

Weekly Topics & Readings

Sept 6: Introduction to conservation genetics

- Ouborg, NJ, P Vergeer, & C Mix. 2006. The rough edges of the conservation genetics paradigm for plants. *Journal of Ecology* 94: 1233–1248.
- Frankham, R. 2010. Challenges and opportunities of genetic approaches to biological conservation. *Biological Conservation* 143: 1919-1927.

Sept 13: Assisted gene flow

- Aitken SN, & MC Whitlock. 2013. Assisted gene flow to facilitate local adaptation to climate change. *Annual Review of Ecology, Evolution, & Systematics* 44:367–388.
- Gargano D, L Bernardo, S Rovito, NG Passalacqua, & T Abeli. 2022. Do marginal plant populations enhance the fitness of larger core units under ongoing climate change? Empirical insights from a rare carnation. *AoB Plants* 14: plac022.

Sept 20: Genetic analysis of invasive species

- Miura, O. 2007. Molecular genetic approaches to elucidate the ecological and evolutionary issues associated with biological invasions. *Ecological Research* 22: 876-883.
- Kolbe, JJ, RE Glor, L Rodríguez Schettino, AC Lara, A Larson, & JB Losos. 2004. Genetic variation increases during biological invasion by a Cuban lizard. *Nature* 431: 177–181.

Sept 27: eDNA in conservation genetics

- Thomsen, PF & E Willerslev. 2015. Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity. *Biological Conservation* 183: 4-18.
- Câmara, PEAS, FLV Bones, FAC Lopes, FS Oliveira, CC Barreto, DK Henriques, LP Campos, M Carvalho-Silva, P Convey & LH Rosa. 2022. DNA metabarcoding reveals cryptic diversity in forest soils on the isolated Brazilian Trindade Island, South Atlantic. *Microbial Ecology* (2022).

Oct 4: Fecal-DNA diet analysis for conservation

- Ando, H, H Mukai, T Komura, T Dewi, M Ando, & Y Isagi. 2020. Methodological trends and perspectives of animal dietary studies by noninvasive fecal DNA metabarcoding. *Environmental DNA* 2: 391– 406.
- Roffler, GH, JM Allen, A Massey, & T Levi. 2021. Metabarcoding of fecal DNA shows dietary diversification in wolves substitutes for ungulates in an island archipelago. *Ecosphere* 12: e03297.

Oct 11: Forensic conservation genetics

- Ogden, R, N Dawnay, & R McEwing. 2009. Wildlife DNA forensics — bridging the gap between conservation genetics and law enforcement. *Endangered Species Research* 9: 179-195. (direct link to PDF)
- Padilla-Jacobo, G, TC Monterrubio-Rico, H Cano-Camacho & MG Zavala-Páramo. 2021. Genealogical relationship inference to identify areas of intensive poaching of the Orange-fronted Parakeet (*Eupsittula canicularis*). *BMC Zoology* 6: 14.

Oct 25: Identifying ESUs (Evolutionarily Significant Units) for conservation

- Crandall, KA, OR Bininda-Emonds, GM Mace, & RK Wayne. 2000. Considering evolutionary processes in conservation biology. *Trends in Ecology & Evolution* 15: 290–295.
- Posso-Terranova, A, & J Andrés. 2018. Multivariate species boundaries and conservation of harlequin poison frogs. *Molecular Ecology* 27: 3432–3451.

Nov 1: Conservation epigenetics

- Rey, O, C Eizaguirre, B Angers, M Baltazar-Soares, K Sagonas, JG Prunier, & S Blanchet. 2020. Linking epigenetics and biological conservation: Towards a conservation epigenetics perspective. *Functional Ecology* 34: 414–427.
- Kitavi, M, R Cashell, M Ferguson, J Lorenzen, M Nyine, PC McKeown & C Spillane. 2020. Heritable epigenetic diversity for conservation and utilization of epigenetic germplasm resources of clonal East African Highland banana (EAHB) accessions. *Theoretical and Applied Genetics* 133: 2605–2625.

