*Supplementary information – Appendix 4*

Is the genomics ‘cart’ before the restoration ecology ‘horse’? Insights from qualitative interviews and trends from the literature

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Appendix 4. Details of the included studies

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| **Reference** | **Country of data collection** | **Country of author affiliation(s)** | **Year(s) of data collection** | **Restoration or conservation (author)** | **Restoration or conservation (reviewer)** | **Type of genomics (see Box 1 for definitions)** |
| Abrams, J.F., Hörig, L.A., Brozovic, R., Axtner, J., Crampton-Platt, A., Mohamed, A., Wong, S.T., Sollmann, R., Yu, D.W. & Wilting, A. 2019 Shifting up a gear with iDNA: from mammal detection events to standardised surveys. Journal of Applied Ecology 56, 1637-1648. (doi:10.1111/1365-2664.13411). | Malaysia | Germany, USA, UK, China | 2015 | Conservation | Conservation | Environmental DNA |
| Ahrendsen, D.L., Aust, S.K. & Kellar, P.R. 2016 Biodiversity assessment using next-generation sequencing: comparison of phylogenetic and functional diversity between Nebraska grasslands. Plant Systematics and Evolution 302, 89-108. (doi:10.1007/s00606-015-1246-6). | USA | USA | NR | Restoration | Restoration | Environmental DNA |
| Allen, J.L., McKenzie, S.K., Sleith, R.S. & Alter, S.E. 2018 First genome-wide analysis of the endangered, endemic lichen Cetradonia linearis reveals isolation by distance and strong population structure. American Journal of Botany 105, 1556-1567. (doi:10.1002/ajb2.1150). | USA | USA | NR | Conservation | Conservation | Population genomics |
| Andersen, L.H., Sunde, P., Pellegrino, I., Loeschcke, V. & Pertoldi, C. 2017 Using population viability analysis, genomics, and habitat suitability to forecast future population patterns of Little Owl Athene noctua across Europe. Ecology and Evolution 7, 10987-11001. (doi:10.1002/ece3.3629). | “Europe” | Denmark, Italy | NR | Conservation | Conservation | Population genomics |
| Ando, H., Setsuko, S., Horikoshi, K., Suzuki, H., Umehara, S., Inoue-Murayama, M. & Isagi, Y. 2013 Diet analysis by next-generation sequencing indicates the frequent consumption of introduced plants by the critically endangered red-headed wood pigeon (Columba janthina nitens) in oceanic island habitats. Ecology and Evolution 3, 4057-4069. (doi:10.1002/ece3.773). | Japan | Japan | 2009-2011 | Conservation | Conservation | Environmental DNA |
| Angeloni, F., Wagemaker, C.A.M., Jetten, M.S.M., Op den Camp, H.J.M., Janssen-Megens, E.M., Francoijs, K.-J., Stunnenberg, H.G. & Ouborg, N.J. 2011 De novo transcriptome characterization and development of genomic tools for Scabiosa columbaria L. using next-generation sequencing techniques. Molecular Ecology Resources 11, 662-674. (doi:10.1111/j.1755-0998.2011.02990.x). | UK | Netherlands | NR | Conservation | Conservation | Population genomics |
| Anthony, M.A., Stinson, K.A., Trautwig, A.N., Coates-Connor, E. & Frey, S.D. 2019 Fungal communities do not recover after removing invasive Alliaria petiolata (garlic mustard). Biological Invasions 21, 2085-2099. (doi:10.1007/s10530-019-02031-8). | USA | USA | 2013-2017 | Restoration | Restoration | Environmental DNA |
| Arrizabalaga-Escudero, A., Garin, I., García-Mudarra, J.L., Alberdi, A., Aihartza, J. & Goiti, U. 2015 Trophic requirements beyond foraging habitats: the importance of prey source habitats in bat conservation. Biological Conservation 191, 512-519. (doi:10.1016/j.biocon.2015.07.043). | Spain | Spain, The Basque Country | 2012 | Conservation | Conservation | Environmental DNA |
