

Supplementary material

Effects of Land Use and Landscape Fragmentation on the Genetic Composition of Arthropods

These are the references for *Gene Flow Disruption and Population Declines in a Soil Arthropod in Fragmented Habitats*

References

- Balkenhol, Niko et al., eds. (2016). *Landscape Genetics: concepts, methods, applications*. Wiley Blackwell. DOI: 10.1002/9781118525258.
- Banks, Sam C. et al. (2013). “How does ecological disturbance influence genetic diversity?” In: *Trends in Ecology and Evolution* 28 (11), pp. 670–679. ISSN: 01695347. DOI: 10.1016/j.tree.2013.08.005.
- Bao, Weidong, Kenji K. Kojima, and Oleksiy Kohany (June 2015). “Repbased Update, a database of repetitive elements in eukaryotic genomes”. In: *Mobile DNA* 6 (11). ISSN: 17598753. DOI: 10.1186/s13100-015-0041-9.
- Bardgett, R D, J B Whittaker, and J C Frankland (1993). “The effect of collembolan grazing on fungal activity in differently managed upland pastures: A microcosm study”. In: *Biology and fertility of soils* 16 (4), pp. 255–262. ISSN: 0178-2762. DOI: 10.1007/BF00369301.
- Bellinger, Peter F., Kenneth A. Christiansen, and Frans Janssens (2024). *Checklist of the Collembola: Collembola Biogeographic Distribution*. URL: <https://www.collembola.org/biogeo/index.php>.
- Bertorelle, Giorgio et al. (Aug. 2022). *Genetic load: genomic estimates and applications in non-model animals*. DOI: 10.1038/s41576-022-00448-x.
- Brůna, Tomáš, Alexandre Lomsadze, and Mark Borodovsky (June 2020). “GeneMark-EP+: Eukaryotic gene prediction with self-training in the space of genes and proteins”. In: *NAR Genomics and Bioinformatics* 2 (2). ISSN: 26319268. DOI: 10.1093/nargab/lqaa026.
- Brůna, Tomáš et al. (Mar. 2021). “BRAKER2: Automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database”. In: *NAR Genomics and Bioinformatics* 3 (1), pp. 1–11. ISSN: 26319268. DOI: 10.1093/nargab/lqaa108.
- Buchfink, Benjamin, Chao Xie, and Daniel H. Huson (Jan. 2015). *Fast and sensitive protein alignment using DIAMOND*. DOI: 10.1038/nmeth.3176.

