

Region	Country	Species	Description	Genetic marker/s	Reference (link)
Central and Southern Asia	India	<i>Taxus contorta</i> West Himalayan yew Gymnosperms	Genetic and climatic data transcribed into conservation management for a Himalayan endangered species.	<b>microsatellites</b>	(Majeed, Singh, & Bhardwaj, 2021)
Central and Southern Asia	India	<i>Penaeus monodon</i> Black tiger shrimp Malacostraca	Population genetic study indicated strong, statistically significant genetic structure among tiger shrimp populations. Study has implications for future domestication of the species in India, including identifying founding stocks for aquaculture, and the potential impacts of release of domesticates into the wild.	<b>microsatellites</b>	(Mandal et al. 2012)
Central and Southern Asia	India	<i>Felis chaus, Panthera pardus, Melursus ursinus</i> and <i>Panthera tigris</i> Jungle cat, leopard, sloth bear and tiger Mammalia	Human footprint differentially impacts genetic connectivity of four wide-ranging mammals in a fragmented landscape.	<b>microsatellites</b>	(Thatte et al., 2020)
Central and Southern Asia	Bangladesh	Multiple fish, aquatic molluscs, crustaceans	Development of a DNA barcoding tool to identify fish, aquatic molluscs, and crustaceans of the Sundarbans mangrove wetland. The resulting inventory will inform future biodiversity studies and a conservation plan.	<b>mtDNA</b> sequence	(Habib et al. 2021)
Central and Southern Asia; Eastern and South-Eastern Asia	Multiple (Pakistan and China)	Libellulidae spp. and Gomphidae spp. Dragonflies Insecta	Sequence data identified 21 different dragonfly species from 15 genera, highlighting the diversity of dragonflies in these regions and the need to develop conservation measures.	<b>mtDNA</b> sequence	(Islam et al., 2018)

Eastern and South-Eastern Asia	China	<i>Pelophylax plancyi</i> The eastern golden frog Amphibia	Genetic data was used to evaluate demographic history and population structure in an area that has undergone urbanization. Results identified bottlenecks, population fragmentation and reductions in genetic diversity related to urbanization, highlighting the need for conservation strategies to incorporate connectivity in rapidly urbanizing environments.	mtDNA sequence; microsatellites	(Wei et al., 2021)
Eastern and South-Eastern Asia	Indonesia	<i>Tridacna crocea</i> Boring giant clam Bivalvia	Framework demonstrating how eight genetic characteristics could be incorporated into spatial conservation prioritization for two contrasting objectives: biodiversity preservation vs. maintaining ecological function and sustainable use.	microsatellites	(Beger et al., 2014)
Eastern and South-Eastern Asia	Indonesia	<i>Sus scrofa vitattus</i> and <i>Sus verrucosus</i> Indonesian banded pig and Java warty pig Mammalia	Evidence of hybridisation between the common Indonesian banded pig and the endangered Java warty pig.	microsatellites	(Drygala, Rode-Margono, Semiadi, Wirdateti, & Frantz, 2020)
Eastern and South-Eastern Asia	Indonesia, Malaysia and Singapore	<i>Manis javanica</i> Sunda pangolin Mammalia	Genomics used to assign pangolins of unknown origin from illegal trade seizures to known populations, with implications for tracing trade patterns, finding populations of origin for rescued animals, and for breeding programs.	RRS	(Nash et al., 2018)
Eastern and South-Eastern Asia	Japan	<i>Heliopora</i> spp. Blue coral Anthozoa	Limited fine-scale larval dispersal of threatened brooding corals as evidenced by population genetics and numerical simulation.	microsatellites	(Taninaka et al., 2019)