Nov 8: Conservation genetics of vertebrate carnivore range expansions

- Chapron G, P Kaczensky, JD Linnell, M von Arx, D Huber, H Andrén, JV López-Bao, M Adamec, F Álvares, O Anders, L Balčiauskas, V Balys, P Bedř, F Bego, JC Blanco, U Breitenmoser, H Brøseth, L Bufka, R Bunikyte, P Ciucci, A Dutsov, T Engleder, C Fuxjäger, C Groff, K Holmala, B Hoxha, Y Iliopoulos, O Ionescu, J Jeremić, K Jerina, G Kluth, F Knauer, I Kojola, I Kos, M Krofel, J Kubala, S Kunovac, J Kusak, M Kutal, O Liberg, A Majić, P Männil, R Manz, E Marboutin, F Marucco, D Melovski, K Mersini, Y Mertzanis, RW Mysłajek, S Nowak, J Odden, J Ozolins, G Palomero, M Paunović, J Persson, H Potočnik, PY Quenette, G Rauer, I Reinhardt, R Rigg, A Ryser, V Salvatori, T Skrbinšek, A Stojanov, JE Swenson, L Szemethy, A Trajçe, E Tsingarska-Sedefcheva, M Váňa, R Veeroja, P Wabakken, M Wölfel, S Wölfel, F Zimmermann, D Zlatanov, & L Boitani. 2014. Recovery of large carnivores in Europe's modern human-dominated landscapes. *Science*. 346: 1517-1519.
- Hagen SB, A Kopatz, J Aspi, I Kojola, & HG Eiken. 2015. Evidence of rapid change in genetic structure and diversity during range expansion in a recovering large terrestrial carnivore. *Proceedings of the Royal Society: B, Biological Sciences* 282: 20150092.

Nov 15: Genetics of ex situ plant conservation

- Abeli, T, S Dalrymple, S Godefroid, A Mondoni, JV Müller, G Rossi & S Orsenigo. 2020. *Ex situ* collections and their potential for the restoration of extinct plants. *Conservation Biology* 34: 303-313.
- Clugston, JAR, M Ruhsam, GJ Kenicer, M Henwood, R Milne & NS Nagalingum. 2022. Conservation genomics of an Australian cycad *Cycas calcicola*, and the absence of key genotypes in botanic gardens. *Conservation Genetics* 23: 449–465.

Nov 2: Genome editing applications to conservation biology

- Phelps MP, LW Seeb, & JE Seeb. 2020. Transforming ecology and conservation biology through genome editing. *Conservation Biology* 34: 54-65.
- Kosch, TA, CNS Silva, LA Brannelly, AA Roberts, Q Lau, G Marantelli, L Berger & LF Skerratt. 2019. Genetic potential for disease resistance in critically endangered amphibians decimated by chytridiomycosis. *Animal Conservation* 22: 238–250.

Nov 29: Movie & snacks (conservation biology themed)

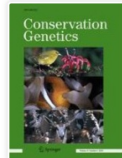
Movie: *Genesis 2.0*

- [in case you are interested in reading further about movies & conservation biology] Silk, MJ, SL Crowley, AJ Woodhead, & A Nuno. 2018. Considering connections between Hollywood and biodiversity conservation. *Conservation Biology* 32: 597-606.

Introduction to Conservation Genetics

Reading: Ouborg, NJ, P Vergeer, & C Mix. 2006. The rough edges of the conservation genetics paradigm for plants. **Journal of Ecology** 94: 1233–1248.
 Frankham, R. 2010. Challenges and opportunities of genetic approaches to biological conservation. **Biological Conservation** 143: 1919-1927.

Additional Papers



Volume 11, issue 2, April 2010

Special Issue: ESF-ConGen: Integrating population Genetics and Conservation Biology / Guest Edited by Kuke Bijlsma, Volker Loeschcke and N. Joop Ouborg

29 articles in this issue

- Ouborg, NJ, F Angeloni & P Vergeer. 2010. An essay on the necessity and feasibility of conservation genomics. **Conservation Genetics** 11: 643-653.
- Hoelzel, AR. 2010. Looking backwards to look forwards: conservation genetics in a changing world. **Conservation Genetics** 11: 655-660.
- Frankham, R. 2010. Where are we in conservation genetics and where do we need to go? **Conservation Genetics** 11: 661-663.
- Avise, JC. 2010. Perspective: conservation genetics enters the genomics era. **Conservation Genetics** 11: 665-669.
- Allendorf, FW. 2016. Genetics and the conservation of natural populations: allozymes to genomes. **Molecular Ecology** 26: 420-430.
- Allendorf, FW, PA Hohenlohe, & G Luikart. 2016. Genomics and the future of conservation genetics. **Nature Reviews Genetics** 11: 697-709.
- Moritz, C. 2002. Strategies to protect biological diversity and the evolutionary processes that sustain it. **Systematic Biology** 51: 238-254,
- Ouborg, NJ, Pertoldi, v Loeschcke, R Bijlsma, & PW Hedrick. 2010. Conservation genetics in transition to conservation genomics. **Trends in Ecology & Evolution** 26: 177-187.

