AMERICAN SOCIETY FOR MICROBIOLOGY
Microbiology Resource Announcements

Draft Genome Sequences of 40 *Dermatophilus congolensis* Isolates from Bovine Dermatophilosis Cases in St. Kitts and Nevis

Ian Branford,[a] Shevaun Johnson,[a] Samantha Zayas,[a] Aspinas Chapwanya,[a] Filip Boyen,[b] Matylda B. Mielcarska,[c] Lidia Szulc-Dąbrowska,[c] Patrick Butaye,[a,b] Felix N. Toka[a,c]

[a]Ross University School of Veterinary Medicine, Basseterre, St. Kitts and Nevis
[b]Ghent University, Faculty of Veterinary Medicine, Department of Pathology, Bacteriology, and Avian Diseases, Merelbeke, Belgium
[c]Warsaw University of Life Sciences-SGGW, Institute of Veterinary Medicine, Warsaw, Poland

ABSTRACT *Dermatophilus congolensis* causes dermatophilosis in cattle, mainly in tropical climates. Despite the economic losses caused by this bacterium, its pathogenic factors are less well understood. We report draft genomes of *D. congolensis* strains isolated during a dermatophilosis outbreak in cattle in St. Kitts and Nevis. Some isolates contain *tet*(Z), which is responsible for resistance to tetracyclines.

Dermatophilus congolensis belongs to the family *Dermatophilaceae* in the genus *Dermatophilus*. It impacts animal health, reduces animal productivity, results in carcass condemnation, and damages the hide. There is no vaccine against this zoonotic pathogen, which may be underdiagnosed in humans (1). The rationale for sequencing is that limited data exist on the molecular characteristics of the *D. congolensis* genome and the 2019 outbreak of disease included animal deaths, suggesting a role for potential emerging virulent strains. We collected 78 scab samples from cattle during a dermatophilosis outbreak in St. Kitts. To isolate the bacteria, the scabs were placed in a sterile mortar and crushed with a pestle. Fragments were transferred to 2 ml of sterile distilled water in a tube and left at room temperature for 3 h. Later, the tube was placed unsealed in a jar with a lit candle for 15 min. A loopful of solution from the surface of the tube contents was inoculated onto blood agar plates, incubated for up to 72 h at 37°C in 5% CO_2, and inspected for growth daily. Suspected colonies, i.e., small, yellow, raised, β-hemolytic, and embedded in agar after 24 to 48 h, were subcultured on blood agar until a pure culture was obtained. To obtain material for identification and genomic DNA isolation, bacteria were cultured in liquid brain heart infusion broth for 48 h at 37°C in 5% CO_2. Bacterial isolates were identified as *D. congolensis* by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) (2). Additionally, PCR confirmed the presence of the *agac* gene, which encodes the *D. congolensis* alkaline ceramide protein (3).

Bacterial DNA was prepared with the AllPrep bacterial DNA/RNA/protein kit (Qiagen, USA). The quality and concentration of DNA were determined with a Qubit 2.0 fluorometer with the following optical density (OD) ratios: OD at 260 nm (OD_{260})/OD_{280} of 1.9 and OD_{260}/OD_{230} of 1.9. Libraries were prepared using the Nextera XT library preparation kit and were sequenced on an Illumina HiSeq system using the 2 × 150-bp strategy. Libraries were sequenced at Admera Health, LLC (South Plainfield, NJ, USA). The genomes were sequenced at a coverage of $\geq 30\times$. Quality control of derived sequences was performed with FastQC v0.11.5 (4) (https://narrative.kbase.us). Adapters and low-quality reads were removed with TrimGalore v0.6.4 (https://github.com/FelixKrueger/TrimGalore) with the following parameters: retain reads with a Phred quality score above 30, discard reads whose length is less than 50 bp after quality

Citation Branford I, Johnson S, Zayas S, Chapwanya A, Boyen F, Mielcarska MB, Szulc-Dąbrowska L, Butaye P, Toka FN. 2021. Draft genome sequences of 40 *Dermatophilus congolensis* isolates from bovine dermatophilosis cases in St. Kitts and Nevis. Microbiol Resour Announc 10:e00334-21. https://doi.org/10.1128/MRA.00334-21.

Editor Julie C. Dunning Hotopp, University of Maryland School of Medicine

Address correspondence to Felix N. Toka, ftoka@rossvet.edu.kn.

