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Review Article

Dermatophilosis research: present status and future prospects

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Abstract

Dermatophilosis is a contagious disease of domestic and wild animals, and recently it has been found to also be of zoonotic importance. Since researchers began attempt to understand the genome and sequences of *Dermatophilus congolensis*, attempt to sequence the entire genome has not been achieved until recently when a series of shotgun sequences were made culminating in a master record of a whole genome sequence of the organism. Scientists started by sequencing the organism in bits and genes and partial sequences of the genes they could identify.

Introduction

Dermatophilosis is a contagious disease of domestic and wild animals, and recently it has been found to also be of zoonotic importance. It is believed to have been first reported in the Belgian Congo present day Zaire, (Van Sacegham 1915). This disease is observed to be more prevalent in the humid tropics and subtropics which are areas with high rainfall, temperatures and humidity. Though it is said to be more prevalent in these areas, it has been reported in all the continents of the world. Interestingly, the disease also has a wide host range. Since the report of dermatophilosis, various researchers and scientists have worked on the disease and the organism causing the disease. The economic importance of the disease is estimated in millions of dollars, due to the loss in productivity in terms of work by infected draft oxen, wool, hides and skin, decreased milk and meat production, a failure in reproduction in cows with severe vulva infection and stud bulls with severe leg lesion making them unable to mount (Oppong, 1976). Because of the serious economic losses associated the disease, it has generated a lot of interest by scientists worldwide. Initial interest on the disease was on how to treat and cure animals with the infection with topical medication and antibiotics.

Susceptibility tests were carried out and the drugs of choice selected used. Then came the era of using serology in trying to diagnose the disease and finding out if there are circulating antibodies, that are protective against the infection. Then scientists began trying to find the existence of other species of the organism from the wide range of the animals, the organism have been known to infect. Epidemiological studies were carried out in various corners of the world to find the prevalence and risk factors associated with the disease. The use of SDS-PAGE and western blotting to separate the proteins of the organism to determine the protein profiles and most immunogenic antigen were also carried out. Following this was the use of restriction enzymes in trying to characterize the organism to study the restriction patterns of different isolates to see if more than one species of the organism existed bearing in mind the wide host range the organism infects. This was in addition to the use of biochemical reactions and sugars to identify and speciate the organism. These series of events were not occurring in isolation with each other but could also be occurring simultaneously or concurrently. The advent of molecular biology brought in renewed interest in the disease and the

causative organism. Scientists began to search for genes of the organism, individual genes of the organism and the sequencing of these genes for possible use in molecular epidemiology. Consequently, polymerase chain reaction was used to either isolate full genes or partial genes sequences and these were used to compare with each other (Shaibuet *al.* 2010). Most recently, the need to sequence the entire genome of the organism has become increasingly more imperative. This is because more work needed to be carried out on its genome. How many genes does the organism contain? What are the basic functions of these genes? Which of these genes are necessary for the survival of the organism? Which of these genes are responsible for the pathogenesis of the organism and so on.

Current state of researches

Different researchers have tried to establish the protein profiles of isolates from different animal species with the aim of differentiating the isolates by the use of polyacrylamide gelelectrophoreses (PAGE) and sodium dodecyl sulphate polyacrylamide gel electrophoreses (SDS-PAGE) (Gogolewski *et al.*, 1992; Masters *et al.*, 1995; Kruger *et al.*, 1998; Makinde Gyles, 1999; Shaibu, *et al.*, 2011). Similarly researchers continue to use other methods such as polymerase chain reaction (PCR), (Buenviaje *et al.*, 2000; Han *et al.*, 2007; Shaibu, 2010) and cloning of serine protease gene, (Mine and Canegie, 1997). Larasa *et al.* (2002) reported the use of a simple Random Amplified polymorphic DNA (RAPD) genotyping method for field isolates of *Dermatophilus congolensis* and suggested that using this technique; they found genotypic variation between isolates, which correlated with host species. Larasa *et al.* (2002) also used other methods in their attempt to type isolates of *Dermatophilus congolensis* by evaluation of randomly amplified polymorphic DNA (RAPD) and Pulse Field Gel Electrophoreses (PFGE) techniques for molecular typing of *Dermatophilus congolensis* and concluded that both methods were good for molecular typing. Researchers have also used restriction enzymes to restrict the DNA of the organisms for genotyping of isolates (Faibra, 1993; Master *et al.*, 1995).

Etiology

Shaibu *et al.* (2011), reported the earlier controversies surrounding the etiology of the organism as reported by the previous workers. Masters, *et al.* (1995) reported the identification of a new species isolated in chelonids in Australia. Similarly Buenvieje *et al.* (2000) reported the identification of another species in crocodiles. Since then no new isolate of the organism has been made. Shaibuet *al.* (2011) also attempted to characterize isolates from cattle, sheep and goats with aim of finding out if new species existed in these animals. Though the organism has been isolated from a king cobra, macau Monkey, blue whale, Agama Lizard and a host of other species, yet no new species has been added to the ones mentioned earlier.

Sequencing/Genomics

Since researchers began attempt to understand the genome and sequences of *Dermatophilus congolensis*, attempt to sequence the entire genome has not been achieved until recently when a series of shotgun sequences were made culminating in a master record of a whole genome sequence of the organism. Scientists started by sequencing the organism in bits and genes and partial sequences of the genes they could identify. Yang and Woese, (1993) sequenced *Dermatophilus congolensis* small subunit ribosomal RNA sequence. Three years later, Normand *et al.* (1996) sequenced the *Dermatophilus congolensis* 16S ribosomal RNA (16S(rRNA) gene and Stackebrandt, and Schumann, (2011) the partial sequence of the same gene and Shaibuet *al.* (2011) sequenced partial sequences of *D. congolensis* 16S ribosomal RNA (16S rRNA) gene from cattle sheep and goats in Nigeria. Then Mine and Caniege, (1997) sequenced a serine protease antigen. Garcia, *et al.* (2004) sequenced an agac alkaline ceramidase gene and also serine protease gene (nasp gene). Kyrpediset *al.* (2013) did a *Dermatophilus congolensis* DSM 44180=NBRC 105199 strain DSM 44180, whole genome shotgun sequencing project, which is the latest work on the sequencing genome of the organism. In conclusion, more whole genome sequences of the organism need to be carried out and also carry out the annotation of the genome to determine the number and functions of the genes the organism contains. This will go a long way in finding prevention, treatment and cure of the clinical disease and control of dermatophilosis infection.

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