Eastern and South-Eastern Asia	Laos, Thailand, Cambodia and Vietnam	<i>Dalbergia cochinchinensis</i> Siamese rosewood Angiosperms	Genetic data used to assess population structure and identify management units, demonstrating the potential for genetics for tracking geographic origin of illegal timber for use in CITES regulation and law enforcement.	<b>microsatellites;</b> <b>RRS</b>	(Hartvig et al., 2020)
Europe	Belgium	<i>Alnus glutinosa</i> Black alder Angiosperms	Population genomic data used to evaluate seed zone delineation for reforestation, with results applied in policy and management.	<b>RRS</b>	(De Kort et al., 2014)
Europe	France	<i>Rana catesbeiana</i> American bullfrog Amphibia	eDNA barcoding was used to identify an invasive species, outperforming traditional field surveys and allowing for early detection at low density. Results suggest that the abundance and distribution of this species has been underestimated, which will be important for control actions.	<b>mtDNA</b> barcoding	(Dejean et al., 2012)
Europe	Multiple (Europe)	<i>Melitta</i> spp. and <i>Bombus</i> spp. European wild bees Insecta	Genetic data used to assess continental scale population structure and gene flow, indicating limited species-range connectivity. This makes these species vulnerable to regional extinction, suggesting conservation efforts should focus on the most distant populations.	<b>mtDNA</b> sequence; <b>nuclear</b> sequence	(Lecocq, Gérard, Michez, & Dellicour, 2017)
Europe	Multiple (Europe)	<i>Canis lupus</i> Wolf Mammalia	Genetic data used to quantify admixture with dogs, and to create a targeted adaptive SNP-panel to quantify admixture in recent wolf-dog hybridization. This provided a management tool to eliminate hybrids from wolf populations.	<b>RRS</b> (targeted sequencing); <b>WGS</b>	(Harmoinen et al., 2021; Smeds et al., 2021)
Europe	Multiple (Baltic Sea)	<i>Esox lucius</i> , <i>Gasterosteus aculeatus</i> , <i>Scophthalmus maximus</i>	Literature review of 61 population genetic studies available for aquatic species in the Baltic Sea. Study examined the protection of genetic diversity by marine protected areas (MPAs) for four species with sufficient	<b>mtDNA</b> sequence; <b>microsatellites</b>	(Wennerström et al. 2016)

		Northern pike, three-spined stickleback, turbot Actinopterygii <i>Fucus vesiculosus</i> Bladderwrack Phaeophyceae	data. No difference was found within vs. outside MPAs, which indicates a more comprehensive study and additional sampling is needed for an in-depth assessment of genetic patterns and connectivity among MPAs.		
Europe	Multiple (Baltic Sea)	<i>Esox lucius</i> Northern pike Actinopterygii	Population genetic study of <i>Esox lucius</i> in the brackish Baltic Sea coastline. Stable, low genetic structure and evidence of gene flow between neighboring populations contrasts with previous studies on anadromous Baltic pike. Study indicates management should assure connectivity among brackish spawning grounds and large population sizes at identified core areas.	microsatellites	(Wennerström et al. 2017)
Latin America and Caribbean	Argentina (western south Atlantic Ocean)	<i>Pontoporia blainvillei</i> Franciscana dolphin Mammalia	Combined genetic and environmental data to understand how geography and environment influence population structure and management of a species threatened by bycatch, and how ecological processes influence genetic patterns in marine species more broadly.	mtDNA sequence; microsatellites	(Mendez, Rosenbaum, Subramaniam, Yackulic, & Bordino, 2010)
Latin America and Caribbean	Colombia	<i>Zamia incognita</i> and <i>Z. melanorrhachis</i> Cycad Gymnosperm	Assessed genetic diversity and structure in remaining populations of two species threatened by deforestation. Populations showed signs of isolation and were highly differentiated. This information was used to help provide guidance on prioritizing populations for ex situ management.	microsatellites	(Aristizábal, Tuberquia, & Sanín, 2018)
Latin America and Caribbean	Ecuador	<i>Geochelone</i> spp. Galapagos Giant Tortoises Reptilia	Evolutionary genetic/genomic approaches to inform <i>in situ</i> and <i>ex situ</i> conservation programs, including the discovery of living individuals with genetic material from extinct lineages, raising the possibility of rescuing species from extinction.	mtDNA sequence; microsatellites; RRS	(Edwards et al., 2013; Gaughran et al., 2018; Jensen, Tapia, Caccone, & Russello, 2015; Poulakakis et al., 2008)

Latin America and Caribbean	Multiple	<i>Chelus</i> spp. Matamata turtles Reptilia	Genetic analyses of animals confiscated from the illegal pet trade in the Amazon revealed they were distinct from other animals from the area. The confiscated animals originated from the Orinoco Basin, where a highly differentiated form was identified using genomic analyses and described as a new species which diverged from the Amazonian taxon roughly 13 million years ago. Molecular data can now be used to guide reintroduction of confiscated animals.	mtDNA sequence; nuclear sequence; RRS	(Vargas-Ramírez et al., 2020)
Latin America and Caribbean; Europe and Northern America	Multiple (western Atlantic Ocean)	<i>Carcharhinus signatus</i> Night shark Chondrichthyes	Investigated genetic diversity, genetic connectivity, and phylogeography of night sharks (IUCN Vulnerable). Evidence of significant population structure, the existence of two matrilineal lineages, and a historical bottleneck support the species being considered as two MUs, with MU-specific catch-quotas.	mtDNA sequence; microsatellites	(Domingues et al., 2019)
Latin America and Caribbean; Europe and Northern America	Multiple (Brazil, USA)	<i>Puma concolor</i> Puma Mammalia	Genomic data used to investigate inbreeding in puma populations, with ROH burden and demographic histories providing insights for translocations.	WGS	(Saremi et al., 2019)
Multiple	Multiple (southeast Atlantic and western Indian Ocean)	<i>Megaptera novaeangliae</i> Humpback whale Mammalia	Genetic data used to determine patterns of population structure and connectivity, including sex-specific gene flow, to inform conservation and management of a highly migratory species recovering from whaling.	mtDNA sequence; microsatellites	(Kershaw et al., 2017)
Northern Africa and Western Asia	Egypt	<i>Parupeneus forsskali</i> , <i>Upeneus pori</i> , <i>Sillago suezensis</i> , <i>Platycephalus indicus</i> , <i>Sphyaena</i>	Identified marine fish species from the Suez Gulf using DNA barcoding, contributing to future fish species identification in the Red Sea and adding to conservation guidelines for gulf fish species in Egypt.	mtDNA barcoding	(Abbas, Ismail, El-Ganainy, & Ali, 2021)