- Charlesworth, D. and B. Charlesworth (Jan. 1987). “Inbreeding Depression and its Evolutionary Consequences”. In: *Annual review of ecology and systematics* 18 (1), pp. 237–268. ISSN: 0066-4162. DOI: 10.1146/annurev.es.18.110187.001321.
- Charlesworth, Deborah, Nicholas H. Barton, and Brian Charlesworth (May 2017). “The sources of adaptive variation”. In: *Proceedings of the Royal Society B: Biological Sciences* 284 (1855). ISSN: 14712954. DOI: 10.1098/rspb.2016.2864.
- Cheng, Haoyu et al. (Feb. 2021). “Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm”. In: *Nature Methods* 18 (2), pp. 170–175. ISSN: 15487105. DOI: 10.1038/s41592-020-01056-5.
- Cheng, Haoyu et al. (Sept. 2022). “Haplotype-resolved assembly of diploid genomes without parental data”. In: *Nature Biotechnology* 40 (9), pp. 1332–1335. ISSN: 15461696. DOI: 10.1038/s41587-022-01261-x.
- Christiansen, Kenneth et al. (Sept. 1992). “Interspecific interactions between Collembolan populations in culture”. In: *Pedobiologia* 36 (5), pp. 274–286. ISSN: 0031-4056. DOI: 10.1016/S0031-4056(24)00788-1.
- Cicconardi, F. et al. (Jan. 2010). “Deep phylogeographic divisions and long-term persistence of forest invertebrates (Hexapoda: Collembola) in the North-Western Mediterranean basin”. In: *Molecular Ecology* 19 (2), pp. 386–400. ISSN: 09621083. DOI: 10.1111/j.1365-294X.2009.04457.x.
- Collins, Gemma E. et al. (Sept. 2020). “Genetic diversity of soil invertebrates corroborates timing estimates for past collapses of the West Antarctic Ice Sheet”. In: *Proceedings of the National Academy of Sciences* 117 (36), pp. 22293–22302. ISSN: 0027-8424. DOI: 10.1073/pnas.2007925117.
- Costa, Dalila et al. (June 2013). “Genetic structure of soil invertebrate populations: Collembolans, earthworms and isopods”. In: *Applied Soil Ecology* 68, pp. 61–66. ISSN: 09291393. DOI: 10.1016/j.apsoil.2013.03.003.
- Cushman, Samuel A. (Mar. 2006). “Effects of habitat loss and fragmentation on amphibians: A review and prospectus”. In: *Biological Conservation* 128 (2), pp. 231–240. ISSN: 00063207. DOI: 10.1016/j.biocon.2005.09.031.
- Cushman, Samuel A., Brad H. McRae, and Kevin McGarigal (Oct. 2015). “Basics of Landscape Ecology: An Introduction to Landscapes and Population Processes for Landscape Geneticists”. In: Wiley, pp. 9–34. DOI: 10.1002/9781118525258.ch02.
- Danecek, Petr et al. (Feb. 2021). “Twelve years of SAMtools and BCFtools”. In: *GigaScience* 10 (2). ISSN: 2047217X. DOI: 10.1093/gigascience/giab008.
- Donald, Paul F. et al. (Sept. 2006). “Further evidence of continent-wide impacts of agricultural intensification on European farmland birds, 1990–2000”. In: *Agriculture, Ecosystems and Environment* 116 (3), pp. 189–196. ISSN: 01678809. DOI: 10.1016/j.agee.2006.02.007.

- Dudchenko, Olga et al. (Apr. 2017). “De novo assembly of the *Aedes aegypti* genome using Hi-C yields chromosome-length scaffolds”. In: *Science* 356 (6333), pp. 92–95. ISSN: 10959203. DOI: 10.1126/science.aal3327.
- Durand, Neva C. et al. (July 2016a). “Juicebox Provides a Visualization System for Hi-C Contact Maps with Unlimited Zoom”. In: *Cell Systems* 3 (1), pp. 99–101. ISSN: 24054720. DOI: 10.1016/j.cels.2015.07.012. URL: <http://dx.doi.org/10.1016/j.cels.2015.07.012>.
- Durand, Neva C. et al. (July 2016b). “Juicer Provides a One-Click System for Analyzing Loop-Resolution Hi-C Experiments”. In: *Cell Systems* 3 (1), pp. 95–98. ISSN: 24054720. DOI: 10.1016/j.cels.2016.07.002.
- Ellegren, Hans and Nicolas Galtier (July 2016). “Determinants of genetic diversity”. In: *Nature Reviews Genetics* 17 (7), pp. 422–433. ISSN: 14710064. DOI: 10.1038/nrg.2016.58.
- England, Phillip R. et al. (Jan. 2003). “Effects of intense versus diffuse population bottlenecks on microsatellite genetic diversity and evolutionary potential”. In: *Conservation Genetics* 4 (5), pp. 595–604. ISSN: 1566-0621. DOI: 10.1023/A:1025639811865.
- Excoffier, Laurent et al. (Oct. 2013). “Robust Demographic Inference from Genomic and SNP Data”. In: *PLoS Genetics* 9 (10). ISSN: 15537390. DOI: 10.1371/journal.pgen.1003905.
- Flynn, Jullien M. et al. (Apr. 2020). “RepeatModeler2 for automated genomic discovery of transposable element families”. In: *PNAS* 117 (17), pp. 9451–9457. URL: <https://doi.org/10.1073/pnas.1921046117>.
- Frampton, Geoff K. (2000). “Recovery responses of soil surface Collembola after spatial and temporal changes in long-term regimes of pesticide use”. In: *Pedobiologia* 44 (3), pp. 489–501. ISSN: 0031-4056. DOI: 10.1078/S0031-4056(04)70066-9.
- Frankham, Richard (Nov. 2005). “Genetics and extinction”. In: *Biological Conservation* 126 (2), pp. 131–140. ISSN: 00063207. DOI: 10.1016/j.biocon.2005.05.002.
- Gabriel, Lars et al. (Dec. 2021). “TSEBRA: transcript selector for BRAKER”. In: *BMC Bioinformatics* 22. ISSN: 14712105. DOI: 10.1186/s12859-021-04482-0.
- Galili, Tal (May 2015). “dendextend: An R package for visualizing, adjusting and comparing trees of hierarchical clustering”. In: *Bioinformatics* 31 (22), pp. 3718–3720. ISSN: 14602059. DOI: 10.1093/bioinformatics/btv428.
- García-Alcalde, Fernando et al. (Oct. 2012). “Qualimap: Evaluating next-generation sequencing alignment data”. In: *Bioinformatics* 28 (20), pp. 2678–2679. ISSN: 13674803. DOI: 10.1093/bioinformatics/bts503.
- Garner, Alisse, Janet L. Rachlow, and Jason F. Hicks (2005). “Patterns of genetic diversity and its loss in mammalian populations”. In: *Conservation Biology* 19 (4), pp. 1215–1221. ISSN: 08888892. DOI: 10.1111/j.1523-1739.2005.00105.x.