Schemske, DW, BC Husband, MH Ruckelshaus, C Goodwillie, IM Parker, & JG Bishop. 1994. Evaluating approaches to the conservation of rare and endangered plants. **Ecology** 75: 584–606.

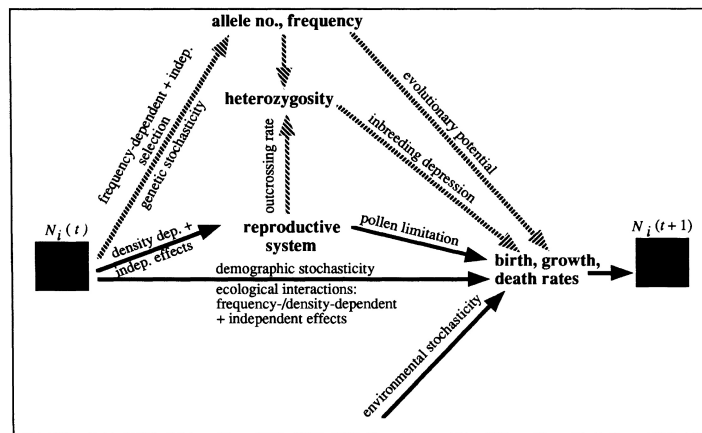


FIG. 1. Schematic of the ecological (solid arrows) and genetic (hatched arrows) processes affecting within-population dynamics in plants. Population size at time t and $t + 1$ is represented by a solid box. Note that processes operating at the scales represented here and in Fig. 2 are not independent. For example, within-population dynamics can affect the size of the metapopulation through local extinctions.

"Nothing in biology makes sense except in the light of evolution."

T. Dobzhanski, T. 1973. The American Biology Teacher 35: 125-129.

"Nothing in conservation biology makes sense except in the light of genetics (and evolution)."

Frankham, 2010. paraphrased

(all images wikipedia.org)



Hypochaeris radicata



Succisa pratensis



Scabiosa columbaria



Salvia pratensis

Conservation/Genetics terms to know from the readings

genetic diversity
molecular genetic variation
population structure
quantitative genetic variation

associative overdominance
background selection
selective sweeps
gene flow
 genetic rescue
 metapopulation
genetic drift
 effective population size (N_e)
inbreeding depression
outbreeding depression

haplo-diploid
polyploidy
 amphidiploid
self-incompatible

evolutionary significant units
management units

allozymes
single-nucleotide polymorphisms (SNPs)
microsatellites (simple sequence repeats, SSRs)

demographic history
Population Viability Analysis (PVA)

Assisted Gene Flow

Reading: Aitken SN, & MC Whitlock. 2013. Assisted gene flow to facilitate local adaptation to climate change. *Annual Review of Ecology, Evolution, & Systematics* 44:367–388.

Gargano D, L Bernardo, S Rovito, NG Passalacqua, & T Abeli. 2022. Do marginal plant populations enhance the fitness of larger core units under ongoing climate change? Empirical insights from a rare carnation. *AoB Plants* 14: plac022.

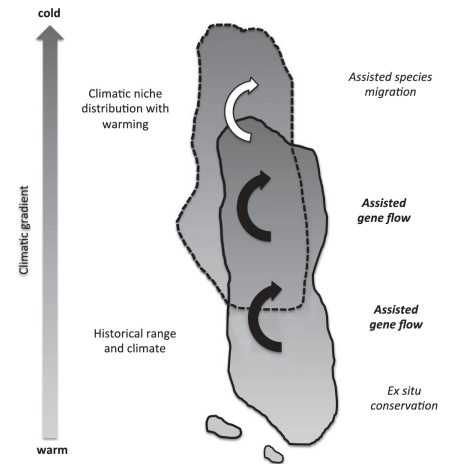


Figure 1 Schematic diagram of management options for reforestation and restoration in a changing climate. While this illustrates the northward movement of individuals, assisted gene flow may also occur along elevational or longitudinal climatic gradients.

