Ecography

ECOG-03235
Wogan, G. O. U. and Wang, I. J. 2017. The value of space-for-time substitution for studying fine-scale microevolutionary processes. – Ecography doi: 10.1111/ecog.03235

Supplementary material

Appendix 1.

Web of Science Search Terms

We used the Web of Science Core Collection to seek out relevant literature for inclusion in this review. We conducted searches June 26-30 2017. We used keyword searches for the following single or combinations of terms: space for time, isolation by time, isolation by distance, temporal FST, known age, colonization history, invasive, urban, habitat fragmentation, altitudinal gradient, latitudinal gradient, cline, genomic, environmental association. We note that while we have attempted to include relevant studies, our search is likely not comprehensive. In addition to the Web of Science search, we also found studies through citation backtracking. Since we are not conducting a meta-analysis of population genetic space for time substitutions, but rather an overview of an emerging topic we believe this to be an appropriate strategy.

"Space for Time": 449 results
filtered by Evolutionary Biology: 10 results
filtered by Ecology: 165 results

"Isolation by time": 31 results (Most of these studies revolve around isolation by reproductive timing, also referenced as IBT; Hendry and Day 2005).

"Temporal FST": 6 results

"Isolation by distance": 3574 results
filtered by "known age": 1 study

"Colonization history" & "Invasive": 55 results

"Urban" & "Fragmentation": 2546 results
filtered by "biodiversity conservation" or "genetics": 381 results

"Genomic" & "Altitudinal Gradient": 28 results

"Genomic" & "Latitudinal Gradient": 60 results

"Genomic" & "Environmental Association": 113 results

"Genomic" & "Cline": 183 results

References:

Hendry, A. and Day, T. 2005. Population structure attributable to reproductive time: isolation by time and adaptation by time. — Molecular Ecology 14: 901-916.

Table A1. A sample of studies that assess population genetic evolutionary processes using space-for-time substitutions

Study Organism	Timespan	Stationary (S) or Non-stationary (N) Landscape	Different Aged Sites (DAS), Spatiotemporal Turnover (ST), Time for Time (TT)	Fit Prediction?	Study Citation
reptiles, birds	13 – 43 years	S	DAS – (Fragmentation)	No	Delaney et al. 2010
amphibian	20 - 1000 years	S	DAS – (Fragmentation)	No	Lourenco et al. 2017
bird	18-305 years	S	DAS – (Fragmentation)	No	Björklund et al. 2010
amphibian	350 years	S	DAS – (Fragmentation)	No	Noël et al. 2007
lizards	10-250 years	S	DAS – (Fragmentation)	No	Littleford-Colquhoun et al. 2017
amphibian	0-160 years	S	DAS – (Fragmentation)	No	Spear and Storfer 2008
arthropod	23 years	S	DAS – (Colonization)	Yes	Haag et al. 2005
fish	55-170 years	S	DAS – (Colonization)	Yes	Bryan et al. 2005
plant	~300 years	S	DAS – (Colonization)	No	Genton et al. 2005
reptile	~200 years	S	DAS – (Colonization)	No	Kolbe et al. 2004
fish	50 years	S	DAS – (Colonization)	No	Lescak et al. 2015
bird	~ 120 years	S	ST	Yes	Peery et al. 2010
plant	150 years	S	ST	Yes	Martin et al. 2014
amphibian	6 years	S	ST	Yes	Wang and Shaffer 2017
insect	77 years	S	ST	Yes	Ugelvig et al. 2011
fish	1-700 years	N	DAS	Yes	Terekhanova et al. 2014
mammal	14 years	N	DAS	No	Brüniche-Olsen et al. 2016
amphibian	N/A	N	ST	N/A	Bonin et al 2006
amphibian	N/A	N	ST	N/A	Guo et al 2016
mammal	N/A	N	ST	N/A	Bi et al. 2013
mammal	N/A	N	ST	N/A	Henry and Russello 2013
insect	< 1 year	N	TT	Yes	Bergland et al 2014

Insect	13-46 years	N	TT	Yes	Balanyá et al. (2006)
fish	55-80 years	N	TT	Yes	Therkildsen et al 2013
insect	experimental	N	TT	Yes	Huang et al. 2014

References

Balanyá, J. et al. 2006. Global genetic change tracks global climate warming in *Drosophila subobscura*. — Science 313: 1773–1775.

Bergland, A. O. et al. 2014. Genomic evidence of rapid and stable adaptive oscillations over seasonal time scales in *Drosophila*. — PLoS Genetics 10: e1004775.

Bi, K. et al. 2013. Unlocking the vault: Next generation museum population genomics. — Molecular Ecology 22: 6018-6032.

Björklund, M. et al. 2010. Genetic differentiation in the urban habitat:The great tits (*Parus major*) of the parks of Barcelona city. — The Biological Journal of the Linnean Society 99: 9-19.

Bonin, A. et al. 2006. Explorative genome scan to detect candidate loci for adaptation along a gradient of altitude in the common frog (*Rana temporaria*). — Molecular Biology and Evolution 23: 773-783.

Brüniche-Olsen, A. et al. 2016. Detecting selection on temporal and spatial scales: A genomic time-series assessment of selective responses to Devil Facial Tumor Disease. — PLoSOne 11: e0147875.

Bryan, M. B. et al. 2005. Patterns of invasion and colonization of the sea lampry (*Petromyzon marinus*) in North America as revealed by microsatellite genotypes. — Molecular Ecology 14: 3757-3773.