| Axtner, J., Crampton-Platt, A., Hörig, L.A., Mohamed, A., Xu, C.C.Y., Yu, D.W. & Wilting, A. 2019 An efficient and robust laboratory workflow and tetrapod database for larger scale environmental DNA studies. GigaScience 8, 1-17. (doi:10.1093/gigascience/giz029). | Malaysia | Germany, China, Netherlands, Canada, UK | Database up until 2015 | Conservation | Conservation | Environmental DNA |
| Bálint, M., Nowak, C., Márton, O., Pauls, S.U., Wittwer, C., Aramayo, J.L., Schulze, A., Chambert, T., Cocchiararo, B. & Jansen, M. 2018 Accuracy, limitations and cost efficiency of eDNA-based community survey in tropical frogs. Molecular Ecology Resources 18, 1415-1426. (doi:10.1111/1755-0998.12934). | Bolivia | Germany, Hungary, Bolivia, USA | 2014 | Conservation | Conservation | Environmental DNA |
| Baloğlu, B., Clews, E. & Meier, R. 2018 NGS barcoding reveals high resistance of a hyperdiverse chironomid (Diptera) swamp fauna against invasion from adjacent freshwater reservoirs. Frontiers in Zoology 15, 31. (doi:10.1186/s12983-018-0276-7). | Singapore | Singapore | 2013-2014 | Conservation | Conservation | Environmental DNA |
| Barboza, A.D.M., Pylro, V.S., Jacques, R.J.S., Gubiani, P.I., de Quadros, F.L.F., da Trindade, J.K., Triplett, E.W. & Foesch, L. 2018 Seasonal dynamics alter taxonomical and functional microbial profiles in Pampa biome soils under natural grasslands. PeerJ 6, e4991. (doi:10.7717/peerj.4991). | Brazil | Brazil, USA | 2014-2015 | Conservation | Conservation | Environmental DNA |
| Bellemain, E., Patricio, H., Gray, T., Guegan, F., Valentini, A., Miaud, C. & Dejean, T. 2016 Trails of river monsters: Detecting critically endangered Mekong giant catfish Pangasianodon gigas using environmental DNA. Global Ecology and Conservation 7, 148-156. (doi:10.1016/j.gecco.2016.06.007). | Thailand | France, Australia, Cambodia, Lao Democratic People’s Republic | 2015 | Conservation | Conservation | Environmental DNA |
| Bessey, C., Jarman, S.N., Stat, M., Rohner, C.A., Bunce, M., Koziol, A., Power, M., Rambahiniarison, J.M., Richardson, A.J. & Berry, O. 2019 DNA metabarcoding assays reveal a diverse prey assemblage for Mobula rays in the Bohol Sea, Philippines. Ecology and Evolution 9, 2459-2474. (doi:10.1002/ece3.4858). | Philippines | Australia, USA, Philippines | 2013-2015 | Conservation | Conservation | Environmental DNA |
| Bi, K., Linderoth, T., Vanderpool, D., Good, J.M., Nielsen, R. & Moritz, C. 2013 Unlocking the vault: next-generation museum population genomics. Molecular Ecology 22, 6018-6032. (doi:10.1111/mec.12516). | USA | USA, Australia | 1915-2012 | Conservation | Conservation | Population genomics |
| Biggs, J., Ewald, N., Valentini, A., Gaboriaud, C., Dejean, T., Griffiths, R.A., Foster, J., Wilkinson, J.W., Arnell, A., Brotherton, P., et al. 2015 Using eDNA to develop a national citizen science-based monitoring programme for the great crested newt (Triturus cristatus). Biological Conservation 183, 19-28. (doi:10.1016/j.biocon.2014.11.029). | UK | UK, France | 2013 | Conservation | Conservation | Environmental DNA |
| Binks, R.M., Byrne, M., McMahon, K., Pitt, G., Murray, K. & Evans, R.D. 2019 Habitat discontinuities form strong barriers to gene flow among mangrove populations, despite the capacity for long-distance dispersal. Diversity and Distributions 25, 298-309. (doi:10.1111/ddi.12851). | Australia | Australia | NR | Conservation | Conservation | Population genomics |
