

Short Research Communication

First Draft Genome Sequence of the Dourine Causative Agent: *Trypanosoma Equiperdum* Strain OVI

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Abstract

Trypanosoma equiperdum is the causative agent of dourine, a sexually-transmitted infection of horses. This parasite belongs to the subgenus Trypanozoon that also includes the agent of sleeping sickness (*Trypanosoma brucei*) and surra (*Trypanosoma evansi*). We herein report the genome sequence of a *T. equiperdum* strain OVI, isolated from a horse in South-Africa in 1976. This is the first genome sequence of the *T. equiperdum* species, and its availability will provide important insights for future studies on genetic classification of the subgenus Trypanozoon.

Key words: Dourine, *Trypanosoma equiperdum*, Whole-genome sequencing, Trypanozoon.

Introduction

Trypanosoma equiperdum is a flagellated protozoan that causes dourine in horses and other members of the Equidae family. This sexually-transmitted infection is a World Organisation for Animal Health (OIE) notifiable disease. The OIE terrestrial animal health code considers dourine as non-treatable and imposes a stamping-out policy for affected animals to recover a country free status [1]. The diagnosis of dourine is problematic since the clinical signs of this disease in horses are in many ways similar to those of surra, a trypanosomosis transmitted by biting flies and caused by *Trypanosoma evansi* [2]. Both dourine and surra are characterised by non-constant symptoms that can include: anemia, edema, lethargy, fever, weight loss, incoordination, paralysis of the hind limbs, facial

paralysis eventually leading to the death of infected animals [3]. To date, phylogenetic analyses show that *T. equiperdum* and *T. evansi* are not monophyletic and should therefore be considered as subspecies of *Trypanosoma brucei*, a parasite causing sleeping sickness in humans and nagana in animals [4]. In this context, we herein report the genome sequence of *T. equiperdum* Onderstepoort Veterinary Institute (OVI), which was isolated in 1976 from the blood of a horse in South Africa [5].

Trypanosomes (*T. equiperdum* OVI) were purified from the blood of infected rats using diethylaminoethyl cellulose (DE52) [6] and genomic DNA was isolated with the Machere-Nagel NucleoSpin® Tissue kit, according to the manufacturer's instructions. The sequencing library

was prepared according to the manufacturer's instructions and sequenced on an Illumina MiSeq instrument with 2×150-bp paired-end reads, according to standard Illumina protocols (carried out by Beckman Coulter Genomics, Danvers, MA). In total, 24,282,070 paired-end reads representing an average coverage of ~104 -fold were generated. Prior to assembly, adapter sequences were trimmed [7] and digital normalisation was performed to reduce the data set without losing information [8]. Following normalisation, 5,770,258 reads were assembled using Velvet version 1.2.03 [9] with a range of k-mer values from 25 to 85. Assembled contigs of less than 1,000 bp were disregarded. Contigs of the best assembly, provided by k-mer length of 33, were extended with SSAKE (default parameter values) using Velvet generated contigs as "seeds" and the short-reads unused by Velvet for their extension [10]. The genome was assembled into 2,026 contigs (>1000 bp) giving a consensus length of 26,228,029 bp. The genomic sequence was then annotated by functional

annotation transfer using the parasite genome annotation pipeline Companion [11] with *Trypanosoma brucei* TREU927 as a reference organism. A total of 7,668 Coding DNA Sequences (CDSs) was predicted. The analysis of orthologous CDS between *Trypanosoma equiperdum* OVI and *Trypanosoma brucei* TREU927 shows that these parasites share a total of 6,805 ortholog clusters, confirming their close relatedness (Figure 1).

The *T. equiperdum* OVI draft genome sequence generated in this study constitutes the first genome of a strain classified as *T. equiperdum*; this represents a new source of knowledge that will be valuable in comparative genomic studies to shed light on the complex biological interplay between the members of the subgenus *Trypanozoon*, their hosts and their diseases.

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession CZPT00000000. The version described in this paper is the second version, CZPT02000000.

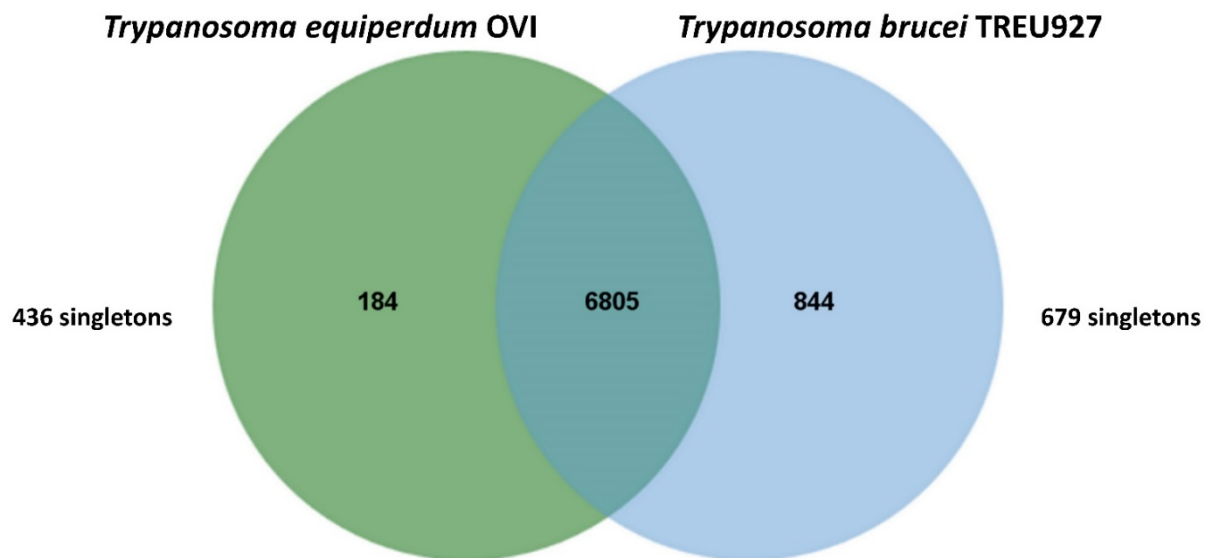


Figure 1. Venn diagram showing the results of OrthoMCL v1.4 analysis of orthologous CDS between *Trypanosoma equiperdum* OVI and *Trypanosoma brucei* TREU927. This Venn diagram show shared and species-specific protein-coding gene clusters in the genomes *T. equiperdum* OVI (left, green) and *Trypanosoma brucei* TREU927 (right, blue). Singletons, i.e. genes without orthologs and paralogs in either species, are placed outside the Venn diagram to the left and right.

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Competing Interests

The authors have declared that no competing interest exists.

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