- Garrick, R. C. et al. (Nov. 2004). “Phylogeography recapitulates topography: Very fine-scale local endemism of a saproxylic ‘giant’ springtail at Tallaganda in the Great Dividing Range of south-east Australia”. In: *Molecular Ecology* 13 (11), pp. 3329–3344. ISSN: 09621083. DOI: 10.1111/j.1365-294X.2004.02340.x.
- Garrison, Erik and Gabor Marth (July 2012). “Haplotype-based variant detection from short-read sequencing”. In: *arXiv*. DOI: 10.48550/arXiv.1207.3907. URL: <http://arxiv.org/abs/1207.3907><https://doi.org/10.48550/arXiv.1207.3907>.
- Gilroy, D. L. et al. (July 2017). “Toll-like receptor variation in the bottlenecked population of the Seychelles warbler: computer simulations see the ‘ghost of selection past’ and quantify the ‘drift debt’”. In: *Journal of Evolutionary Biology* 30 (7), pp. 1276–1287. ISSN: 14209101. DOI: 10.1111/jeb.13077.
- Goldewijk, Kees Klein et al. (Jan. 2011). “The HYDE 3.1 spatially explicit database of human-induced global land-use change over the past 12,000 years”. In: *Global Ecology and Biogeography* 20 (1), pp. 73–86. ISSN: 1466822X. DOI: 10.1111/j.1466-8238.2010.00587.x.
- Gomulkiewicz, Richard and Robert D Holt (1995). “When does Evolution by Natural Selection Prevent Extinction?” In: *Evolution* 49 (1), pp. 201–207. ISSN: 0014-3820. DOI: 10.1111/j.1558-5646.1995.tb05971.x.
- Gotoh, Osamu (May 2008). “A space-efficient and accurate method for mapping and aligning cDNA sequences onto genomic sequence”. In: *Nucleic Acids Research* 36 (8), pp. 2630–2638. ISSN: 03051048. DOI: 10.1093/nar/gkn105.
- Guan, Dengfeng et al. (May 2020). “Identifying and removing haplotypic duplication in primary genome assemblies”. In: *Bioinformatics* 36 (9), pp. 2896–2898. ISSN: 14602059. DOI: 10.1093/bioinformatics/btaa025.
- Gustafson, Kyle D. et al. (May 2017). “A single migrant enhances the genetic diversity of an inbred puma population”. In: *Royal Society Open Science* 4 (5). ISSN: 20545703. DOI: 10.1098/rsos.170115.
- Hardy, Olivier J. and Xavier Vekemans (Aug. 1999). “Isolation by distance in a continuous population: Reconciliation between spatial autocorrelation analysis and population genetics models”. In: *Heredity* 83 (2), pp. 145–154. ISSN: 0018067X. DOI: 10.1046/j.1365-2540.1999.00558.x.
- Hartfield, M. (Jan. 2016). “Evolutionary genetic consequences of facultative sex and outcrossing”. In: *Journal of Evolutionary Biology* 29 (1), pp. 5–22. ISSN: 14209101. DOI: 10.1111/jeb.12770.
- Hartl, Daniel L. and Andrew G. Clark (2007). *Principles of Population Genetics*. 4. Sinauer and Associates. ISBN: 9780878933082.
- Hijmans, Robert J. et al. (2024). *geosphere: Spherical Trigonometry*. DOI: 10.32614/CRAN.package.geosphere. URL: <https://CRAN.R-project.org/package=geosphere>.