| Boeraeve, M., Honnay, O., Mullens, N., Vandekerkhove, K., De Keersmaeker, L., Thomaes, A. & Jacquemyn, H. 2018 The impact of spatial isolation and local habitat conditions on colonization of recent forest stands by ectomycorrhizal fungi. Forest Ecology and Management 429, 84-92. (doi:10.1016/j.foreco.2018.06.043). | Belgium | Belgium | NR | Restoration | Restoration | Environmental DNA |
| Boessenkool, S., McGlynn, G., Epp, L.S., Taylor, D., Pimentel, M., Gizaw, A., Nemomissa, S., Brochmann, C. & Popp, M. 2014 Use of ancient sedimentary DNA as a novel conservation tool for high-altitude tropical biodiversity. Conservation Biology 28, 446-455. (doi:10.1111/cobi.12195). | Uganda, Rwanda | Norway, Ireland, Singapore, Ethiopia | 2018 | Both | Both | Environmental DNA |
| Boscari, E., Abbiati, M., Badalamenti, F., Bavestrello, G., Benedetti-Cecchi, L., Cannas, R., Cau, A., Cerrano, C., Chimienti, G., Costantini, F., et al. 2019 A population genomics insight by 2b-RAD reveals populations' uniqueness along the Italian coastline in Leptopsammia pruvoti (Scleractinia, Dendrophylliidae). Diversity and Distributions 25, 1101-1117. (doi:10.1111/ddi.12918). | Italy | Italy | 2014-2015 | Conservation | Conservation | Population genomics |
| Brauer, C.J., Hammer, M.P. & Beheregaray, L.B. 2016 Riverscape genomics of a threatened fish across a hydroclimatically heterogeneous river basin. Molecular Ecology 25, 5093-5113. (doi:10.1111/mec.13830).  ] | Australia | Australia | 2000-2013 | Conservation | Conservation | Population genomics |
| Brozio, S., Manson, C., Gourevitch, E., Burns, T.J., Greener, M.S., Downie, J.D. & Hoskinsson, P.A. 2017 Development and application of an eDNA method to detect the critically endangered Trinidad golden tree frog (Phytotriades auratus) in Bromeliad Phytotelmata. PLoS One 12, e0170619. (doi:10.1371/journal.pone.0170619). | Trinidad | UK | 2015 | Conservation | Conservation | Environmental DNA |
| Brunbjerg, A.K., Bruun, H.H., Dalby, L., Fløjgaard, C., Frøslev, T.G., Høye, T.T., Goldberg, I., Læssøe, T., Hansen, M.D.D., Brøndum, L., et al. 2018 Vascular plant species richness and bioindication predict multi-taxon species richness. Methods in Ecology and Evolution 9, 2372-2382. (doi:10.1111/2041-210X.13087). | Denmark | Denmark | NR | Conservation | Both | Environmental DNA |
| Brüniche-Olsen, A., Austin, J.J., Jones, M.E., Holland, B.R. & Burridge, C.P. 2016 Detecting selection on temporal and spatial scales: a genomic time-series assessment of selective responses to devil facial tumor disease PLoS One 11, e0147875. (doi:10.1371/journal.pone.0147875). | Australia | Australia | 1999-2013 | Conservation | Conservation | Population genomics |
| Brüniche‐Olsen, A., Kellner, K.F. & DeWoody, J.A. 2019 Island area, body size and demographic history shape genomic diversity in Darwin's finches and related tanagers. Molecular Ecology 28, 4914-4925. (doi:10.1111/mec.15266). | Ecuador | USA | 1988-2001 | Conservation | Both | Population genomics |
| Burgar, J.M., Murray, D.C., Craig, M.D., Haile, J., Houston, J., Stokes, V. & Bunce, M. 2014 Who's for dinner? High-throughput sequencing reveals bat dietary differentiation in a biodiversity hotspot where prey taxonomy in largely undescribed. Molecular Ecology 23, 3605-3617. (doi:10.1111/mec.12531). | Australia | Australia | 2010-2011 | Conservation | Conservation | Environmental DNA |