		<i>chrysotaenia</i> , <i>Atherinomorus forskalii</i> , <i>Stephanolepis diaspros</i> , <i>Pomadasys stridens</i> , <i>Lagocephalus suezensis</i> and <i>L. sceleratus</i> Marine fishes Actinopterygii			
Northern Africa and Western Asia	Morocco	<i>Argania spinosa</i> The Argan Angiosperms	Genetic data used to assess variation in an overexploited tree, revealing strong population differentiation across its range. This provided guidance for the best source populations for seed storage for ex situ conservation programs.	<b>AFLP</b> (ISSR and IRAP)	(Pakhrou et al., 2017)
Northern America	USA	<i>Conradina cygniflora</i> Angiosperms	Genetic data helped to identify a new species, leading to its classification as endangered.	<b>microsatellites</b>	(Edwards, Judd, Ionta, & Herring, 2009)
Northern America	USA	<i>Quercus</i> spp. Oak Angiosperms	Genetic data used to determine if two populations of a Critically Endangered oak are safeguarded in botanic garden collections. DNA shows that only one population was collected historically, highlighting a need to collect seed from the other.	<b>microsatellites</b>	(Hoban et al., 2020)
Northern America	USA	<i>Haliotis fulgens</i> <i>Philippi</i> Green abalone Gastropoda	Genetic data were used to investigate population structure in a species that has undergone intensive harvesting to inform a management plan. Analyses revealed one large panmictic population, suggesting that it may not be necessary to source local broodstocks for translocations and restocking in hatchery populations.	<b>RRS</b>	(Gruenthal et al., 2014)

Northern America	USA	<i>Gymnogyps californianus</i> California condor Aves	Sex determination and parentage analysis was executed to inform the California Condor recovery program. Having a high quality pedigree will support decision making in captive pairing and release recommendations.	<b>microsatellites</b>	(Moran et al., 2021)
Northern America	USA	<i>Brachylagus idahoensis</i> Pygmy rabbit Mammalia	Genetic monitoring was used to evaluate survival and reproduction of reintroduced rabbits, assess the percentage of local ancestry retained and track the spatial expansion and population size.	<b>mtDNA</b> sequence; <b>microsatellites</b>	(DeMay, Becker, Rachlow, & Waits, 2017)
Northern America	USA	<i>Canis rufus</i> Red wolf Mammalia	Genetic monitoring was used to monitor and minimize hybridization with coyotes. This included fecal DNA monitoring, rapid genetic analyses of pups and cross fostering, and genetic analysis of all captured individuals.	<b>microsatellites</b>	(Gese et al., 2015)
Oceania	Australia	<i>Natator depressus</i> Flatback turtle Reptilia	Used genetic data to investigate range-wide phylogeography and population structure among rookeries. This led to the identification of different stocks, with implications for assessing stock-specific threats (including climate change) along migratory routes and foraging habitat.	<b>mtDNA</b> sequence; <b>microsatellites</b>	(FitzSimmons et al., 2020)
Oceania	Australia	<i>Tympanocryptis</i> spp. Grassland earless dragons Reptilia	Genetic data was used to resolve uncertain taxonomy of threatened species. One possible extinction was identified, highlighting the need for surveys to locate any remaining populations of this species.	<b>mtDNA</b> sequence; <b>RRS</b>	(Melville et al., 2019)
Oceania	Australia	<i>Macquarie australasica</i> Macquarie perch Actinopterygii	Genetic data were used to assess effective population size and the need for genetic rescue and restoration. Results of the augmentation were monitored with reduced representation genome-wide markers. Further a sexing array was designed based on whole genome resequencing.	<b>mtDNA</b> sequence; <b>microsatellites</b> ; <b>RRS</b> ; <b>WGS</b>	(Pavlova et al. 2017; <a href="#">Lutz et al. 2021</a> ; <a href="#">Pavlova et al. 2022</a> )