- Hoff, Katharina J. et al. (Mar. 2016). “BRAKER1: Unsupervised RNA-Seq-based genome annotation with GeneMark-ET and AUGUSTUS”. In: *Bioinformatics* 32 (5), pp. 767–769. ISSN: 14602059. DOI: 10.1093/bioinformatics/btv661.
- Hoff, Katharina J. et al. (Jan. 2019). “Whole-Genome Annotation with BRAKER”. In: vol. 1962. Springer, pp. 65–95. ISBN: 9781493991723. DOI: 10.1007/978-1-4939-9173-0_5.
- Hoffmann, Ary A. et al. (May 2021). “An endangered flightless grasshopper with strong genetic structure maintains population genetic variation despite extensive habitat loss”. In: *Ecology and Evolution* 11 (10), pp. 5364–5380. ISSN: 20457758. DOI: 10.1002/ece3.7428.
- Holland, J. M. (June 2004). “The environmental consequences of adopting conservation tillage in Europe: Reviewing the evidence”. In: *Agriculture, Ecosystems and Environment* 103 (1), pp. 1–25. ISSN: 01678809. DOI: 10.1016/j.agee.2003.12.018.
- Hopkin, Stephen P. (1997). *Biology of the springtails (Insecta, Collembola)*. Oxford University Press. ISBN: 0198540841.
- IPBES (2019). *Global assessment report of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services*. Ed. by Eduardo S. Brondízio et al. IPBES secretariat, p. 1144. ISBN: 9783947851201.
- Iwata, Hiroaki and Osamu Gotoh (Nov. 2012). “Benchmarking spliced alignment programs including Spaln2, an extended version of Spaln that incorporates additional species-specific features”. In: *Nucleic Acids Research* 40 (20), e161. ISSN: 03051048. DOI: 10.1093/nar/gks708.
- Jaureguiberry, Pedro et al. (Nov. 2022). “The direct drivers of recent global anthropogenic biodiversity loss”. In: *Science Advances* 8 (45). ISSN: 2375-2548. DOI: 10.1126/sciadv.abm9982.
- Kardos, Marty et al. (2021). “The crucial role of genome-wide genetic variation in conservation”. In: *PNAS* 118 (48). URL: <https://doi.org/10.1073/pnas.2104642118>.
- Keightley, Peter D. et al. (Jan. 2015). “Estimation of the Spontaneous Mutation Rate in *Heliconius melpomene*”. In: *Molecular Biology and Evolution* 32 (1), pp. 239–243. ISSN: 15371719. DOI: 10.1093/molbev/msu302.
- Kimura, Motoo (Apr. 1969). “THE NUMBER OF HETEROZYGOUS NUCLEOTIDE SITES MAINTAINED IN A FINITE POPULATION DUE TO STEADY FLUX OF MUTATIONS”. In: *Genetics* 61 (4), pp. 893–903. ISSN: 0016-6731. DOI: 10.1093/genetics/61.4.893.
- Klink, Roel van et al. (Apr. 2024). “Disproportionate declines of formerly abundant species underlie insect loss”. In: *Nature* 628 (8007), pp. 359–364. ISSN: 14764687. DOI: 10.1038/s41586-023-06861-4.
- Kofler, Robert, Ram Vinay Pandey, and Christian Schlötterer (Dec. 2011). “PoPoolation2: Identifying differentiation between populations using sequencing of pooled DNA samples (Pool-Seq)”. In: *Bioinformatics* 27

