**Supplementary Materials**

Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the U.S. Government.

**Table S1**: Year of first *Batrachochytrium dendrobatidis* (Bd) detection and prevalence for 36 breeding sites where 231 toads were sampled and genotyped in 2018 and 2019. “Na” denotes sites where Bd has never been detected. Sampling sites were grouped into 15 regions for population genomic measures, consisting of Wyoming (WY), Elkhead Mountains (Elkhead), Front Range north (FR\_N), Zimmerman Lake (Zim), Rocky Mountain National Park (RMNP), Gore Range north and south (Gore\_N and Gore\_S), I-70 north and south (I70\_N and I70\_S), Grand Mesa (Grand), Elk Mountains (Elk), Mosquito Range (Mosq), and Sawatch Range north, central, and south (Saw\_N, Saw\_C, and Saw\_S). See Figure 1 for map of these regions. ‘*N*’ refers to number of individuals sequenced using double-digest, restriction site-associated DNA sequencing (ddRAD). ‘Unknown’ refers to Wyoming site where we do not have Prevalence data, whereas ‘Na” refers to Colorado sites where Bd has been tested for but has never been detected.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Site | Region | *N* | Genomic Sampling | Year of First Bd Detection | Prevalence |
| WY01 | WY | 3 | 2019 | 2004 | Unknown |
| RO04 | Elkhead | 6 | 2019 | 2003 | 1.00 |
| LR06 | FR\_N | 4 | 2018, 2019 | 2014 | 0.45 |
| LR10 | FR\_N | 3 | 2019 | 2014 | 0.57 |
| LR07 | FR\_N | 9 | 2018 | 2016 | 0.38 |
| Zim | Zim | 36 | 2018 | Na | Na |
| LR01 | RMNP | 16 | 2018, 2019 | 2022 | 1.0 |
| LR03 | RMNP | 3 | 2019 | Na | Na |
| RED | RMNP | 8 | 2018 | 2016 | 0.43§ |
| RO07 | Gore\_N | 4 | 2019 | Na | Na |
| RO05 | Gore\_N | 3 | 2018 | Na | Na |
| RO08 | Gore\_N | 3 | 2018 | Na | Na |
| SU04A | Gore\_S | 12 | 2018, 2019 | Na | Na |
| SU04B | Gore\_S | 3 | 2018 | Na | Na |
| SU05 | Gore\_S | 1 | 2019 | 2021 | 1.0 |
| CC02 | I70\_N | 1 | 2018 | 2007 | 0.53 |
| GR07 | I70\_N | 5 | 2018 | Na | Na |
| SU08 | I70\_S | 10 | 2018 | Na | Na |
| SU06 | I70\_S | 2 | 2018 | Na | Na |
| CCLC | I70\_S | 7 | 2018 | 2018 | 0.25\* |
| CC06 | I70\_S | 3 | 2019 | Na | Na |
| ME01 | Grand | 14 | 2018, 2019 | 2007 | 0.20 |
| PI02 | Elk | 12 | 2018 | Na | Na |
| GU01 | Elk | 11 | 2018 | Na | Na |
| CF07 | Mosq | 2 | 2019 | 2014 | 0.5 |
| CF20 | Mosq | 1 | 2019 | Na | Na |
| EA04 | Saw\_N | 5 | 2019 | 2016 | 0.67\* |
| EA06 | Saw\_N | 5 | 2018 | 2014 | 0.18 |
| LA02 | Saw\_N | 1 | 2018 | Na | Na |
| PI07 | Saw\_C | 2 | 2019 | Na | Na |
| PI04 | Saw\_C | 4 | 2018, 2019 | Na | Na |
| GU03 | Saw\_S | 11 | 2018 | 2017 | 0.39 |
| GU06 | Saw\_S | 2 | 2018, 2019 | Na | Na |
| CF04 | Saw\_S | 7 | 2018, 2019 | 2014 | 1.00\* |
| CF10 | Saw\_S | 6 | 2018, 2019 | 2015 | 0.05 |
| CF08 | Saw\_S | 6 | 2019 | 2014 | 0.33 |

\* Denotes a year when multiple Bd samples were pooled. Value reflects the proportion of sample pools that tested positive for Bd.