Oceania	New Caledonia (French territory)	<i>Araucaria</i> spp. Gymnosperms	Genetic data used to resolve phylogenetic relationships, and within species genetic diversity among diverse endemic taxa. High levels of within species genetic structure were detected, likely due to low gene flow and inbreeding. This information was used to provide recommendations for defining ESUs.	chloroplast sequence; microsatellites	(Gaudeul, Gardner, Thomas, Ennos, & Hollingsworth, 2014)
Oceania	New Zealand	<i>Strigops habroptilus</i> Kākapō Aves	Genetic sexing has been used to inform management about the effect of supplemental feeding on the sex ratio of the offspring. Supplemental feeding was found to lead to an excess of males, suggesting that feeding regimes needed to be updated.	nuclear sequence	(Clout, Elliott, & Robertson, 2002)
Oceania	USA (Hawai'i)	<i>Eretmochelys imbricata</i> Hawksbill turtle Reptilia	Genetic data revealed strong differentiation between the Hawaiian nesting colony and those in the west and east Pacific. This indicates that the Hawaiian nesting colony is demographically isolated and warrants recognition as a demographically distinct management unit.	mtDNA sequence	(Gaos et al., 2020)
Sub-Saharan Africa	Ethiopia and South Africa	<i>Sarothrura ayresi</i> White-winged flufftail Aves	Genetic data used to determine population connectivity, revealing that the two populations are one population occupying different seasonal ranges, rather than separate species/subspecies. Low genetic diversity suggests that this population may be at risk of extinction.	mtDNA; microsatellites	(Dalton, Smit-Robinson, Vermaak, Jarvis, & Kotze, 2018)
Sub-Saharan Africa	Madagascar	<i>Dracaena umbraculifera</i> Angiosperms	Phylogenetic data from the wild and from botanic gardens helped identify populations of a previously presumed extinct plant species, which led to its reclassification as Critically Endangered by the IUCN.	chloroplast sequence	(Edwards et al., 2018)



Sub-Saharan Africa	Multiple (West and East Africa)	<i>Lates niloticus</i> Nile perch Actinopterygii	Genetic data used to delineate management units and population structure, to explore the possibility of multiple species. The data suggested a single management unit and a single bottlenecked and possibly endangered species within Lake Victoria. Geographic genetic structure across West and East Africa corroborated signatures of a recent bottleneck.	<b>mtDNA</b> sequence; <b>microsatellites</b>	(Basiita et al. 2018)
Sub-Saharan Africa	Multiple (Cameroon and Equatorial Guinea)	<i>Andropadus virens</i> Little greenbul Aves	Genetic data used to assess how sexual selection and mate choice are influenced by anthropogenic habitat change, and to assess genomic vulnerability. Found divergent selection/genetic differentiation across different habitats, and areas where climate and land use are predicted to change will require the greatest shifts in adaptive genomic variation.	<b>AFLP</b> ; <b>RRS</b>	(Smith et al., 2021, 2008)
Sub-Saharan Africa	Multiple (Mozambique and South Africa)	<i>Cercopithecus</i> spp. Samango monkeys Mammalia	Genetic data was used to determine the number and timing of radiation events of <i>Cercopithecus</i> monkeys in southern Africa, adding to taxonomic knowledge and phylogeographic history of these species.	<b>mtDNA</b> sequence; <b>microsatellites</b>	(Linden et al., 2020)
Sub-Saharan Africa	Multiple	<i>Diceros bicornis</i> and <i>Ceratotherium simum</i> Black rhinoceros and white rhinoceros Mammalia	Genetic data used to date and reconstruct historical events, past demographic history, estimate historical and current effective population sizes, contemporary and historical gene flow, define population structure and identify conservation units. Results suggest that divergence time does not necessarily correlate with cessation of genetic contact, while exploring contemporary vs. historical gene flow allowed for assessment of lost genetic diversity.	<b>mtDNA</b> sequence; <b>microsatellites</b> ; <b>WGS</b>	(Moodley et al., 2017, 2018, 2020)