- (24), pp. 3435–3436. ISSN: 13674803. DOI: 10.1093/bioinformatics/btr589.
- Kremen, Claire (Feb. 2018). “The value of pollinator species diversity”. In: *Science* 359 (6377), pp. 741–742. ISSN: 0036-8075. DOI: 10.1126/science.aar7614.
- Leffler, Ellen M. et al. (Sept. 2012). “Revisiting an Old Riddle: What Determines Genetic Diversity Levels within Species?” In: *PLoS Biology* 10 (9). ISSN: 15449173. DOI: 10.1371/journal.pbio.1001388.
- Levins, Richard (Sept. 1969). “Some Demographic and Genetic Consequences of Environmental Heterogeneity for Biological Control”. In: *Bulletin of the Entomological Society of America* 15 (3), pp. 237–240. DOI: 10.1093/besa/15.3.237.
- Li, Heng (Mar. 2013). “Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM”. In: URL: <http://arxiv.org/abs/1303.3997>.
- (Sept. 2018). “Minimap2: Pairwise alignment for nucleotide sequences”. In: *Bioinformatics* 34 (18), pp. 3094–3100. ISSN: 14602059. DOI: 10.1093/bioinformatics/bty191.
- Liu, Haoxuan et al. (Jan. 2017). “Direct determination of the mutation rate in the bumblebee reveals evidence for weak recombination-associated mutation and an approximate rate constancy in insects”. In: *Molecular Biology and Evolution* 34 (1), pp. 119–130. ISSN: 15371719. DOI: 10.1093/molbev/msw226.
- Liu, Xiaoming and Yun Xin Fu (Dec. 2020). “Stairway Plot 2: demographic history inference with folded SNP frequency spectra”. In: *Genome Biology* 21 (1). ISSN: 1474760X. DOI: 10.1186/s13059-020-02196-9.
- Lohrum, Nele et al. (May 2024). “Unveiling the frontiers: Historical expansion and modern implications of agricultural land use in Denmark”. In: *Journal of Environmental Management* 359. ISSN: 10958630. DOI: 10.1016/j.jenvman.2024.120934.
- Lomsadze, Alexandre et al. (2005). “Gene identification in novel eukaryotic genomes by self-training algorithm”. In: *Nucleic Acids Research* 33 (20), pp. 6494–6506. ISSN: 03051048. DOI: 10.1093/nar/gki937.
- Losey, John E. and Mace Vaughan (Apr. 2006). “The Economic Value of Ecological Services Provided by Insects”. In: *Bioscience* 56 (4), pp. 311–323. ISSN: 0006-3568. DOI: 10.1641/0006-3568(2006)56[311:TEVOES]2.0.CO;2.
- Lynch, Michael, John Conery, and Reinhard Bürger (Oct. 1995). “Mutation Accumulation and the Extinction of Small Populations”. In: *The American Naturalist* 146 (4), pp. 489–518. ISSN: 0003-0147. DOI: 10.1086/285812.
- Manni, Mosè et al. (Oct. 2021). “BUSCO Update: Novel and Streamlined Workflows along with Broader and Deeper Phylogenetic Coverage for Scoring of Eukaryotic, Prokaryotic, and Viral Genomes”. In: *Molecular*