§ Prevalence measures based on sampled *Pseudacris maculata*

**Table S2**: Genetic distances (FST) of boreal toads in the southern Rocky Mountains (SRM) of Colorado and southern Wyoming, USA.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | WY | Elkhead | FR\_N | Zim | RMNP | Gore\_N | I70\_N | I70\_S | Gore\_S | Grand | Elk | Saw\_C | Mosq | Saw\_N | Saw\_S |
| WY | -- | 0.08 | 0.04 | 0.04 | 0.08 | 0.06 | 0.07 | 0.03 | 0.04 | 0.05 | 0.04 | 0.03 | 0.08 | 0.13 | 0.02 |
| Elkhead |  | -- | 0.03 | 0.03 | 0.05 | 0.04 | 0.05 | 0.03 | 0.04 | 0.05 | 0.04 | 0.03 | 0.06 | 0.06 | 0.02 |
| FR\_N |  |  | -- | 0.03 | 0.03 | 0.03 | 0.03 | 0.01 | 0.02 | 0.03 | 0.02 | 0.01 | 0.03 | 0.03 | 0.01 |
| Zim |  |  |  | -- | 0.02 | 0.03 | 0.04 | 0.02 | 0.03 | 0.03 | 0.03 | 0.03 | 0.03 | 0.03 | 0.03 |
| RMNP |  |  |  |  | -- | 0.04 | 0.05 | 0.02 | 0.03 | 0.04 | 0.03 | 0.02 | 0.05 | 0.05 | 0.02 |
| Gore\_N |  |  |  |  |  | -- | 0.04 | 0.02 | 0.03 | 0.04 | 0.03 | 0.02 | 0.05 | 0.05 | 0.02 |
| I70\_N |  |  |  |  |  |  | -- | 0.02 | 0.03 | 0.05 | 0.03 | 0.02 | 0.05 | 0.07 | 0.02 |
| I70\_S |  |  |  |  |  |  |  | -- | 0.02 | 0.02 | 0.02 | 0.02 | 0.02 | 0.03 | 0.01 |
| Gore\_S |  |  |  |  |  |  |  |  | -- | 0.03 | 0.02 | 0.01 | 0.03 | 0.03 | 0.01 |
| Grand |  |  |  |  |  |  |  |  |  | -- | 0.03 | 0.02 | 0.04 | 0.04 | 0.02 |
| Elk |  |  |  |  |  |  |  |  |  |  | -- | 0.02 | 0.04 | 0.04 | 0.01 |
| Saw\_C |  |  |  |  |  |  |  |  |  |  |  | -- | 0.02 | 0.03 | 0.01 |
| Mosq |  |  |  |  |  |  |  |  |  |  |  |  | -- | 0.08 | 0.02 |
| Saw\_N |  |  |  |  |  |  |  |  |  |  |  |  |  | -- | 0.02 |
| Saw\_S |  |  |  |  |  |  |  |  |  |  |  |  |  |  | -- |

