

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement
☒	☐ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ A description of all covariates tested
☒	☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☐	☒ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒ Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection	Climatic data from 2010 to 2023 across six provinces in China (Gansu, Inner Mongolia, Ningxia, Qinghai, Shaanxi and Xinjiang) and six neighbouring countries (Afghanistan, Kazakhstan, Kyrgyzstan, Mongolia, Pakistan and Tajikistan) were sourced from the Global Surface Summary of Day Data archive. Global grid data on elevation at a spatial resolution of 30 meters were downloaded from the Land Processes Distributed Active Archive Center. Global grid data for land cover at a spatial resolution of 30 meters were downloaded from the ESA WorldCover 2021 archive. We downloaded global livestock grid data at a spatial resolution of 10 kilometres from the Food and Agriculture Organization of the United Nations. Finally, we downloaded population density and the proportion of the rural population at the county level for provinces in China and at the district level for neighbouring countries from an online website City Population.
Data analysis	We used Fastp v0.20.0, Trimmomatic v0.36, Bowtie2 v2.4.1, SAMtools v1.10, Geneious Prime v2023.2.1, Trinity v2.5.1, MAFFT v7.490, IQ-TREE v1.6.1241, and MrBayes 3 to analyse the sequencing data and viral genomes. We used BRT model to predict the probabilities of occurrence of ticks and TBVs. The codes used in this study are archived on Zenodo with the https://doi.org/10.5281/zenodo.17385901 . The corresponding GitHub repository can be found at https://github.com/HengcongLiu/NorthWestBRTmodel .

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The sequence reads generated in this study have been deposited in the NCBI Sequence Read Archive (SRA) database under BioProject accession number PRJNA1190384 (SRA accession numbers: SRR32560802- SRR32561316) [<https://dataview.ncbi.nlm.nih.gov/object/PRJNA1190384>]. The assembled sequences are available at GenBank under accession numbers PV023382-PV023575 [add hyperlink here]. The study data is also available in an openly available repository Figshare [<https://doi.org/10.6084/m9.figshare.28831238>]. All data required to develop the BRT model in this study are provided in the Supplementary Data or are accessible via the provided source links.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	This study does not involve information about sex and gender.
Reporting on race, ethnicity, or other socially relevant groupings	This study does not involve information about race, ethnicity, or other socially relevant groupings.
Population characteristics	Only a tick was collected from a patient in 2019, who presented clinical symptoms of severe edema, partial necrosis, and monocytosis.
Recruitment	Only a tick was collected from a patient in 2019, who presented clinical symptoms of severe edema, partial necrosis, and monocytosis.
Ethics oversight	The study of a tick collected from a patient was approved by the ethics committee of the First Affiliated Hospital of Shihezi Medical University.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	This is a vector, genomic, and modelling study of the risk of human- and mammal-infecting tick-borne viruses in Northwest China and adjacent countries.
Research sample	From 2012 to 2024, a total of 100,406 ticks were collected from 82 counties in Xinjiang Uygur Autonomous Region (XUAR, n=85,960), Qinghai (n=475), Gansu (n=55), and West Inner Mongolia Autonomous Region (IMAR, n=1,602), China, and Kazakhstan (n=12,314).
Sampling strategy	A total of 41,847 unfed ticks were collected by flagging. A total of 58,559 blood-feeding ticks were removed from different domestic or wild animals. A total of 9,610 ticks containing 3,493 unfed and 6,117 feeding ticks from 30 counties in XUAR (n=7,486), Qinghai (n=402), Gansu (n=55), and West IMAR (n=1,068), China, and Kazakhstan (n=599) were used for meta-transcriptomic sequencing.
Data collection	The collection sites of 82 counties selected to cover the main eco-regions of north-western China and Kazakhstan, such as desert, shrubland, steppe, and farmland. The latitude and longitude of each collection site were recorded. H.Z., Y.-X.W., S.Z., M.G., J.C., M.C., S.W., X.Z., J.Q., Z.L., Z.M., R.Z., and B.Z. collected the samples and relevant data.
Timing and spatial scale	We collected samples from 2012 to 2024 in Northwest China and Kazakhstan, and sampling time was mainly during the peak period of ticks every year (from March to October).
Data exclusions	Any ambiguous information of TBVs and ticks reported in the studies was excluded if the ambiguity could not be clarified.
Reproducibility	This study does not involves reproducible experiment.
Randomization	All samples were randomly pooled into different groups according their biological characteristics, such as tick species, bloodmeal

status, collection location and date.

Blinding

This study does not involve blinding.

Did the study involve field work?

☒ Yes ☐ No

Field work, collection and transport

Field conditions

The collection sites included different ecological environments, such as desert, shrubland, steppe, and farmland.

Location

The latitude and longitude of each collection site were recorded and shown in Supplementary Data 1.

Access & import/export

We only enter the permitted habitats for sample collection.

Disturbance

No disturbance were caused.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

Methods

- | | |
|-------------------------------------|---|
| n/a | Involved in the study |
| ☒ | ☐ Antibodies |
| ☒ | ☐ Eukaryotic cell lines |
| ☒ | ☐ Palaeontology and archaeology |
| ☐ | ☒ Animals and other organisms |
| ☒ | ☐ Clinical data |
| ☒ | ☐ Dual use research of concern |
| ☒ | ☐ Plants |

- | | |
|-------------------------------------|---|
| n/a | Involved in the study |
| ☒ | ☐ ChIP-seq |
| ☒ | ☐ Flow cytometry |
| ☒ | ☐ MRI-based neuroimaging |

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals

The study did not involve laboratory animals.

Wild animals

Wild animals were captured by cages in the field, and the parasitic ticks on their bodies were collected. Host animals were subsequently released. The study has been reviewed and approved by the ethic committee of Shihezi University and Shandong First Medical University.

Reporting on sex

Sex was not considered in the study design.

Field-collected samples

A total of >100,000 ticks of 28 different tick species from 82 counties across diverse environments in Northwest China and adjacent countries were collected.

Ethics oversight

The study was approved by the ethics committee of the First Affiliated Hospital of Shihezi Medical University, including the procedures and protocols of specimen collection and processing, and informed consent was obtained from the patient involved (No. A2018-144-01).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.