- Biology and Evolution* 38 (10), pp. 4647–4654. ISSN: 15371719. DOI: 10.1093/molbev/msab199.
- Nielsen, Tora Finderup, Kaj Sand-Jensen, and Hans Henrik Bruun (July 2021). “Drier, darker and more fertile: 140 years of plant habitat change driven by land-use intensification”. In: *Journal of Vegetation Science* 32 (4). ISSN: 16541103. DOI: 10.1111/jvs.13066.
- Odgaard, Bent Vad and Peter Rasmussen (Oct. 2000). “Origin and temporal development of macro-scale vegetation patterns in the cultural landscape of Denmark”. In: *Journal of Ecology* 88 (5), pp. 733–748. ISSN: 00220477. DOI: 10.1046/j.1365-2745.2000.00490.x.
- Potapov, Anton M. et al. (Feb. 2023). “Globally invariant metabolism but density-diversity mismatch in springtails”. In: *Nature Communications* 14 (1). ISSN: 20411723. DOI: 10.1038/s41467-023-36216-6.
- Potapov, Anton M. et al. (Jan. 2024). “Global fine-resolution data on spring-tail abundance and community structure”. In: *Scientific Data* 11 (1). ISSN: 20524463. DOI: 10.1038/s41597-023-02784-x.
- Quinlan, Aaron R. and Ira M. Hall (Jan. 2010). “BEDTools: A flexible suite of utilities for comparing genomic features”. In: *Bioinformatics* 26 (6), pp. 841–842. ISSN: 13674803. DOI: 10.1093/bioinformatics/btq033.
- Riva, Federico, Nicola Koper, and Lenore Fahrig (Aug. 2024). “Overcoming confusion and stigma in habitat fragmentation research”. In: *Biological Reviews* 99 (4), pp. 1411–1424. ISSN: 1469185X. DOI: 10.1111/brv.13073.
- Roberts, John M.K. and Andrew R. Weeks (Feb. 2011). “Genetic structure and long-distance dispersal in populations of the wingless pest springtail, *Sminthurus viridis* (Collembola: Sminthuridae).” In: *Genetics research* 93 (1), pp. 1–12. ISSN: 14695073. DOI: 10.1017/S0016672310000510.
- Romiguier, J. et al. (Nov. 2014). “Comparative population genomics in animals uncovers the determinants of genetic diversity”. In: *Nature* 515 (7526), pp. 261–263. ISSN: 14764687. DOI: 10.1038/nature13685.
- Rosenberg, Yuval et al. (Feb. 2023). “The global biomass and number of terrestrial arthropods”. In: *Science Advances* 9 (5). ISSN: 2375-2548. DOI: 10.1126/sciadv.abq4049.
- Saltzweid, Helge Von, Stefan Scheu, and Ina Schaefer (July 2016). “Founder events and pre-glacial divergences shape the genetic structure of European Collembola species”. In: *BMC Evolutionary Biology* 16 (1). ISSN: 14712148. DOI: 10.1186/s12862-016-0719-8.
- Schubert, Mikkel, Stinus Lindgreen, and Ludovic Orlando (Feb. 2016). “Adapter-Removal v2: Rapid adapter trimming, identification, and read merging”. In: *BMC Research Notes* 9. ISSN: 17560500. DOI: 10.1186/s13104-016-1900-2.
- Seastedt, T. R. (Jan. 1984). “The Role of Microarthropods in Decomposition and Mineralization Processes”. In: *Annual Review of Entomology* 29 (1),