| Burgess, T.I., White, D., McDougall, K.M., Garnas, J., Dunstan, W.A., Català, S., Carnegie, A.J., Worboys, S., Cahill, D., Vettraino, A.-M., et al. 2017 Distribution and diversity of Phytophthora across Australia. Pacific Conservation Biology 23, 150-162. (doi:10.1071/PC16032). | Australia | Australia, Italy, Spain, South Africa | 2013-2015 | Conservation | Conservation | Environmental DNA |
| Callicrate, T., Dikow, R., Thomas, J.W., Mullikin, J.C., Jarvis, E.D., Fleischer, R.C. & NISC Comparative Sequencing Program. 2014 Genomic resources for the endangered Hawaiian honeycreepers. BMC Genomics 15, 1098. (doi:10.1186/1471-2164-15-1098). | USA | USA | 2002 | Conservation | Conservation | Comparative genomics |
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| Chen, J., Mo, L., Zhang, Z., Nan, J., Xu, D., Chao, L., Zhang, X. & Bao, Y. 2020 Evaluation of the ecological restoration of a coal mine dump by exploring the characteristics of microbial communities. Applied Soil Ecology 147, 103430. (doi:10.1016/j.apsoil.2019.103430). | China | China | 2018 | Restoration | Restoration | Environmental DNA |
| Chen, N., Cosgrove, E.J., Bowman, R., Fitzpatrick, J.W. & Clark, A.G. 2016 Genomic consequences of population decline in the endangered Florida scrub-jay. Current Biology 26, 2974-2979. (doi:10.1016/j.cub.2016.08.062). | USA | USA | 1995-2013 | Conservation | Conservation | Population genomics |
| Çilingir, F.G., Rheindt, F.E., Garg, K.M., Platt, K., Platt, S.G. & Bickford, D.P. 2017 Conservation genomics of the endangered Burmese roofed turtle. Conservation Biology 31, 1469-1476. (doi:10.1111/cobi.12921). | Myanmar | Singapore, Myanmar, USA | 2006-2011 | Conservation | Conservation | Population genomics |
| Cilleros, K., Valentini, A., Allard, L., Dejean, T., Etienne, R., Grenouillet, G., Iribar, A., Taberlet, P., Vigouroux, R. & Brosse, S. 2019 Unlocking biodiversity and conservation studies in high-diversity environments using environmental DNA (eDNA): a test with Guianese freshwater fishes. Molecular Ecology Resources 19, 27-46. (doi:10.1111/1755-0998.12900). | French Guiana | France, French Guiana | 2010-2015 | Conservation | Conservation | Environmental DNA |
| Cordeiro, E.M.G., Macrini, C.M., Sujii, P.S., Schwarcz, K.D., Pinheiro, J.B., Rodrigues, R.R., Brancalion, P.H.S. & Zucchi, M.I. 2019 Diversity, genetic structure, and population genomics of the tropical tree Centrolobium tomentosum in remnant and restored Atlantic forests. Conservation Genetics 20, 1073-1085. (doi:10.1007/s10592-019-01195-z). | Brazil | Brazil | 2013-2014 | Both | Both | Population genomics |
| Cristofari, R., Plaza, P., Fernández, C.E., Trucchi, E., Gouin, N., Le Bohec, C., Zavalaga, C., Alfaro-Shigueto, J. & Luna-Jorquera, G. 2019 Unexpected population fragmentation in an endangered seabird: the case of the Peruvian diving-petrel. Scientific Reports 9, 2021. (doi:10.1038/s41598-019-38682-9). | Chile | Finland, France, Monaco, Norway, Chile, Austria, Italy, Peru | 2012 | Conservation | Conservation | Population genomics |
| Cruz, M.V., Mori, G.M., Signori-Müller, C., da Silva, C.C., Oh, D.-H., Dassanayake, M., Zucchi, M.I., Oliveira, R.S. & de Souza, A.P. 2019 Local adaptation of a dominant coastal tree to freshwater availability and solar radiation suggested by genomic and ecophysiological approaches. Scientific Reports 9, 19936. (doi:10.1038/s41598-019-56469-w). | “South America” | Brazil, USA | 2014 | Conservation | Conservation | Population genomics |