**Table S3**: Genes within 25 thousand base pairs (Kbp) of environmentally- and *Batrachochytrium dendrobatidis* (Bd)-related single nucleotide polymorphisms (SNPs). The boreal toad scaffold, SNP ID, and SNP position, and correlation (absolute values) are shown with the predictor variable each SNP was most strongly correlated with, consisting of *Bd* prevalence, years since first *Bd* detection, minimum temperature of the coldest month, heat load index, streams and rivers, and percent tree canopy cover in the Predictor Variable column. Gene names from the new boreal toad reference genome annotation are listed in the Gene column. In total, 88 genes were found to be putatively under selection, out of 41,174 genes total (i.e., proportion of genes under selection = 0.002).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Scaffold** | **SNP ID** | **Position** | **Correlation** | **Predictor** | **Gene** |
| 5 | 784425:285:+ | 158060195 | 0.85 | years since detection | Lire1 |
| 3 | 7221882:308:- | 155773933 | 0.81 | years since detection | LINE-1 retrotransposable element ORF2 protein |
| 5 | 784093:12:- | 158000214 | 0.76 | years since detection | mppe1 |
| 4 | 15547554:185:+ | 409290783 | 0.75 | years since detection | LINE-1 retrotransposable element ORF2 protein |
| 7 | 19182368:197:+ | 196342704 | 0.75 | bd prevalence | Cnih1 |
| 2 | 13473662:251:- | 760516432 | 0.75 | bd prevalence | Ffar2 |
| 3 | 8820773:247:+ | 481558559 | 0.73 | years since detection | an3 |
| 5 | 1660598:96:- | 340877059 | 0.73 | bd prevalence | PSMG4 |
| 2 | 10009620:104:+ | 69715314 | 0.72 | years since detection | LINE-1 reverse transcriptase homolog |
| 6 | 17481093:257:- | 201286706 | 0.72 | bd prevalence | PRP2 |
| 2 | 10737699:80:- | 210172280 | 0.71 | bd prevalence | Violet-sensitive opsin |
| 1 | 5019260:42:+ | 509429790 | 0.69 | years since detection | Lire1 |
| 7 | 19050451:114:+ | 173913086 | 0.69 | years since detection | PCNX1 |
| 2 | 12461695:104:- | 559532605 | 0.67 | bd prevalence | Iapp |
| 1 | 6275312:100:- | 764204051 | 0.67 | bd prevalence | ST3GAL5 |
| 7 | 19170663:78:- | 194407563 | 0.67 | years since detection | Dync1h1 |
| 1 | 4568300:231:- | 416919603 | 0.67 | years since detection | LINE-1 reverse transcriptase homolog |
| 5 | 592435:259:+ | 120492951 | 0.65 | bd prevalence | PGBD4 |
| 1 | 3723042:238:+ | 246776192 | 0.65 | bd prevalence | Lire1 |
| 4 | 16266053:68:- | 551053122 | 0.65 | years since detection | ATF3 |
| 3 | 9052427:75:- | 529159882 | 0.64 | bd prevalence | ACOT9 |
| 4 | 14238600:94:+ | 144682531 | 0.64 | bd prevalence | atr |
| 3 | 7007366:277:+ | 112074286 | 0.64 | bd prevalence | Gdf11 |
| 5 | 630398:261:- | 127366706 | 0.64 | bd prevalence | DSG2 |
| 9 | 20470180:203:+ | 45371169 | 0.64 | bd prevalence | NOX1 |
| 4 | 13771101:285:- | 51849544 | 0.64 | bd prevalence | ASTL |
| 5 | 737494:226:- | 149445858 | 0.63 | years since detection | Dlgap1 |
| 1 | 5822721:39:- | 675591847 | 0.63 | bd prevalence | Helt |
| 2 | 11371507:73:- | 335981288 | 0.62 | bd prevalence | DUSP6 |
| 7 | 18692658:118:- | 103599575 | 0.62 | bd prevalence | trappc2l |
| 3 | 8040806:20:- | 321180401 | 0.61 | bd prevalence | Gjb3 |
| 9 | 21020869:262:- | 156685132 | 0.60 | bd prevalence | Sipa1l3 |
| 6 | 17930304:244:+ | 284374751 | 0.59 | years since detection | hhex |
| 10 | 21270924:281:- | 12756963 | 0.56 | years since detection | gata2 |
| 5 | 1483807:146:- | 303433599 | 0.55 | bd prevalence | L1TD1 |
| 1 | 5088498:111:+ | 523184399 | 0.54 | years since detection | Elastase-1 |
| 1 | 2623728:80:- | 27135190 | 0.54 | years since detection | NIPBL |
| 3 | 7048437:130:+ | 119051399 | 0.53 | years since detection | Fmnl3 |
| 6 | 17495780:245:- | 204497987 | 0.52 | bd prevalence | L1td1 |
| 3 | 6849039:300:+ | 82583006 | 0.51 | years since detection | CELA1 |
| 2 | 13489768:34:- | 764148865 | 0.50 | bd prevalence | Pol |
| 6 | 17329610:126:- | 169421286 | 0.50 | min temp coldest month | BMS1 |
| 2 | 11394312:58:- | 340591205 | 0.49 | bd prevalence | HNRNPAB |
| 4 | 15979106:48:+ | 496315815 | 0.48 | bd prevalence | REL |