- pp. 25–46. ISSN: 0066-4170. DOI: 10.1146/annurev.en.29.010184.000325.
- Seibold, Sebastian et al. (Oct. 2019). “Arthropod decline in grasslands and forests is associated with landscape-level drivers”. In: *Nature* 574 (7780), pp. 671–674. ISSN: 14764687. DOI: 10.1038/s41586-019-1684-3.
- Sim, Sheina B. et al. (Dec. 2022). “HiFiAdapterFilt, a memory efficient read processing pipeline, prevents occurrence of adapter sequence in PacBio HiFi reads and their negative impacts on genome assembly”. In: *BMC Genomics* 23 (1). ISSN: 14712164. DOI: 10.1186/s12864-022-08375-1.
- Slotte, Tanja et al. (July 2013). “The *Capsella rubella* genome and the genomic consequences of rapid mating system evolution”. In: *Nature Genetics* 45 (7), pp. 831–835. ISSN: 10614036. DOI: 10.1038/ng.2669.
- Smit, A. F. A., R. Hubley, and P. Green (2013). *RepeatMasker Open-4.0. 2013-2015*. URL: <http://repeatmasker.org>.
- Stanke, Mario et al. (Jan. 2008). “Using native and syntenically mapped cDNA alignments to improve de novo gene finding”. In: *Bioinformatics* 24 (5), pp. 637–644. ISSN: 13674803. DOI: 10.1093/bioinformatics/btn013.
- Stevens, Kate et al. (Feb. 2018). “Reduced gene flow in a vulnerable species reflects two centuries of habitat loss and fragmentation.” in: *Ecosphere* 9 (2). ISSN: 21508925. DOI: 10.1002/ecs2.2114.
- Team, R Core (2024). *R: A language and environment for statistical computing*. URL: <https://www.R-project.org/>.
- Thorbek, P. and T. Bilde (June 2004). “Reduced numbers of generalist arthropod predators after crop management”. In: *Journal of Applied Ecology* 41 (3), pp. 526–538. ISSN: 00218901. DOI: 10.1111/j.0021-8901.2004.00913.x.
- Timmermans, M. J.T.N. et al. (June 2005). “Genetic structure in *Orchesella cincta* (Collembola): Strong subdivision of European populations inferred from mtDNA and AFLP markers”. In: *Molecular Ecology* 14 (7), pp. 2017–2024. ISSN: 09621083. DOI: 10.1111/j.1365-294X.2005.02548.x.
- Turner, Monica G. (Oct. 2010). “Disturbance and landscape dynamics in a changing world”. In: *Ecology* 91 (10), pp. 2833–2849. ISSN: 00129658. DOI: 10.1890/10-0097.1.
- Vanbergen, Adam J. et al. (June 2013). “Threats to an ecosystem service: Pressures on pollinators”. In: *Frontiers in Ecology and the Environment* 11 (5), pp. 251–259. ISSN: 15409309. DOI: 10.1890/120126.
- Wagner, David L. (Jan. 2020). “Insect Declines in the Anthropocene”. In: *Annual Review of Entomology* 65 (1), pp. 457–480. ISSN: 0066-4170. DOI: 10.1146/annurev-ento-011019-025151.
- Webster, Matthew T. et al. (Feb. 2023). “Population Genomics for Insect Conservation”. In: *Annual Review of Animal Biosciences* 11 (1), pp. 115–140. ISSN: 2165-8110. DOI: 10.1146/annurev-animal-122221-075025.

- Welch, David Mark and Matthew Meselson (May 2000). “Evidence for the Evolution of Bdelloid Rotifers Without Sexual Reproduction or Genetic Exchange”. In: *Science* 288 (5469), pp. 1211–1215. ISSN: 0036-8075. DOI: 10.1126/science.288.5469.1211.
- Willi, Yvonne, Josh Van Buskirk, and Ary A. Hoffmann (Jan. 2006). “Limits to the adaptive potential of small populations”. In: *Annual Review of Ecology, Evolution, and Systematics* 37 (1), pp. 433–458. ISSN: 1543592X. DOI: 10.1146/annurev.ecolsys.37.091305.110145.
- Wurff, André W.G. Van Der et al. (Jan. 2005). “Population genetic structure of *Orchesella cincta* (Collembola; Hexapoda) in NW Europe, as revealed by microsatellite markers”. In: *Pedobiologia* 49 (2), pp. 167–174. ISSN: 00314056. DOI: 10.1016/j.pedobi.2004.10.004.
- Yang, Louie H. and Claudio Gratton (Aug. 2014). “Insects as drivers of ecosystem processes”. In: *Current Opinion in Insect Science* 2, pp. 26–32. ISSN: 22145745. DOI: 10.1016/j.cois.2014.06.004.
- Ørsted, Michael et al. (June 2019). “Genomic variation predicts adaptive evolutionary responses better than population bottleneck history”. In: *PLoS Genetics* 15 (6). ISSN: 15537404. DOI: 10.1371/journal.pgen.1008205.