| De Barba, M., Miquel, C., Boyer, F., Mercier, C., Rioux, D., Coissac, E. & Taberlet, P. 2014 DNA metabarcoding multiplexing and validation of data accuracy for diet assessment: application to omnivorous diet. Molecular Ecology Resources 14, 306-323. (doi:10.1111/1755-0998.12188). | Italy | Moscow | 2002-2008 | Conservation | Conservation | Environmental DNA |
| de Villemereuil, P., Rutschmann, A., Lee, K.D., Ewen, J.G., Brekke, P. & Santure, A.W. 2019 Little adaptive potential in a threatened passerine bird. Current Biology 29, 889-894. (doi:10.1016/j.cub.2019.01.072). | New Zealand | New Zealand, France, UK | 2004-2015 | Conservation | Conservation | Population genomics |
| Devitt, T.J., Wright, A.M., Cannatella, D.C. & Hillis, D.M. 2019 Species delimitation in endangered groundwater salamanders: implications for aquifer management and biodiversity conservation. Proceedings of the National Academy of Science 116, 2624-2633. (doi:10.1073/pnas.1815014116). | USA | USA | NR | Conservation | Conservation | Population genomics |
| DeWoody, J.A., Fernandez, N.B., Brüniche‐Olsen, A., Antonides, J.D., Doyle, J.M., San Miguel, P., Westerman, R., Vertyankin, V.V., Godard-Codding, C.A.J. & Bickham, J.W. 2017 Characterization of the grey whale Eschrichtius robustus genome and a genotyping array based on single-nucleotide polymorphisms in candidate genes. The Biological Bulletin 232, 186-197. (doi:10.1086/693483). | “Pacific” | USA, Russia | NR | Conservation | Conservation | Population genomics |
| Dittberner, H., Becker, C., Jiao, W.-B., Schneeberger, K., Hölzel, N., Tellier, A. & de Meaux, J. 2019 Strengths and potential pitfalls of hay transfer for ecological restoration revealed by RAD‐seq analysis in floodplain Arabis species. Molecular Ecology 28, 3887-3901. (doi:10.1111/mec.15194). | Germany | Germany | 1997-2016 | Restoration | Restoration | Population genomics & environmental DNA |
| Dobrynin, P., Liu, S., Tamazian, G., Xiong, Z., Yurchenko, A.A., Krasheninnikova, K., Kliver, S., Schmidt-Küntzel, A., Koepfli, K.-P., Johnson, W., et al. 2015 Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology 16, 277. (doi:10.1186/s13059-015-0837-4). | Namibia, Tanzania | Russia, China, Namibia, USA, Spain, Portugal, Puerto Rico, Brazil, Korea, Denmark, Saudi Arabia | NR | Conservation | Conservation | Population genomics |
| Docherty, K.M. & Gutknecht, J.L.M. 2019 Soil microbial restoration strategies for promoting climate‐ready prairie ecosystems. Ecological Applications 29, e01858. (doi:10.1002/eap.1858). | USA | USA | 2015 | Restoration | Restoration | Environmental DNA |
| Drinkwater, R., Bærholm Schnell, I., Bohmann, K., Bernard, H., Veron, G., Clare, E., Gilbert, M.T.P. & Rossiter, S.J. 2019 Using metabarcoding to compare the suitability of two blood‐feeding leech species for sampling mammalian diversity in North Borneo. Molecular Ecology Resources 19, 105-117. (doi:10.1111/1755-0998.12943). | Malaysia | UK, Denmark, Malaysia, France, Norway | 2015 | Conservation | Conservation | Environmental DNA |
| Drury, C., Schopmeyer, S., Goergen, E., Bartels, E., Nedimyer, K., Johnson, M., Maxwell, K., Galvan, V., Manfrino, C. & Lirman, D. 2017 Genomic patterns in Acropora cervicornis show extensive population structure and variable genetic diversity Ecology and Evolution 7, 6188-6200. (doi:10.1002/ece3.3184). | USA | Dominican Republic, USA, Cayman Islands | 2012-2015 | Conservation | Conservation | Population genomics |