Delaney, K. S. et al. 2010. A rapid, strong, and convergent genetic response to urban habitat fragmentation in four divergent and widespread vertebrates. — PLoSOne 5: e12767.

Genton, B. J. et al. 2005. High genetic diversity in french invasive populations of common ragweed, *Ambrosia artemsiifolia*, as a result of multiple sources of introduction. — Molecular Ecology 14: 4275-4285.

Guo, B. et al. 2016. Genomewide scan for adaptive differnetiation along altitudinal gradient in the Andrew's toad *Bufo andrewsi*. — Molecular Ecology 25: 3884-3900.

Haag, C. R. et al. 2005. Genetic diversity and genetic differentiation in daphnia metapopulations with subpopulations of known age. — Genetics 170: 1809-1820.

Henry, P. and Russello, M. 2013. Adaptive divergence along environmental gradients in a climate-change-sensitive mammal. — Ecology and Evolution 3906-3917.

Huang, Y. et al. 2014. Genome-wide patterns of genetic variation within and among alternative selective regimes. — PLoS Genetics 10: e1004527.
Kolbe, J. J. et al. 2004. Genetic variation increases during biological invasion by a Cuban lizard. — Nature 431: 177-181.
Lescak, E. A. et al. 2015. Evolution of stickleback in 50 years on earthquake-uplifted islands. — Proceedings of the National Academy of Sciences 112: E7204–E7212.
Littleford-Colquhoun, B. L. et al. 2017. Archipelagos of the Anthropocene: Rapid and extensive differentiation of native terrestrial vertebrates in a single metropolis. — Molecular Ecology 26: 2466-2481
Lourenco, A. et al. 2017. Trapped within the city: Integrating demography, time since isolation and population-specific traits to assess the genetic effects of urbanization. — Molecular Ecology 26: 1498-1514
Martin, M. D. et al. 2014. Herbarium specimens reveal a historical shift in phylogeographic structure of common ragweed during native range disturbance. — Molecular Ecology 23: 1701-1716.
Noël, S. et al. 2007. Impact of urban fragmentation on the genetic structure of the eastern red-backed salamander. — Conservation Genetics 8: 599-606.
Peery, M. Z. et al. 2010. Genetic analyses of historic and modern marbled murrelets suggest decoupling of migration and gene flow after habitat fragmnetation. — Proceeding of the Royal Society B 277: 697-706.
Spear, S. F. and Storfer, A. 2008. Landscape genetic structure of coastal tailed frogs (*Ascaphus truei*) in protected vs. Managed forests. — Molecular Ecology 17: 4642-4656.
Terekhanova, N. V. et al. 2014. Fast evolution from precast bricks: Genomics of young freshwater populations of threespine stickleback *Gasterosteus aculeatus*. — PL0S Genetics 10: e1004696.
Therkildsen, N. O. et al. 2013. Spatiotemporal SNP analysis reveals pronounced biocomplexity at the northern range margin of Atlantic cod *Gadus morhua*. — Evolutionary Applications 6: 690-705.
Ugelvig, L. V. et al. 2011. Reconstructing eight decades of genetic variation in an isolated danish population of the large blue butterfly *Maculinea arion*. — BMC Evolutionary Biology 11: 201.
Wang, I. J. and Shaffer, H. B. 2017. Population genetic and field-ecological analyses return similar estimates of dispersal over space and time in an endangered amphibian. — Evolutionary Applications 10: 630-639.

Table A2. Examples of studies that evaluate isolation by time

Organism	Time	IBT estimation (FST)	Study Citation
Mammal: Mountain goat	14 years	0.031	Ortego et al. 2011
Mammal: Chipmunks	90 years	0.023	Bi et al. 2013
Bird: Black grouse	~170 years	0.111	Larsson et al. 2008
Fish: perch	23 years	0.022	Demandt 2010
Fish: roach	23 years	0.018	Demandt 2010
Insect: beetle	20 years	0.000 – 0.0603	Drees et al. 2011
Fish: cod	~69 years	0.000 – 0.006	Nielsen et al. 2007
Amphibian: salamander	6 years	0.002 – 0.044	Wang and Shaffer 2017

References

Bi, K. et al. 2013. Unlocking the vault: Next generation museum population genomics. — Molecular Ecology 22: 6018-6032.

Demandt, M. H. 2010. Temporal changes in genetic diversity of isolated populations of perch and roach. — Conservation Genetics 11: 249-255.

Drees, C. et al. 2011. Repeated sampling detects gene flow in a flightless ground beetle in a fragmented landscape. — Herediitas 148: 36-45.

Larsson, J. K. et al. 2008. Genetic impoverishment of the last black grouse (*Tetrao tetrix*) population in the netherlands: Detectable only with a reference from the past. — Molecular Ecology 1897-1904.

Nielsen, E. E. et al. 2007. Historical analysis of *Pan I* in atlantic cod (*Gadus morhua*): Temproal stability of allele frequencies in the southeastern part of the species distribution. — Canadian Journal of Fisheries and Aquatic Sciences 64: 1448-1455.

Ortego, J. et al. 2011. Temporal dynamics of genetic variability in a mountain goat (*Oreamnos americanus*) population. — Molecular Ecology 20: 1601-1611.

Wang, I. J. and Shaffer, H. B. 2017. Population genetic and field-ecological analyses return similar estimates of dispersal over space and time in an endangered amphibian. — Evolutionary Applications 10: 630-639.