

Molecular Description of a Novel *Orientia* Species Causing Scrub Typhus in Chile

Appendix

Appendix Table 1. Primers and amplification conditions of semi-nested PCR assays

Target	Primer ID	Sequence (5'-3')	Annealing temp.	Ref.
16S rRNA (<i>rrs</i>)	16sO79F*	ATTAATGCTGAGCTTGCTTAGCAT	51°C	(1)
	16sOR1198R*,†	TTTCCTATAGTTCCCGGCATT	51°C	(1)
	16s155F†	TCAGTACGGAATAACWTTTAGAAATAA	51°C	(2)
47-kDa (<i>htrA</i>)	Otr47_263F*	GTGCTAAGAAARGATGATACTTC	51°C	(3)
	Otr47_1133R*,†	ACATTTAACATACCACGACGAAT	51°C	(3)
	Otr47F†	TAAAGGTTAAGTTTATGAAAAAGGCATT	51°C	(4)
56-kDa (<i>tsa</i>)	Otr56_498F*	AATTAGTTTAGAATGGTTACCAC	54°C	(4)
	r56_1459R*,†	TCTGTATCTGTTTCGACAGATGCACTATTA	54°C	(5)
	Otr56_585F†	GAATGTCTGCGTTGTCGTTGC	54°C	(4)

*PCR.

†Semi-nested PCR.

Appendix Table 2. Identity matrix of *rrs* (upper right) and *htrA* (lower left). Percentage of pairwise identity of sequences and *rrs*/*htrA* genotypes of 18 *Orientia* isolates from Chile

Genotypes	BM 2016- ‡	LC 2016- ‡	MS 2016- M*‡	IS 2017- M‡	NV 2017- ‡	AE 2018- M‡	FC 2018- M‡	AF 2018- M‡	EC 2018- M‡	VP 2018- M‡	SH 2018- M§	GM 2019- I*¶	JC 2019- I¶	CC 2019- M¶	CV 2019- M¶	MA 2019- M§	MV 2019- M§	SG 2019- M*§
BM2016-I#		100	100	100	100	100	100	100	100	100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
LC2016-I#	100		100	100	100	100	100	100	100	100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
MS2016-M#	100	100		100	100	100	100	100	100	100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
IS2017-M#	100	100	100		100	100	100	100	100	100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
NV2017-I#	100	100	100	100		100	100	100	100	100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
AE2018-M#	100	100	100	100	100		100	100	100	100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
FC2018-M#	100	100	100	100	100	100		100	100	100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
AF2018-M#	100	100	100	100	100	100	100		100	100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
EC2018-M#	100	100	100	100	100	100	100	100		100	99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
VP2018-M*#	100	100	100	100	100	100	100	100	100		99.8	99.7	99.7	99.7	99.7	99.8	99.8	99.8
SH2018-M	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		99.8	99.8	99.8	99.8	100	100	100
GM2019-I#	100	100	100	100	100	100	100	100	100	100	NA		100	100	100	99.8	99.8	99.8
JC2019-I††	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	NA	99.8		100	100	99.8	99.8	99.8
CC2019-M††	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	NA	99.8	100		100	99.8	99.8	99.8
CV2019-M††	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	NA	99.8	100	100		99.8	99.8	99.8
MA2019-M††	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	NA	99.8	100	100	100		100	100
MV2019-M††	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	NA	99.8	100	100	100	100		100
SG2019-M*††	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	NA	99.8	100	100	100	100	100	

NA, not amplified

*Deposited at GenBank

‡*rrs* 1 genotype

§*rrs* 2 genotype

¶*rrs* 3 genotype

#*htrA* a genotype

††*htrA* b genotype

References

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