| Dupuis, J.R., Oliver, J.C., Brunet, B.M.T., Longcore, T., Johnson, J.J. & Sperling, F.A.H. 2018 Genomic data indicate ubiquitous evolutionary distinctiveness among populations of California metalmark butterflies. Conservation Genetics 19, 1097-1108. (doi:10.1007/s10592-018-1081-8). | USA | USA, Canada | 1995-2014 | Conservation | Conservation | Population genomics |
| Dupuis, J.R., Peigler, R.S., Geib, S.M. & Rubinoff, D. 2018 Phylogenomics supports incongruence between ecological specialization and taxonomy in a charismatic clade of buck moths. Molecular Ecology 27, 4417-4429. (doi:10.1111/mec.14883). | USA | USA | 1997-2015 | Conservation | Conservation | Population genomics |
| Eaton, W.D., Shokralla, S., McGee, K.M. & Hajibabaei, M. 2017 Using metagenomics to show the efficacy of forest restoration in the New Jersey Pine Barrens. Genome 60, 825-836. (doi:10.1139/gen-2015-0199). | USA | USA, Canada, Egypt | 2011 | Restoration | Restoration | Environmental DNA |
| Ejrnæs, R., Frøslev, T.G., Høye, T.T., Kjøller, R., Oddershede, A., Brunbjerg, A.K., Hansen, A.J. & Bruun, H.H. 2018 Uniquity: A general metric for biotic uniqueness of sites. Biological Conservation 225, 98-105. (doi:10.1016/j.biocon.2018.06.034). | Denmark | Denmark | 2014-2016 | Conservation | Both | Environmental DNA |
| Ekblom, R., Brechlin, B., Persson, J., Smeds, L., Johansson, M., Magnusson, J., Flagstad, Ø. & Ellegren, H. 2018 Genome sequencing and conservation genomics in the Scandinavian wolverine population Conservation Biology 32, 1301-1312. (doi:10.1111/cobi.13157). | Sweden | Sweden, Norway | 2005-2010 | Conservation | Conservation | Population genomics |
| Esnaola, A., Arrizabalaga-Escudero, A., González-Esteban, J., Elosegi, A. & Aihartza, J. 2018 Determining diet from faeces: Selection of metabarcoding primers for the insectivore Pyrenean desman (Galemys pyrenaicus). PLoS One 13, e0208986. (doi:10.1371/journal.pone.0208986). | Spain | Spain | 2015-2016 | Conservation | Conservation | Environmental DNA |
| Ezeokoli, O.T., Bezuidenhout, C.C., Maboeta, M.S., Khasa, D.P. & Adeleke, R.A. 2020 Structural and functional differentiation of bacterial communities in post-coal mining reclamation soils of South Africa: bioindicators of soil ecosystem restoration. Scientific Reports 10, 1759. (doi:10.1038/s41598-020-58576-5). | South Africa | South Africa, Canada | 2016 | Restoration | Restoration | Environmental DNA |
| Feng, S., Fang, Z., Barnett, R., Li, C., Han, S., Kuhlwilm, M., Zhou, L., Pan, H., Deng, Y., Chen, G., et al. 2019 The genomic footprints of the fall and recovery of the crested ibis. Current Biology 29, 340-349. (doi:10.1016/j.cub.2018.12.008). | China, Korea, Japan, Russia | China, Denmark, UK, Spain, Austria, Germany, Norway | 1841-1922 | Conservation | Conservation | Population genomics |
| Fernandes, K., van der Heyde, M., Coghlan, M., Wardell-Johnson, G., Bunce, M., Harris, R. & Nevill. 2019 Invertebrate DNA metabarcoding reveals changes in communities across mine site restoration chronosequences. Restoration Ecology 27, 1177-1186. (doi:10.1111/rec.12976). | Australia | Australia | 2017 | Restoration | Restoration | Environmental DNA |
| Feutry, P., Berry, O., Kyne, P.M., Pillans, R.D., Hillary, R.M., Grewe, P.M., Marthick, J.R., Johnson, G., Gunasekera, R.M., Bax, N.J., et al. 2017 Inferring contemporary and historical genetic connectivity from juveniles. Molecular Ecology 26, 444-456. (doi:10.1111/mec.13929). | Australia | Australia | 2012-2014 | Conservation | Conservation | Population genomics |
