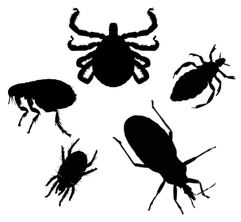
Metagenomic surveillance for veterinary and public health relevant bacterial agents carried by blood-sucking arthropods in Chile



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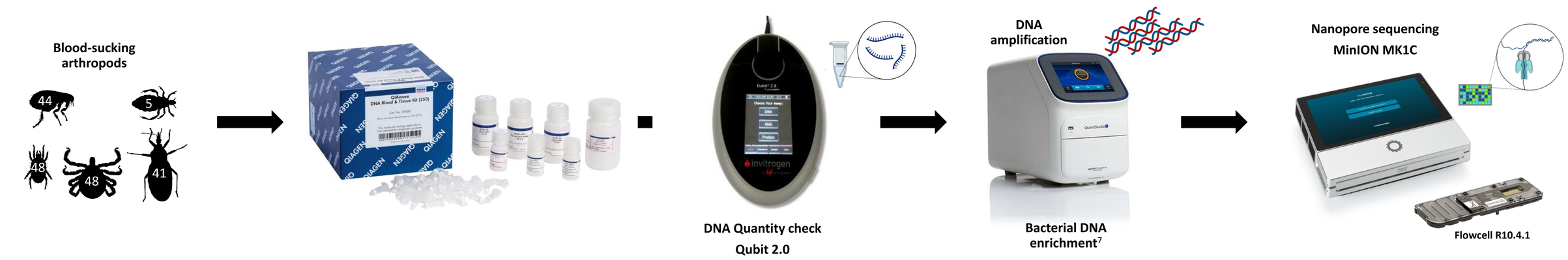
BACKGROUND

As vector of many neglected diseases, blood-sucking arthropods pose an unseen threat until symptomatic cases in humans or animals emerge, or when local epidemics occur.[1,2,3] With the current climate change scenario creating an environment conducive to the emergence, re-emergence, and spread of arthropod-borne infectious agents, continuous surveillance and timely identification of microorganisms with pathogenic potential become permanent tasks.[4] Nanopore sequencing has emerged as a powerful tool for epidemiological surveillance in diverse settings, offering rapid and real-time processing of a relatively large number of samples.[5,6] Our study utilises long-read sequencing to enhance our understanding of the potential vectorial role that blood-sucking arthropods – fleas, lice, mites, ticks, and triatomines – play across Chilean ecosystems regarding Bacteria.

METHODS



RESULTS

Map of Chile.
Denotes the approximate location of the samples that presented reads for potentially pathogenic Bacteria. Colour code: blue, *Rickettsia*; yellow, *Orientia*; pink, *Borrelia*.

2 Fleas — 1,242 reads *Orientia* sp.

Orientia tsutsugamushi - CP044031

	BLASTn	Length	Identities	Query Cover	Gaps
Average	95.27%	1476	1286/1352	98	13.5/1352
Min	88.97%	1409	754/775	92	2/775
Max	97.29%	1572	1412/1495	99	44/1495

14 Ticks — 51 reads *Rickettsia* sp. SFGI

Rickettsia parkeri strain Black Gap - CP044031
Rickettsia parkeri strain Atlantic Rainforest - CP040325

	BLASTn	Length	Identities	Query Cover	Gaps
Average	98.43%	1384	1355/1376	99.03	10/1376
Min	96.32%	919	775/1470	99	3/795
Max	99.25%	1463	1451/1470	100	25/1470

Orientia tsutsugamushi - CP044031

	BLASTn	Length	Identities	Query Cover	Gaps
Average	94.64%	1189	1071.5/1127	98.5	17/1127
Min	93.14%	927	747/802	98	9/802
Max	96.14%	1451	1396/1452	99	25/1452

2 reads *Orientia* sp. — **2 Triatomines**

12 Fleas — 29 reads *Rickettsia* sp. SFGI

Rickettsia parkeri strain Black Gap - CP044031
Rickettsia parkeri strain Atlantic Rainforest - CP040325

	BLASTn	Length	Identities	Query Cover	Gaps
Average	97.82%	1304	1234/1261		12/1261
Min	96.15%	929	700/728	99	1/728
Max	97.82%	1460	1440/1464		18/1464

1 Mites — 2 reads *Borrelia* sp. RFG

Borrelia sp. R57 - AY626138

	BLASTn	Length	Identities	Query Cover	Gaps
Average	96.50%	1467	1391.5/1442		9/1442
Min	96.19%	1440	1388/1441	96	6/1441
Max	96.81%	1494	1395/1443		12/1443

Rickettsia parkeri strain Black Gap - CP044031
Rickettsia parkeri strain Atlantic Rainforest - CP040325

	BLASTn	Length	Identities	Query Cover	Gaps
Average	98.43%	1384	1355/1376	99.03	10/1376
Min	96.32%	919	775/1470	99	3/795
Max	99.25%	1463	1451/1470	100	25/1470

2 Lice — 11 reads *Rickettsia* sp. SFGI

Rickettsia parkeri strain Atlantic Rainforest - CP040325

	BLASTn	Length	Identities	Query Cover	Gaps
Average	97.89%	1161	869/888		6.3/888
Min	97.70%	1053	766/784	99	4/784
Max	98.24%	1353	1062/1081		8/1081

1 Mites — 3 reads *Rickettsia* sp. SFGI

DISCUSSION AND CONCLUSIONS

Although the detection of *Orientia* DNA in fleas and triatomines was unexpected, the identification of *Borrelia* DNA in mites[13] and *Rickettsia* DNA in ticks,[14] fleas,[15] lice,[16] and mites[17] has been previously reported. In this sense, our next steps involve the use of taxa-specific primers to confirm our findings. Metabarcoding based on 16S rRNA is useful for profiling arthropod-borne bacterial agents, capturing not only a snapshot of potential pathogens circulating among these arthropods but also establishing the foundation for future genetic analyses.

REFERENCES

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