Sub-Saharan Africa	Multiple (Namibia and South Africa)	<i>Equus zebra</i> Mountain zebras Mammalia	Genetic data informed choice of suitable populations for reintroductions and translocations, and used to monitor temporal changes in genetic diversity.	<b>mtDNA</b> sequence; <b>microsatellites</b>	(Kotzé et al., 2019; Moodley & Harley, 2005)
Sub-Saharan Africa	Multiple (West and Central Africa)	<i>Loxodonta africana cyclotis</i> and <i>L. a. africana</i> African elephant (forest and savanna subspecies) Mammalia	Genetic data revealed that hybridization between forest and savanna elephants is more important than thought and hybrids are fertile, highlighting the need to consider them as two separate species and the potential effect of human pressure on the species' distribution.	<b>mtDNA</b> sequence; <b>nuclear</b> sequence	(Mondol et al., 2015)
Sub-Saharan Africa	South Africa	<i>Acinonyx jubatus</i> Cheetah Mammalia	Developed a SNP array to monitor legal and illegal trade of cheetah in South Africa, including individual identification and parentage testing.	<b>microsatellites</b> ; <b>RRS</b> (targeted sequencing)	(Magliolo et al., 2021)
Sub-Saharan Africa	South Africa	<i>Damaliscus pygargus pygargus</i> and <i>D. p. phillips</i> Bontebok and blesbok Mammalia	Genetic data used to identify pure and hybrid animals to mitigate hybridisation risk, demonstrating how genetics can be used as a tool to help conserve the integrity of both subspecies.	<b>microsatellites</b>	(van Wyk, Kotzé, Randi, & Dalton, 2013)
Sub-Saharan Africa	South Africa	<i>Panthera pardus</i> Leopard Mammalia	Used genetic data to understand population structure and gene flow in a human dominated landscape, identifying fragmented populations with low genetic diversity. This highlights the need for management of these populations to mediate human impact.	<b>microsatellites</b>	(McManus et al., 2015)

## References

- Abbas, E. M., Ismail, M., El-Ganainy, A., & Ali, F. S. (2021). First DNA Barcoding-based Inventory of Suez Gulf Fishes in Egypt and its Implication for Species Diversity. *Journal of Ichthyology*, *61*, 386–395.
- Aristizábal, A., Tuberquia, D. J., & Sanín, M. J. (2018). Conservation Genetics of Two Highly Endangered and Poorly Known Species of *Zamia* (Zamiaceae: Cycadales) in Colombia. *The Journal of Heredity*, *109*, 438–445.
- Basiita, R. K., Zenger, K. R., Mwanja, M. T., & Jerry, D. R. (2018). Gene flow and genetic structure in Nile perch, *Lates niloticus*, from African freshwater rivers and lakes. *PLoS One*, *13*, e0200001.
- Beger, M., Selkoe, K. A., Treml, E., Barber, P. H., von der Heyden, S., Crandall, E. D., ... Riginos, C. (2014). Evolving coral reef conservation with genetic information. *Bulletin of Marine Science*, *90*, 159–185.
- Clout, M. N., Elliott, G. P., & Robertson, B. C. (2002). Effects of supplementary feeding on the offspring sex ratio of kakapo: a dilemma for the conservation of a polygynous parrot. *Biological Conservation*, *107*, 13–18.
- Dalton, D. L., Smit-Robinson, H. A., Vermaak, E., Jarvis, E., & Kotze, A. (2018). Is there genetic connectivity among the critically endangered White-winged Flufftail (*Sarothrura ayresi*) populations from South Africa and Ethiopia? *African Journal of Ecology*, *56*, 28–37.
- Dejean, T., Valentini, A., Miquel, C., Taberlet, P., Bellemain, E., & Miaud, C. (2012). Improved detection of an alien invasive species through environmental DNA barcoding: the example of the American bullfrog *Lithobates catesbeianus*. *The Journal of Applied Ecology*, *49*, 953–959.
- De Kort, H., Mergeay, J., Vander Mijnsbrugge, K., Decocq, G., Maccherini, S., Kehlet Bruun, H. H., ... Vandepitte, K. (2014). An evaluation of seed zone delineation using phenotypic and population genomic data on black alder *Alnus glutinosa*. *The Journal of Applied Ecology*, *51*, 1218–1227.
- DeMay, S. M., Becker, P. A., Rachlow, J. L., & Waits, L. P. (2017). Genetic monitoring of an endangered species recovery: demographic and genetic trends for reintroduced pygmy rabbits (*Brachylagus idahoensis*). *Journal of Mammalogy*, *98*, 350–364.
- Domingues, R. R., Bruels, C. C., Gadig, O. B. F., Chapman, D. D., Hilsdorf, A. W. S., & Shivji, M. S. (2019). Genetic connectivity and phylogeography of the night shark (*Carcharhinus signatus*) in the western Atlantic Ocean: Implications for conservation management. *Aquatic Conservation: Marine and Freshwater Ecosystems*, *29*, 102–114.
- Drygala, F., Rode-Margono, J., Semiadi, G., Wirdateti, & Frantz, A. C. (2020). Evidence of hybridisation between the common Indonesian banded pig (*Sus scrofa vitattus*) and the endangered Java warty pig (*Sus verrucosus*). *Conservation Genetics*, *21*, 1073–1078.
- Edwards, C. E., Bassüner, B., Birkinshaw, C., Camara, C., Lehavana, A., Lowry, P. P., ... Jackson, P. W. (2018). A botanical mystery solved by phylogenetic analysis of botanical garden collections: the rediscovery of the presumed-extinct *Dracaena umbraculifera*. *Oryx: The Journal of the Fauna Preservation Society*, *52*, 427–436.
- Edwards, C. E., Judd, W. S., Ionta, G. M., & Herring, B. (2009). Using Population Genetic Data as a Tool to Identify New Species: *Conradina cygniflora* (Lamiaceae), a New, Endangered Species from Florida. *Systematic Botany*, *34*, 747–759.
- Edwards, D. L., Benavides, E., Garrick, R. C., Gibbs, J. P., Russello, M. A., Dion, K. B., ... Caccone, A. (2013). The genetic legacy of Lonesome George survives: Giant tortoises with Pinta Island ancestry identified in Galápagos. *Biological Conservation*, *157*, 225–228.
- FitzSimmons, N. N., Pittard, S. D., McIntyre, N., Jensen, M. P., Guinea, M., Hamann, M., ... Whiting, S. (2020). Phylogeography, genetic stocks, and