| Ficetola, G.F., Miaud, C., Pompanon, F. & Taberlet, P. 2008 Species detection using environmental DNA from water samples. Biology Letters 4, 423-425. (doi:10.1098/rsbl.2008.0118). | France | France | NR | Conservation | Both | Environmental DNA |
| Fløjgaard, C., De Barba, M., Taberlet, P. & Ejrnæs, R. 2017 Body condition, diet and ecosystem function of red deer (Cervus elaphus) in a fenced nature reserve. Global Ecology and Conservation 11, 312-323. (doi:10.1016/j.gecco.2017.07.003). | Denmark | Denmark, France | 2013-2014 | Conservation | Conservation | Environmental DNA |
| Garbe, J.R., Prakapenka, D., Tan, C. & Da, Y. 2016 Genomic inbreeding and relatedness in wild panda populations. PLoS One 11, e0160496. (doi:10.1371/journal.pone.0160496). | China | USA, China | NR | Conservation | Conservation | Population genomics |
| Gellie, N.J.C., Mills, J.G., Breed, M.F. & Lowe, A.J. 2017 Revegetation rewilds the soil bacterial microbiome of an old field. Molecular Ecology 26, 2895-2904. (doi:10.1111/mec.14081). | Australia | Australia | 2015 | Restoration | Restoration | Environmental DNA |
| Geml, J., Gravendeel, B., van der Gaag, K., Neilen, M., Lammers, Y., Raes, N., Semenova, T.A., de Knijff, P. & Noordeloos, M.E. 2014 The contribution of DNA metabarcoding to fungal conservation: diversity assessment, habitat partitioning and mapping red-listed fungi in protected coastal Salix repens communities in the Netherlands. PLoS One 9, e99852. (doi:10.1371/journal.pone.0099852). | Netherlands | Netherlands | 2010 | Conservation | Conservation | Environmental DNA |
| Grange, Z.L., Biggs, P.J., Rose, S.P., Gartrell, B.D., Nelson, N.J. & French, N.P. 2017 Genomic epidemiology and management of Salmonella in island ecosystems used for takahe conservation. Microbial Ecology 74, 735-744. (doi:10.1007/s00248-017-0959-1). | New Zealand | New Zealand, USA | 2011-2013 | Conservation | Conservation | Comparative genomics |
| Grange, Z.L., Gartrell, B.D., Biggs, P.J., Nelson, N.J., Anderson, M. & French, N.P. 2016 Microbial genomics of a host-assocated commensal bacterium in fragmented populations of endangered takahe. Microbial Ecology 71, 1020-1029. (doi:10.1007/s00248-015-0721-5). | New Zealand | New Zealand | 2011-2013 | Conservation | Conservation | Comparative genomics |
| Gueuning, M., Ganser, D., Blaser, S., Albrecht, M., Knop, E., Praz, C. & Frey, J.E. 2019 Evaluating next-generation sequencing (NGS) methods for routine monitoring of wild bees: Metabarcoding, mitogenomics or NGS barcoding. Molecular Ecology Resources 19, 847-862. (doi:10.1111/1755-0998.13013). | Switzerland | Switzerland | 2017 | Conservation | Both | Environmental DNA |
| Guo, W., Mishra, S., Wang, C., Zhang, H., Ning, R., Kong, F., Zeng, B., Zhao, J. & Li, Y. 2019 Comparative Study of Gut Microbiota in Wild and Captive Giant Pandas (Ailuropoda melanoleuca). Genes (Basel) 10, 827. (doi:10.3390/genes10100827). | China | China, USA | 2013-2015 | Conservation | Conservation | Environmental DNA |
| Guo, Y., Chen, X., Wu, Y., Zhang, L., Cheng, J., Wei, G. & Lin, Y. 2018 Natural revegetation of a semiarid habitat alters taxonomic and functional diversity of soil microbial communities. Science of the Total Environment 635, 598-606. (doi:10.1016/j.scitotenv.2018.04.171). | China | China | 2014 | Restoration | Restoration | Environmental DNA |
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