| 3 | 9652875:200:+ | 648477876 | 0.48 | min temp coldest month | USF3, FP1, SIDT1 |
| 7 | 18224599:180:- | 15873753 | 0.47 | heat load index | Fadd |
| 1 | 3310078:133:- | 163783515 | 0.47 | bd prevalence | tc1a |
| 3 | 8789509:101:- | 475503718 | 0.46 | years since detection | NME7 |
| 2 | 10960427:261:- | 254626701 | 0.46 | bd prevalence | L1RE1 |
| 5 | 1492094:114:- | 305260550 | 0.46 | bd prevalence | pol |
| 2 | 12837935:42:- | 633393541 | 0.46 | heat load index | Lire1 |
| 7 | 18556308:47:- | 78548277 | 0.46 | min temp coldest month | Necab2 |
| 4 | 15878213:89:- | 476261136 | 0.44 | tree canopy | ENTPD6 |
| 4 | 14607578:36:- | 218415238 | 0.43 | bd prevalence | LINE-1 retrotransposable element ORF2 protein |
| 6 | 16984997:48:+ | 100515237 | 0.41 | heat load index | LINE-1 reverse transcriptase homolog |
| 9 | 21213391:227:+ | 193782566 | 0.41 | bd prevalence | eif3a |
| 5 | 1594500:50:- | 328293286 | 0.41 | bd prevalence | LINE-1 retrotransposable element ORF2 protein |
| 9 | 21051779:351:+ | 162437961 | 0.41 | min temp coldest month | Olfactomedin, Hnrnpul1 |
| 3 | 7512345:37:- | 215985478 | 0.40 | years since detection | ARHGEF7 |
| 10 | 21359937:67:- | 28042901 | 0.39 | bd prevalence | ATp6v1fnb |
| 7 | 18348368:57:- | 36855950 | 0.39 | bd prevalence | Phrf1 |
| 6 | 17969378:71:- | 291616319 | 0.39 | streams/rivers | ADAM9, PSTK, ikzf5 |
| 5 | 1606965:119:- | 330811346 | 0.36 | bd prevalence | L1td1 |
| 9 | 20341041:146:- | 20624027 | 0.36 | bd prevalence | RAB7A |
| 2 | 10718282:248:+ | 206510868 | 0.36 | bd prevalence | UBE2Q2 |
| 4 | 14966471:205:+ | 289665319 | 0.36 | bd prevalence | TRIOBP |
| 9 | 20411539:218:- | 33131212 | 0.36 | years since detection | unnamed |
| 6 | 16822876:68:+ | 71565453 | 0.35 | bd prevalence | E2F1 |
| 1 | 3577831:258:+ | 217210098 | 0.33 | bd prevalence | ydjc |
| 3 | 8288204:339:+ | 371958818 | 0.33 | bd prevalence | CNKSR1 |
| 8 | 19256719:242:+ | 8742609 | 0.33 | bd prevalence | BIN1 |
| 6 | 17260606:104:- | 153936294 | 0.33 | bd prevalence | Gtf2ird2 |
| 5 | 2190776:139:- | 444058114 | 0.31 | bd prevalence | Larp4b |
| 1 | 3179227:83:- | 136477213 | 0.31 | min temp coldest month | Pol |
| 5 | 2298589:42:+ | 464893807 | 0.30 | heat load index | LINE-1 retrotransposable element ORF2 protein |
| 5 | 1488661:260:+ | 304592682 | 0.30 | years since detection | LINE-1 retrotransposable element ORF2 protein |
| 8 | 19427220:109:- | 39536820 | 0.29 | years since detection | cybrd1 |
| 38 | 22151262:307:+ | 225926 | 0.29 | bd prevalence | TY3B-I |
| 6 | 16772187:251:- | 60864767 | 0.29 | bd prevalence | Utp18 |
| 7 | 19081764:100:+ | 178980659 | 0.29 | bd prevalence | naa30 |
| 2 | 10381022:176:+ | 141823084 | 0.29 | bd prevalence | rasef |
| 7 | 18806938:309:- | 127624410 | 0.28 | years since detection | PPOX |
| 9 | 20475026:30:- | 46262260 | 0.28 | min temp coldest month | tmem35a |
| 1 | 6385615:27:- | 788059406 | 0.28 | years since detection | Vmn2r26 |
| 5 | 223149:222:- | 47793877 | 0.28 | bd prevalence | Transposon TX1 uncharacterized 149 kDa protein |
| 2 | 10697674:139:+ | 202891180 | 0.28 | bd prevalence | LACTB |
| 2 | 11215864:179:+ | 306325149 | 0.28 | years since detection | nell2 |
| 2 | 10330564:135:- | 132608398 | 0.27 | years since detection | Acan |
| 5 | 1483767:41:- | 303428166 | 0.27 | bd prevalence | L1TD1 |
| 7 | 18231715:80:+ | 16987803 | 0.27 | bd prevalence | chst1 |
| 2 | 12369964:285:+ | 541538759 | 0.27 | bd prevalence | samm50 |
| 2 | 12721059:11:- | 611273801 | 0.26 | bd prevalence | DUSP8 |
| 9 | 21130128:175:+ | 176464388 | 0.26 | years since detection | Carboxy-terminal kinesin 2 |
| 8 | 19369001:241:- | 29483298 | 0.26 | bd prevalence | Tanc1 |
| 2 | 12093678:59:+ | 485985273 | 0.25 | years since detection | slc35a4 |
| 4 | 16351188:5:- | 568183121 | 0.24 | years since detection | CAPN2 |
| 1 | 3590025:201:- | 219607888 | 0.24 | years since detection | mmp11 |
| 1 | 3772933:290:- | 256343906 | 0.24 | years since detection | MED13L |
| 10 | 22094870:55:- | 171996690 | 0.22 | years since detection | caiap |
| 5 | 1484056:44:+ | 303474693 | 0.22 | years since detection | LINE-1 reverse transcriptase homolog |