- conservation implications for an Australian endemic marine turtle. *Aquatic Conservation: Marine and Freshwater Ecosystems*, *30*, 440–460.
- Gaos, A. R., LaCasella, E. L., Kurpita, L., Balazs, G., Hargrove, S., King, C., ... Dutton, P. H. (2020). Hawaiian hawksbills: a distinct and isolated nesting colony in the Central North Pacific Ocean revealed by mitochondrial DNA. *Conservation Genetics*, *21*, 771–783.
- Gaudeul, M., Gardner, M. F., Thomas, P., Ennos, R. A., & Hollingsworth, P. M. (2014). Evolutionary dynamics of emblematic Araucaria species (Araucariaceae) in New Caledonia: nuclear and chloroplast markers suggest recent diversification, introgression, and a tight link between genetics and geography within species. *BMC Evolutionary Biology*, *14*, 171.
- Gaughran, S. J., Quinzin, M. C., Miller, J. M., Garrick, R. C., Edwards, D. L., Russello, M. A., ... Caccone, A. (2018). Theory, practice, and conservation in the age of genomics: The Galápagos giant tortoise as a case study. *Evolutionary Applications*, *11*, 1084–1093.
- Gese, E. M., Knowlton, F. F., Adams, J. R., Beck, K., Fuller, T. K., Murray, D. L., ... Waits, L. P. (2015). Managing hybridization of a recovering endangered species: The red wolf *Canis rufus* as a case study. *Current Zoology*, *61*, 191–205.
- Gruenthal, K. M., Witting, D. A., Ford, T., Neuman, M. J., Williams, J. P., Pondella, D. J., ... Larson, W. A. (2014). Development and application of genomic tools to the restoration of green abalone in southern California. *Conservation Genetics*, *15*, 109–121.
- Harmoinen, J., von Thaden, A., Aspi, J., Kvist, L., Cocchiararo, B., Jaraus, A., ... Nowak, C. (2021). Reliable wolf-dog hybrid detection in Europe using a reduced SNP panel developed for non-invasively collected samples. *BMC Genomics*, *22*, 473.
- Habib, Kazi Ahsan, Amit Kumer Neogi, Muntasir Rahman, Jina Oh, Youn-Ho Lee, and Chong-Gon Kim. 2021. DNA barcoding of brackish and marine water fishes and shellfishes of Sundarbans, the world's largest mangrove ecosystem. *PloS ONE* *16*(8): e0255110.
- Hartvig, I., So, T., Changtragoon, S., Tran, H. T., Bouamanivong, S., Ogden, R., ... Kjær, E. D. (2020). Conservation genetics of the critically endangered Siamese rosewood (*Dalbergia cochinchinensis*): recommendations for management and sustainable use. *Conservation Genetics*, *21*, 677–692.
- Hoban, S., Callicrate, T., Clark, J., Deans, S., Dosmann, M., Fant, J., ... Griffith, M. P. (2020). Taxonomic similarity does not predict necessary sample size for ex situ conservation: a comparison among five genera. *Proceedings. Biological Sciences / The Royal Society*, *287*, 20200102.
- Islam, S. U., Qasim, M., Lin, W., Islam, W., Arif, M., Ali, H., ... Wu, Z. (2018). Genetic interaction and diversity of the families Libellulidae and Gomphidae through COI gene from China and Pakistan. *Acta Tropica*, *182*, 92–99.
- Jensen, E. L., Tapia, W., Caccone, A., & Russello, M. A. (2015). Genetics of a head-start program to guide conservation of an endangered Galápagos tortoise (*Chelonoidis ephippium*). *Conservation Genetics*, *16*, 823–832.
- Kershaw, F., Carvalho, I., Loo, J., Pomilla, C., Best, P. B., Findlay, K. P., ... Rosenbaum, H. C. (2017). [Review of *Multiple processes drive genetic structure of humpback whale (Megaptera novaeangliae) populations across spatial scales*]. *Molecular ecology*, *26*, 977–994.
- Kotzé, A., Smith, R. M., Moodley, Y., Luikart, G., Birss, C., Van Wyk, A. M., ... Dalton, D. L. (2019). Lessons for conservation management: Monitoring temporal changes in genetic diversity of Cape mountain zebra (*Equus zebra zebra*). *PloS One*, *14*, e0220331.
- Lecocq, T., Gérard, M., Michez, D., & Dellicour, S. (2017). Conservation genetics of European bees: new insights from the continental scale. *Conservation Genetics*, *18*, 585–596.
- Linden, B., Dalton, D. L., Ralph, T. M. C., Silva, I., Kotze, A., & Taylor, P. J. (2020). Adding another piece to the southern African Cercopithecus monkey phylogeography puzzle. *African Zoology*, *55*, 351–362.
- Magliolo, M., Prost, S., Orozco-terWengel, P., Burger, P., Kropff, A. S., Kotze, A., ... Dalton, D. L. (2021). Unlocking the potential of a validated