Additional Papers

Aitken SN, & JB Bemmels. 2015. Time to get moving: assisted gene flow of forest trees. *Evolutionary Applications* 9: 271-290.

Browne, L, JW Wright, S Fitz-Gibbon, PF Gugger, & VL Sork. 2019. Adaptational lag to temperature in valley oak (*Quercus lobata*) can be mitigated by genome-informed assisted gene flow. *Proceedings of the National Academy of Sciences, USA* 116: 25179-25185. **Valley oak**

Grummer, JA, TR Booker, R Matthey-Doret, P Nietlisbach, AT Thomaz, & MC Whitlock. 2022. The immediate costs and long-term benefits of assisted gene flow in large populations. *Conservation Biology* 36: e13911. **model**

Hamilton, JA, R Royauté, JW Wright, P Hodgskiss, & FT Ledig. 2017. Genetic conservation and management of the California endemic, Torrey pine (*Pinus torreyana* Parry): Implications of genetic rescue in a genetically depauperate species. *Ecology and Evolution* 7 :7370-7381. **Torrey pine**

Kelly, E, & BL Phillips. 2016. Targeted gene flow for conservation. *Conservation Biology* 30: 259-267.

Kelly, E, & BL Phillips. 2019. Targeted gene flow and rapid adaptation in an endangered marsupial. *Conservation Biology* 33: 112-121. **northern quoll**

Kronenberg, JA, JC Gerberich, SW Fitzpatrick, ED Broder, LM Angeloni, & WC Funk. 2018. An experimental test of alternative population augmentation scenarios. *Conservation Biology* 32: 838-848. **Trinidadian guppy**

McKay JK, CE Christian, S Harrison, & KJ Rice. 2005. "How local is local?"—A review of practical and conceptual issues in the genetics of restoration. *Restoration Ecology* 13: 432–440.

Shryock, DF, LK Washburn, LA DeFalco, & TC Esque TC. 2021. Harnessing landscape genomics to identify future climate resilient genotypes in a desert annual. *Molecular Ecology* 30: 698-717. **desert Indianwheat**

Weeks, AR, CM Sgro, AG Young, R Frankham, NJ Mitchell, KA Miller, M Byrne, DJ Coates, MDB Eldridge, P Sunnucks, MF Breed, EA James, & AA Hoffmann. 2011. Assessing the benefits and risks of translocations in changing environments: a genetic perspective. *Evolutionary Applications* 4: 709–725.

Pinus torreyana
Torrey Pine



Dasyurus hallucatus
northern quall



Plantago ovata
desert Indianwheat



Poecilia reticulata
Trinidadian guppy



Quercus lobata
Valley oak

[all images wikipedia.com]

Gargano, D, G Pellegrino, & L Bernardo. 2015. Conservation Genetics 16:1127–1138.

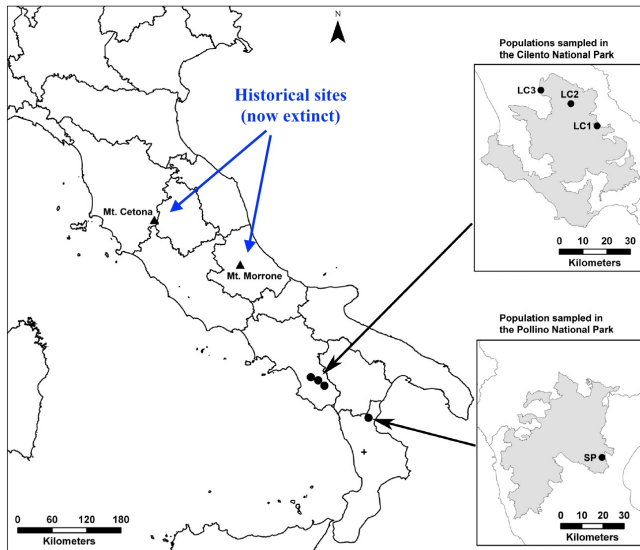


Fig. 1 Italian peninsula with sites of historical presence of *Dianthus guliae* Janka (black triangles), and sampled populations in areas with current presence of the species (on the left). Details of the boundaries of the national parks (gray areas) hosting the remnant populations of *D. guliae* (on the right). LC1, LC2, LC3, SP population code used in the text to distinguish the sampled units. '+' location of the Botanical Garden of University of Calabria