**Table S4**: Gene list and gene ontology (GO) information from biomaRt output gene ontology names for all candidate genes flagged by our RDA-*Batrachochytrium dendrobatidis* (Bd) and redundancy analysis (RDA)-env that were assigned GO terms based on the western clawed frog ensemble database. We searched annotation reports for GO terms for traits hypothesized to be associated with *Bd* and disease (GO search terms: skin, keratin, collagen, osmoregulation, osmo, membrane, inflammation, immune, histo, heart, cardiac, MHC) and physiological tolerance to environmental variation (GO search terms: heat shock, temperature, heat load). The boreal toad scaffold, SNP ID, and SNP position are shown relative to the correlation to the respective variable each SNP was most strongly correlated with in the Predictor column. Genes within 25 Kbp of the SNP are listed in the gene-name column. The ensemble and entrezgene idís, entrezgene accession and descriptions for *Xenopus tropicalis* and *Homo sapiens* are reported as well as the GO ids, names and functional information from the *X. tropicalis* and *H. sapiens* ensemble databases. In total, 88 genes were found to be putatively under selection, out of 41,174 genes total (i.e., proportion of genes under selection = 0.002).

\*Large Table; see google drive:

<https://docs.google.com/spreadsheets/d/1pn4zwui6Pl90PuVIo0iT6lENkg3WKdeM/edit#gid=1164766778>



**Figure S1**: Little population genomic structure was detected in boreal toads across the southern Rocky Mountains using a neighbor-net tree constructed with Splitstree.