Received 30 March 2021
Accepted 29 April 2021
Published 27 May 2021

TABLE 1 Statistics for draft genome assemblies of *D. congolensis* strains isolated from acute cases of dermatophilosis on the island of St. Kitts

Isolate name	Species	GenBank accession no.	SRA accession no.	Total no. of reads	Final coverage (×)	N_{50} (bp)	Genome size (bp)	No. of contigs	No. of coding sequences	G+C content (%)
BTSK1	*D. congolensis*	JAAFOV000000000	SRX7208580	1,977,952	225	62,641	2,636,036	2	2,482	58.8
BTSK2	*D. congolensis*	JAAFOU000000000	SRX7208581	2,047,090	233	36,669	2,635,845	2	2,501	58.8
BTSK3	*D. congolensis*	JAAFOT000000000	SRX7208592	2,181,622	247	36,669	2,645,506	4	2,506	59.2
BTSK4	*D. congolensis*	JAAFOS000000000	SRX7208603	2,005,910	228	36,032	2,644,574	6	2,504	59.2
BTSK5	*D. congolensis*	JAAFOR000000000	SRX7208614	2,376,664	263	35,808	2,707,787	4	2,566	59.2
BTSK6	*D. congolensis*	JAAFOQ000000000	SRX7208615	2,071,660	230	36,699	2,707,101	4	2,580	59.1
BTSK7	*D. congolensis*	JAAFOP000000000	SRX7208616	2,023,060	230	46,334	2,634,952	2	2,546	58.8
BTSK8	*D. congolensis*	JAAFOO000000000	SRX7208617	2,081,650	239	39,504	2,610,909	2	2,530	58.8
BTSK9	*D. congolensis*	JAAFON000000000	SRX7208618	1,964,496	218	34,393	2,705,920	5	2,577	59.1
BTSK10	*D. congolensis*	JAAFOM000000000	SRX7208619	2,086,030	231	36,071	2,706,861	7	2,581	59.1
BTSK11	*D. congolensis*	JAAFOL000000000	SRX7208582	1,977,630	219	34,352	2,704,542	9	2,564	59.1
BTSK12	*D. congolensis*	JAAFOK000000000	SRX7208583	1,940,046	215	35,040	2,706,162	8	2,567	59.1
BTSK13	*D. congolensis*	JAAFOJ000000000	SRX7208584	2,298,664	255	39,414	2,705,629	6	2,562	59.1
BTSK14	*D. congolensis*	JAAFOI000000000	SRX7208585	1,947,074	216	36,055	2,706,605	5	2,520	59.1
BTSK15	*D. congolensis*	JAAFOH000000000	SRX7208586	1,914,556	212	35,867	2,706,691	4	2,553	59.1
BTSK16	*D. congolensis*	JAAFOG000000000	SRX7208587	2,085,600	231	35,425	2,704,123	4	2,561	59.1
BTSK17	*D. congolensis*	JAAFOF000000000	SRX7208588	1,974,306	225	40,401	2,635,364	2	2,551	58.8
BTSK18	*D. congolensis*	JAAFOE000000000	SRX7208589	2,022,336	230	34,301	2,643,372	3	2,486	59.2
BTSK19	*D. congolensis*	JAAFOD000000000	SRX7208590	2,102,574	238	36,056	2,646,426	5	2,505	59.2
BTSK20	*D. congolensis*	JAAFOC000000000	SRX7208591	1,835,522	208	40,084	2,643,778	3	2,498	59.2
BTSK21	*D. congolensis*	JAAFOB000000000	SRX7208593	2,478,552	285	43,043	2,609,406	3	2,513	58.8
BTSK22	*D. congolensis*	JAAFOA000000000	SRX7208594	2,125,938	236	35,872	2,705,748	4	2,584	59.1
BTSK23	*D. congolensis*	JAAFNZ000000000	SRX7208595	1,812,266	201	36,023	2,707,702	5	2,584	59.1
BTSK24	*D. congolensis*	JAAFNY000000000	SRX7208596	2,157,370	245	36,132	2,644,395	4	2,480	59.2
BTSK25	*D. congolensis*	JAAFNX000000000	SRX7208597	1,876,270	213	39,840	2,644,659	4	2,481	59.2
BTSK26	*D. congolensis*	JAAFNW000000000	SRX7208598	2,120,640	236	40,081	2,690,948	5	2,546	59.1
BTSK27	*D. congolensis*	JAAFNV000000000	SRX7208599	1,990,734	227	42,739	2,635,575	2	2,505	58.8
BTSK28	*D. congolensis*	JAAFNU000000000	SRX7208600	2,055,712	233	36,892	2,644,675	4	2,536	59.2
BTSK29	*D. congolensis*	JAAFNT000000000	SRX7208601	2,009,138	228	35,918	2,641,543	5	2,518	59.2
BTSK30	*D. congolensis*	JAAFNS000000000	SRX7208602	2,059,488	229	37,662	2,692,568	4	2,526	59.1
BTSK31	*D. congolensis*	JAAFNR000000000	SRX7208604	1,800,378	205	38,314	2,635,532	2	2,536	58.8
BTSK32	*D. congolensis*	JAAFNQ000000000	SRX7208605	2,589,746	294	52,013	2,640,714	3	2,499	59.2
BTSK33	*D. congolensis*	JAAFNP000000000	SRX7208606	1,724,744	196	35,444	2,640,994	4	2,490	59.2
BTSK34	*D. congolensis*	JAAFNO000000000	SRX7208607	1,967,536	224	44,591	2,635,305	2	2,527	58.8
BTSK35	*D. congolensis*	JAAFNN000000000	SRX7208608	1,965,800	223	36,107	2,642,663	2	2,488	59.2
BTSK36	*D. congolensis*	JAAFNM000000000	SRX7208609	1,928,268	218	35,350	2,649,493	4	2,496	59.2
BTSK37	*D. congolensis*	JAAFNL000000000	SRX7208610	1,958,350	222	36,093	2,642,605	4	2,517	59.2
BTSK38	*D. congolensis*	JAAFNK000000000	SRX7208611	1,940,290	220	38,501	2,640,313	3	2,503	59.2
BTSK39	*D. congolensis*	JAAFNJ000000000	SRX7208612	1,781,368	202	34,368	2,640,884	4	2,540	59.2
BTSK40	*D. congolensis*	JAAFNI000000000	SRX7208613	1,999,598	227	38,550	2,640,858	4	2,510	59.2