Sample sizes (based on raw data in Supplementary Appendix S3)

| | agar | | | dry | | | wet | | | |
|------|------|----|----|-----|----|----|-----|----|----|-----|
| | S | wC | bC | S | wC | bC | S | wC | bC | |
| COR1 | 4 | 4 | 4 | 8 | 8 | 8 | 8 | 8 | 8 | 60 |
| COR2 | 4 | 4 | 4 | 8 | 8 | 8 | 9 | 8 | 8 | 61 |
| COR3 | 4 | 4 | 4 | 8 | 9 | 8 | 8 | 8 | 8 | 61 |
| COR4 | 4 | 4 | 4 | 8 | 8 | 8 | 8 | 8 | 8 | 60 |
| COR5 | 4 | 3 | 5 | 7 | 8 | 8 | 8 | 8 | 7 | 58 |
| PER1 | 8 | 4 | 8 | 4 | 8 | 8 | 8 | 8 | 4 | 60 |
| PER2 | 8 | 4 | 8 | 4 | 8 | 8 | 8 | 8 | 4 | 60 |
| PER3 | 8 | 4 | 8 | 4 | 8 | 8 | 8 | 8 | 4 | 60 |
| PER4 | 8 | 4 | 8 | 4 | 8 | 8 | 8 | 8 | 4 | 60 |
| PER5 | 8 | 4 | 8 | 4 | 8 | 8 | 8 | 8 | 4 | 60 |
| | 60 | 39 | 61 | 59 | 81 | 80 | 81 | 80 | 59 | |
| | | | | 160 | | | 220 | | | 600 |

Table S2.2. Between-lineage fitness variations and related patterns of inbreeding depression and heterosis in the two populations for each trait and experimental treatment. Inbred (S), offspring obtained by self-pollination; Outbred (wC), offspring obtained by within-population cross-pollination; Hybrid (bC), offspring obtained by between-population cross-pollination; further details are provided in the main text.

| Population | Treatment | Trait | agar | | | | | wet | | | | | dry | | | | |
|------------|-----------|----------------------|------------|--------------|-------------|--------------------|------|------------|--------------|-------------|-------------------|-------|------------|--------------|-------------|-------------------|-------|
| | | | Inbred (S) | Outbred (wC) | Hybrid (bC) | ID _{AGAR} | H | Inbred (S) | Outbred (wC) | Hybrid (bC) | ID _{WET} | H | Inbred (S) | Outbred (wC) | Hybrid (bC) | ID _{DRY} | H |
| Core | | Seed germination (%) | 0,85 | 1,00 | 0,90 | 0,15 | 0,11 | 0,73 | 0,95 | 0,82 | 0,23 | -0,16 | 0,67 | 0,71 | 0,90 | 0,06 | 0,21 |
| Peripheral | | Seed germination (%) | 0,70 | 0,85 | 0,90 | 0,18 | 0,06 | 0,60 | 0,83 | 0,85 | 0,28 | 0,02 | 0,55 | 0,70 | 0,63 | 0,21 | -0,11 |
| Core | | Early survival (%) | - | - | - | - | - | 0,56 | 0,85 | 0,79 | 0,34 | -0,08 | 0,54 | 0,68 | 0,77 | 0,21 | 0,12 |
| Peripheral | | Early survival (%) | - | - | - | - | - | 0,60 | 0,70 | 0,83 | 0,14 | 0,16 | 0,48 | 0,62 | 0,45 | 0,23 | -0,38 |
| Core | | Radicle length (mm) | - | - | - | - | - | 15,55 | 23,94 | 18,41 | 0,35 | -0,30 | 14,68 | 18,16 | 19,15 | 0,19 | 0,05 |
| Peripheral | | Radicle length (mm) | - | - | - | - | - | 16,37 | 20,99 | 21,41 | 0,22 | 0,02 | 14,97 | 19,40 | 18,34 | 0,23 | -0,06 |
| Core | | Shoot size (mm) | - | - | - | - | - | 28,74 | 39,13 | 34,74 | 0,27 | -0,13 | 29,07 | 34,28 | 38,04 | 0,15 | 0,10 |
| Peripheral | | Shoot size (mm) | - | - | - | - | - | 30,31 | 37,19 | 39,67 | 0,18 | 0,06 | 29,18 | 37,08 | 33,49 | 0,21 | -0,11 |