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**Figure S2**: Subtle trend of isolation by distance (*IBD*) was detected in boreal toads in the southern Rocky Mountains (SRM) of Colorado and southern Wyoming using (a) Admixture membership plots (K=2) and (b) a Mantel test. The Mantel test was not significant (p = 0.48, Mantel’s r = 0.08).

A screen shot of a graph

Description automatically generated

**Figure S3a.** Demographic analysis of boreal toads in the Wyoming (WY) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A white grid with red lines

Description automatically generated

**Figure S3b.** Demographic analysis of boreal toads in the Elkhead Mountains (Elkhead) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A screen shot of a graph

Description automatically generated

**Figure S3c.** Demographic analysis of boreal toads in the Front Range north (FR\_N) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A graph with red line

Description automatically generated

**Figure S3d.** Demographic analysis of boreal toads in the Zimmerman Lake (Zim) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A graph with a line going up

Description automatically generated

**Figure S3e.** Demographic analysis of boreal toads in the Rocky Mountain National Park (RMNP) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A graph with red line

Description automatically generated

**Figure S3f.** Demographic analysis of boreal toads in the Gore Range north (Gore\_N) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A screen shot of a graph

Description automatically generated

**Figure S3g.** Demographic analysis of boreal toads in the Gore Range south (Gore\_S) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A screen shot of a graph

Description automatically generated

**Figure S3h.** Demographic analysis of boreal toads in the I-70 north (I70\_N) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A screen shot of a graph

Description automatically generated

**Figure S3i.** Demographic analysis of boreal toads in the I-70 south (I70\_S) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A screen shot of a graph

Description automatically generated

**Figure S3j.** Demographic analysis of boreal toads in the Grand Mesa (Grand) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A white screen with red lines

Description automatically generated

**Figure S3k.** Demographic analysis of boreal toads in the Elk Mountains (Elk) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A screen shot of a graph

Description automatically generated

**Figure S3l.** Demographic analysis of boreal toads in the Mosquito Range (Mosq) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A screen shot of a graph

Description automatically generated

**Figure S3m.** Demographic analysis of boreal toads in the Sawatch Range north (Saw\_N) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A graph with a red line

Description automatically generated

**Figure S3n.** Demographic analysis of boreal toads in the Sawatch Range central (Saw\_C) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

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Description automatically generated

**Figure S3o.** Demographic analysis of boreal toads in the Sawatch Range south (Saw\_S) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

A graph with red line

Description automatically generated

**Figure S3p.** Demographic analysis of boreal toads in the southern Rocky Mountains (SRM) region. Generation time of toads is assumed to be 5 years, and mutation rate is 2.52e-9. The bars represent the median demographic model (red), 75% confidence intervals (dark gray), and 95% confidence intervals (light gray) across 10,000 simulations.

**Chart, scatter chart

Description automatically generatedFigure S4**: Correlations among landscape predictor variables for genotype-environment associations (GEA) and redundancy analysis (RDA) consisting of *Batrachochytrium dendrobatidis* (*Bd*) prevalence (PREV) and years since first detection (YSFD), annual precipitation (AP), minimum temperature of the coldest month (MTCM), maximum temperature of the warmest month (MTWM), percent tree canopy cover (CC), compound topographic index of wetness (CTI), heat load index (HLI), streams and rivers (STR), roads (RDS), and percent impervious surface (IMP).

Scatter chart, qr code

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**Figure S5**: Linkage disequilibrium (LD) as a function of genomic distance (base pairs) calculated using VCFtools v0.1.17 calculated within a 1 million base pair (bp) sliding window across the boreal toad reference genome. Red dashed line corresponds to 25 thousand base pairs (Kbp).