- single nucleotide polymorphism array for genomic monitoring of trade in cheetahs (*Acinonyx jubatus*). *Molecular Biology Reports*, *48*, 171–181.
- Majeed, A., Singh, A., & Bhardwaj, P. (2021). Transcribing molecular and climatic data into conservation management for the Himalayan endangered species, *Taxus contorta* (Griff.). *Conservation Genetics*, *22*, 53–66.
- Mandal, Anup, Divya Rao, Deepa Karuppaiah, Achamveetil Gopalakrishnan, Jayagopal Pozhoth, Yohannan Chellamma Thampi Samraj, and Roger W. Doyle. 2012. *Gene* 491: 149-157.
- McManus, J. S., Dalton, D. L., Kotzé, A., Smuts, B., Dickman, A., Marshal, J. P., & Keith, M. (2015). Gene flow and population structure of a solitary top carnivore in a human-dominated landscape. *Ecology and Evolution*, *5*, 335–344.
- Melville, J., Chaplin, K., Hutchinson, M., Sumner, J., Gruber, B., MacDonald, A. J., & Sarre, S. D. (2019). Taxonomy and conservation of grassland earless dragons: new species and an assessment of the first possible extinction of a reptile on mainland Australia. *Royal Society Open Science*, *6*, 190233.
- Mendez, M., Rosenbaum, H. C., Subramaniam, A., Yackulic, C., & Bordino, P. (2010). Isolation by environmental distance in mobile marine species: molecular ecology of franciscana dolphins at their southern range. *Molecular Ecology*, *19*, 2212–2228.
- Mondol, S., Moltke, I., Hart, J., Keigwin, M., Brown, L., Stephens, M., & Wasser, S. K. (2015). New evidence for hybrid zones of forest and savanna elephants in Central and West Africa. *Molecular Ecology*, *24*, 6134–6147.
- Moodley, Y., & Harley, E. H. (2005). Population structuring in mountain zebras (*Equus zebra*): The molecular consequences of divergent demographic histories. *Conservation Genetics*, *6*, 953–968.
- Moodley, Y., Russo, I.-R. M., Dalton, D. L., Kotzé, A., Muya, S., Haubensak, P., ... Bruford, M. W. (2017). Extinctions, genetic erosion and conservation options for the black rhinoceros (*Diceros bicornis*). *Scientific Reports*, *7*, 41417.
- Moodley, Y., Russo, I.-R. M., Robovský, J., Dalton, D. L., Kotzé, A., Smith, S., ... Bruford, M. W. (2018). Contrasting evolutionary history, anthropogenic declines and genetic contact in the northern and southern white rhinoceros (*Ceratotherium simum*). *Proceedings. Biological Sciences / The Royal Society*, *285*. <https://doi.org/10.1098/rspb.2018.1567>
- Moodley, Y., Westbury, M. V., Russo, I.-R. M., Gopalakrishnan, S., Rakotoarivelo, A., Olsen, R.-A., ... Bruford, M. W. (2020). Interspecific Gene Flow and the Evolution of Specialization in Black and White Rhinoceros. *Molecular Biology and Evolution*, *37*, 3105–3117.
- Moran, B. M., Thomas, S. M., Judson, J. M., Navarro, A., Davis, H., Sidak-Loftis, L., ... Steiner, C. C. (2021). Correcting parentage relationships in the endangered California Condor: Improving mean kinship estimates for conservation management. *Ornithological Applications*, *123*. <https://doi.org/10.1093/ornithapp/duab017>
- Nash, H. C., Wirdateti, Low, G. W., Choo, S. W., Chong, J. L., Semiadi, G., ... Rheindt, F. E. (2018). Conservation genomics reveals possible illegal trade routes and admixture across pangolin lineages in Southeast Asia. *Conservation Genetics*, *19*, 1083–1095.
- Pakhrou, O., Medraoui, L., Yatrib, C., Alami, M., Filali-Maltouf, A., & Belkadi, B. (2017). Assessment of genetic diversity and population structure of an endemic Moroccan tree (*Argania spinosa* L.) based in IRAP and ISSR markers and implications for conservation. *Physiology and Molecular Biology of Plants: An International Journal of Functional Plant Biology*, *23*, 651–661.
- Poulakakis, N., Glaberman, S., Russello, M., Beheregaray, L. B., Ciofi, C., Powell, J. R., & Caccone, A. (2008). Historical DNA analysis reveals living descendants of an extinct species of Galápagos tortoise. *Proceedings of the National Academy of Sciences of the United States of America*,