Stockten Blanco
BIO 432
K. Karoly
20 September 2022

GENETIC ANALYSIS OF INVASIVE SPECIES

- Kolbe, J. J., Glor, R. E., Rodríguez Schettino, L., Lara, A. C., Larson, A., & Losos, J. B. (2004). Genetic variation increases during biological invasion by a Cuban lizard. *Nature*, *431*(7005), 177–181. <https://doi.org/10/b7nkn4>
- Miura, O. (2007). Molecular genetic approaches to elucidate the ecological and evolutionary issues associated with biological invasions. *Ecological Research*, *22*(6), 876–883. <https://doi.org/10.1007/s11284-007-0389-5>

ADDITIONAL READINGS

- te Beest, M., Le Roux, J. J., Richardson, D. M., Brysting, A. K., Suda, J., Kubesova, M., & Pysek, P. (2012). The more the better? The role of polyploidy in facilitating plant invasions. *Annals of Botany*, *109*(1), 19–45. <https://doi.org/10/crw8d9>
- whole genome duplication and evolutionary potential in plants
- Lavergne, S., & Molofsky, J. (2007). Increased Genetic Variation and Evolutionary Potential Drive the Success of an Invasive Grass. *Proceedings of the National Academy of Sciences of the United States of America*, *104*(10), 3883–3888. <https://doi.org/10/dfj9vz>
- evolutionary potential linked to genetic diversity of *P. arundinacea*
- Tsutsui, N. D., Suarez, A. V., Holway, D. A., & Case, T. J. (2000). Reduced genetic variation and the success of an invasive species. *Proceedings of the National Academy of Sciences*, *97*(11), 5948–5953. <https://doi.org/10/dxnzcm>
- lack of genetic diversity in *L. humile* increases fitness due to reduced intraspecific aggression associated w/ kinship
- Voisin, M., Engel, C. R., & Viard, F. (2005). Differential shuffling of native genetic diversity across introduced regions in a brown alga: Aquaculture vs. maritime traffic effects. *Proceedings of the National Academy of Sciences*, *102*(15), 5432–5437. <https://doi.org/10/bcmsx4>
- # of introductions & invasion vectors explain genetic variation/structure of invasives
- Williams, E. E. (1969). The Ecology of Colonization as Seen in the Zoogeography of Anoline Lizards on Small Islands. *The Quarterly Review of Biology*, *44*(4), 345–389. <https://doi.org/10/d8ftv8>
- dispersal barriers to genetic variation in *A. sagrei*

TERMS

cryptic species: morphologically indistinguishable but genetically unique

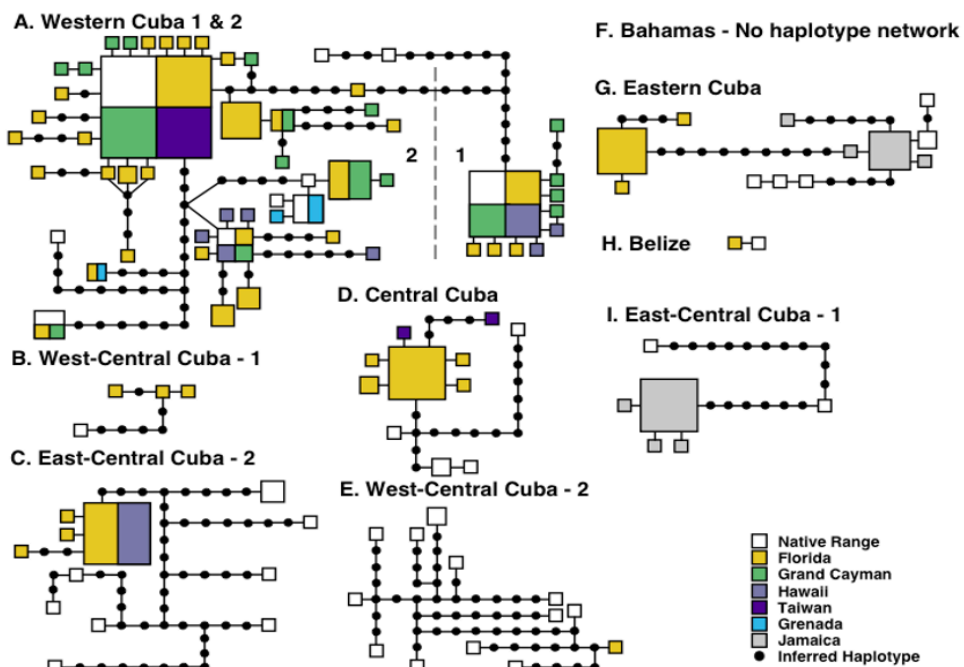
haplotype: group of alleles that are inherited together