control, and maintain paired-end read order. Genome assembly was performed with SPAdes v3.13.0 (https://narrative.kbase.us) or MEGAHIT v1.1.1, and the assembly quality was determined with QUAST v4.4 (5). Annotation was performed with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.11 (6). GenBank and SRA accession numbers for each isolate and assembly statistics are presented in Table 1. For easy identification, we have named the isolates BTSK followed by a number.

We used the Comprehensive Antibiotic Resistance Database (CARD) v3.0.7 (Resistance Gene Identifier [RGI] v5.1.0; https://card.mcmaster.ca/analyze/rgi) (7) and ResFinder v3.2 (https://cge.cbs.dtu.dk/services/ResFinder) (8) to search for antimicrobial resistance genes. The two databases identified the *tet*(Z) gene in 12 isolates of *D. congolensis*. The gene confers resistance to tetracyclines. PHASTER (BLAST+ v2.3.0+) (https://phaster.ca) (9) identified prophage sequences.

Data availability. The whole-genome sequencing data and raw read data have been deposited in GenBank under the BioProject accession number PRJNA590056. Table 1 lists the accession numbers for draft genome assemblies and Sequence Read Archive (SRA) data.

ACKNOWLEDGMENTS

This study was supported by grant 41003-2019 to F.N.T. from the One Health Centre for Zoonoses and Tropical Veterinary Medicine, Ross University School of Veterinary Medicine. Bacterial species identification was performed by MALDI-TOF MS financed by the Research Foundation Flanders (FWO-Vlaanderen) as Hercules project AUGE/15/05 (grant G0H2516N). The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

REFERENCES

1. Amor A, Enríquez A, Corcuera MT, Toro C, Herrero D, Baquero M. 2011. Is infection by *Dermatophilus congolensis* underdiagnosed? J Clin Microbiol 49:449–451. https://doi.org/10.1128/JCM.01117-10.
2. Van Driessche L, Vanneste K, Bogaerts B, De Keersmaecker SCJ, Roosens NH, Haesebrouck F, De Cremer L, Deprez P, Pardon B, Boyen F. 2020. Isolation of drug-resistant *Gallibacterium anatis* from calves with unresponsive bronchopneumonia, Belgium. Emerg Infect Dis 26:721–730. https://doi.org/10.3201/eid2604.190962.
3. García A, Martínez R, Benitez-Medina JM, Risco D, García WL, Rey J, Alonso JM, de Mendoza JH. 2013. Development of a real-time SYBR Green PCR assay for the rapid detection of *Dermatophilus congolensis*. J Vet Sci 14:491–494. https://doi.org/10.4142/jvs.2013.14.4.491.
4. Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. http://www.bioinformatics.babraham.ac.uk/projects/fastqc.
5. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086.
6. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.
7. Alcock BP, Raphenya AR, Lau TTY, Tsang KK, Bouchard M, Edalatmand A, Huynh W, Nguyen A-LV, Cheng AA, Liu S, Min SY, Miroshnichenko A, Tran H-K, Werfalli RE, Nasir JA, Oloni M, Speicher DJ, Florescu A, Singh B, Faltyn M, Hernandez-Koutoucheva A, Sharma AN, Bordeleau E, Pawlowski AC, Zubyk HL, Dooley D, Griffiths E, Maguire F, Winsor GL, Beiko RG, Brinkman FSL, Hsiao WWL, Domselaar GV, McArthur AG. 2020. CARD 2020: antibiotic resistome surveillance with the Comprehensive Antibiotic Resistance Database. Nucleic Acids Res 48:D517–D525. https://doi.org/10.1093/nar/gkz935.
8. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. J Antimicrob Chemother 67:2640–2644. https://doi.org/10.1093/jac/dks261.
9. Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. Nucleic Acids Res 44:W16–W21. https://doi.org/10.1093/nar/gkw387.