUCTION

Woese et al. first proposed that life on earth is composed of three primary divisions, or domains to which all organisms belong. These domains are named Archaea (or archaeabacteria), Bacteria (or eubacteria), and Eucarya (or eukaryotes), with Eucarya being relatives (or descendants) of Archaea (Woese & Fox, 1977; Woese et al., 1990). This proposal was
based on 16S ribosomal RNA sequences and later confirmed by the comparison of many protein sequences (Pohlschroder et al., 1997; Scamardella, 1999; Woese & Fox, 1977; Woese et al., 1990). This proposal is currently widely accepted, although some sequence features and phyllogenies derived from many highly conserved proteins are inconsistent (Gupta, 1998).

Prokaryotes and eukaryotes differ from each other in many respects, with the most important criteria of their distinction being the type of their cells; eukaryotes’ cells contain a membrane-bounded nucleus, while prokaryotes not (Gupta, 1998). Archaea resemble morphologically with bacteria (e.g. both of them are prokaryotes), but they are evolutionary distinct from them and other prokaryotes and constitute a fundamentally different form of life (i.e., life’s third domain) (Gupta, 1998; Olsen & Woese, 1993; Pohlschroder et al., 1997; Woese & Fox, 1977; Woese et al., 1990).

Eukaryotes are organisms composed of one or more cells with nuclei which have inhabited Earth for approximately 1.2 billion to 1.8 billion years (Knoll et al., 2006). Eukaryotes dominate the visible landscapes of terrestrial and marine systems and are major players in biogeochemical cycling and cause numerous global diseases (e.g., malaria, African sleeping sickness, amoebic dysentery). Eukaryotes clearly differentiate from prokaryotes as all of eukaryotes share the main features of cellular architecture (e.g. the complex intracellular compartmentalization) and the regulatory circuitry (Koonin, 2010). Plants, animals, fungi and protists are the most familiar eukaryotes (Tekle et al., 2009).

The small size of some of Eukaryotes has traditionally made these groups recalcitrant to study. In addition, their evolution exhibits a vast timescale that obscures evolutionary events during their origin and early diversification. However, advances in molecular techniques (e.g., multigene sequencing, genomics) are transforming our views on eukaryotic evolution (Tekle et al., 2009).

Protozoa are single-celled eukaryotes that commonly show characteristics usually associated with animals, most notably mobility and heterotrophy (Flynn et al., 2007; Pink et al., 2005). Protozoa combine cell and organism in one (Vickerman & Coombs, 1999). The kingdom Protozoa belongs to Protists that contains also algae, and lower fungi (Corliss, 2002). The term “protist” is often used instead of “protozoa” because many protozoa have features in common with fungi or algae (Flynn et al., 2007).

They are a multiphyletic group of organisms, whose members differ in structure, morphology, biochemistry and genetics (Flynn et al., 2007; Scamardella, 1999) and their vast diversity of cellular organization provides an endless supply of material for biologists to investigate (Vickerman & Coombs, 1999). Protozoa adapt to changing environments by modifying form and function to achieve homeostasis (Vickerman & Coombs, 1999).

A few protozoa are important parasites (Pink et al., 2005) that are responsible for diseases of humans and other mammals, lower animals and higher plants (Vickerman & Coombs, 1999). Such protozoa experience devastating changes of environment during the course of their life cycles. Protozoa may leave the host to face the outside world before infecting another host or move directly from one host to another (e.g vector-transmitted parasites such as the trypanosomes, leishmanias and malaria parasites) (Vickerman & Coombs, 1999). In addition, some parasitic protozoa must avoid elimination by host defences, innate or acquired (Vickerman & Coombs, 1999).

Parasitic diseases are caused mainly by protozoa and continue to take an enormous toll on human health, particularly in tropical regions (Pink et al., 2005). Parasitic diseases also provoke crop damage and problems in livestock health (Adl et al., 2007).

**EPIZOOTIC DISEASE AND ZOONOSIS**

Epizootic (from Greek epi- upon + zoon animal) is a disease that occasionally occur at higher than normal rates in animal populations (in correspondence with the term epidemic applied to
Towards Healthy Public Policy: GIS and Food Systems Analysis
Julie Yang (2014). Research Perspectives on the Role of Informatics in Health Policy and Management (pp. 135-152).
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