105, 15464–15469.

- Saremi, N. F., Supple, M. A., Byrne, A., Cahill, J. A., Coutinho, L. L., Dalén, L., ... Shapiro, B. (2019). Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. *Nature Communications*, *10*, 4769.
- Smeds, L., Aspi, J., Berglund, J., Kojola, I., Tirronen, K., & Ellegren, H. (2021). Whole-genome analyses provide no evidence for dog introgression in Fennoscandian wolf populations. *Evolutionary Applications*, *14*, 721–734.
- Smith, T. B., Fuller, T. L., Zhen, Y., Zaunbrecher, V., Thomassen, H. A., Njabo, K., ... Harrigan, R. J. (2021). Genomic vulnerability and socio-economic threats under climate change in an African rainforest bird. *Evolutionary Applications*, *14*, 1239–1247.
- Smith, T. B., Milá, B., Grether, G. F., Slabbekoorn, H., Sepil, I., Buermann, W., ... Pollinger, J. P. (2008). Evolutionary consequences of human disturbance in a rainforest bird species from Central Africa. *Molecular Ecology*, *17*, 58–71.
- Taninaka, H., Bernardo, L. P. C., Saito, Y., Nagai, S., Ueno, M., Kitano, Y. F., ... Yasuda, N. (2019). Limited fine-scale larval dispersal of the threatened brooding corals *Heliopora* spp. as evidenced by population genetics and numerical simulation. *Conservation Genetics*, *20*, 1449–1463.
- Thatte, P., Chandramouli, A., Tyagi, A., Patel, K., Baro, P., Chhattani, H., & Ramakrishnan, U. (2020). Human footprint differentially impacts genetic connectivity of four wide-ranging mammals in a fragmented landscape. *Diversity & Distributions*, *26*, 299–314.
- van Wyk, A. M., Kotzé, A., Randi, E., & Dalton, D. L. (2013). A hybrid dilemma: a molecular investigation of South African bontebok (*Damaliscus pygargus pygargus*) and blesbok (*Damaliscus pygargus phillipsi*). *Conservation Genetics*, Vol. 14, pp. 589–599.
- Vargas-Ramírez, M., Caballero, S., Morales-Betancourt, M. A., Lasso, C. A., Amaya, L., Martínez, J. G., ... Fritz, U. (2020). Genomic analyses reveal two species of the matamata (Testudines: Chelidae: *Chelus* spp.) and clarify their phylogeography. *Molecular Phylogenetics and Evolution*, *148*, 106823.
- Wennerström, Lovisa, Eeva Jansson, and Linda Laikre. 2017. Baltic Sea genetic biodiversity: Current knowledge relating to conservation management. *Aquatic Conservation: Marine and Freshwater Ecosystems* 27: 1069-1090.
- Wennerström, Lovisa, Jens Olsson, Nils Ryman, and Linda Laikre. 2017. Temporally stable, weak genetic structuring om brackish northern pike (*Esox lucius*) in the Baltic Sea indicates a contrasting divergence pattern relative to freshwater populations. *Canadian Journal of Fisheries and Aquatic Sciences* 74: 562-571.
- Wei, X., Huang, M., Yue, Q., Ma, S., Li, B., Mu, Z., ... Wang, Z. (2021). Long-term urbanization impacts the eastern golden frog (*Pelophylax plancyi*) in Shanghai City: Demographic history, genetic structure, and implications for amphibian conservation in intensively urbanizing environments. *Evolutionary Applications*, *14*, 117-135.