microsatellite markers: repetitive nucleotide sequences that constitute co-dominant, polymorphic loci (1-10 bp long; A.K.A. simple sequence repeats (SSRs) or short tandem repeats (STRs))

phylogenetic tree: diagram that represents hypothesized evolutionary relationships

Fig. S2. Statistical parsimony networks connecting introduced and native-range haplotypes^{S2}.

Letters for each network correspond to native-range clades identified in Figs. 1 and 2. Each square is a unique haplotype with its size proportional to the haplotype's frequency; its color indicates the geographic origin of the sample, and black dots represent inferred mutational steps between haplotypes. The haplotype network from the Western Cuba clade (A) was divided into two sub-networks (1 & 2) to recognize the haplotype divergence within the network. All native-range haplotypes are from Cuba except for one haplotype from each of the Bahamas (F) and Belize (H). The one haplotype nested within the Bahamian clade (F) was too distantly related to the closest haplotypes sampled from San Salvador, Bahamas to form a haplotype network with 95% confidence. |



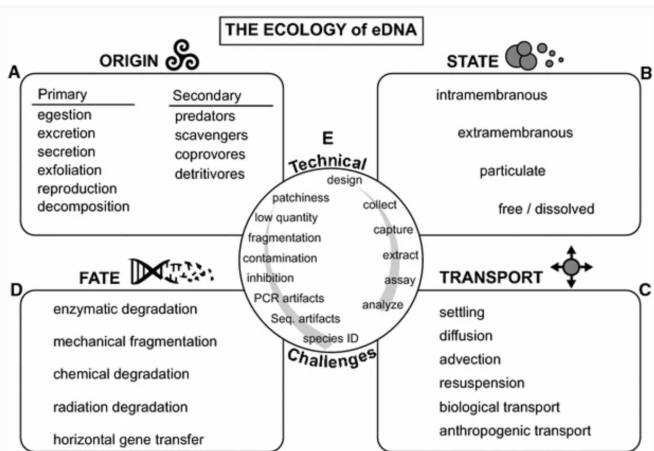
Environmental DNA

Papers from Class:

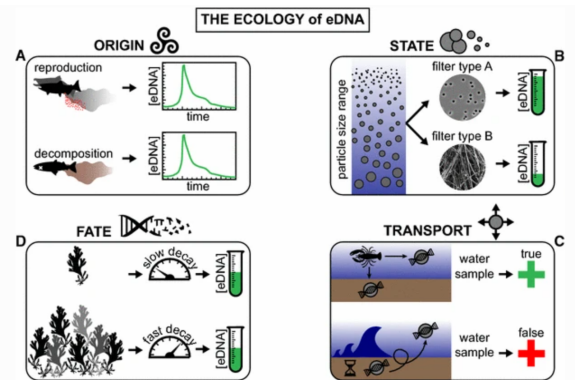
Thomsen, P. F., & Willerslev, E. (2015). Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity. *Biological Conservation*, 183, 4–18. <https://doi.org/10.1016/j.biocon.2014.11.019>

Câmara, P. E. A. S., Bones, F. L. V., Lopes, F. A. C., Oliveira, F. S., Barreto, C. C., Knop Henriques, D., Campos, L. P., Carvalho-Silva, M., Convey, P., & Rosa, L. H. (2022). DNA Metabarcoding Reveals Cryptic Diversity in Forest Soils on the Isolated Brazilian Trindade Island, South Atlantic. *Microbial Ecology*. <https://doi.org/10.1007/s00248-022-02018-4>

Extra Images from Barnes Paper



Processes and properties within four domains of eDNA ecology (a–d) and key technical challenges (e) can guide eDNA conservation and research applications

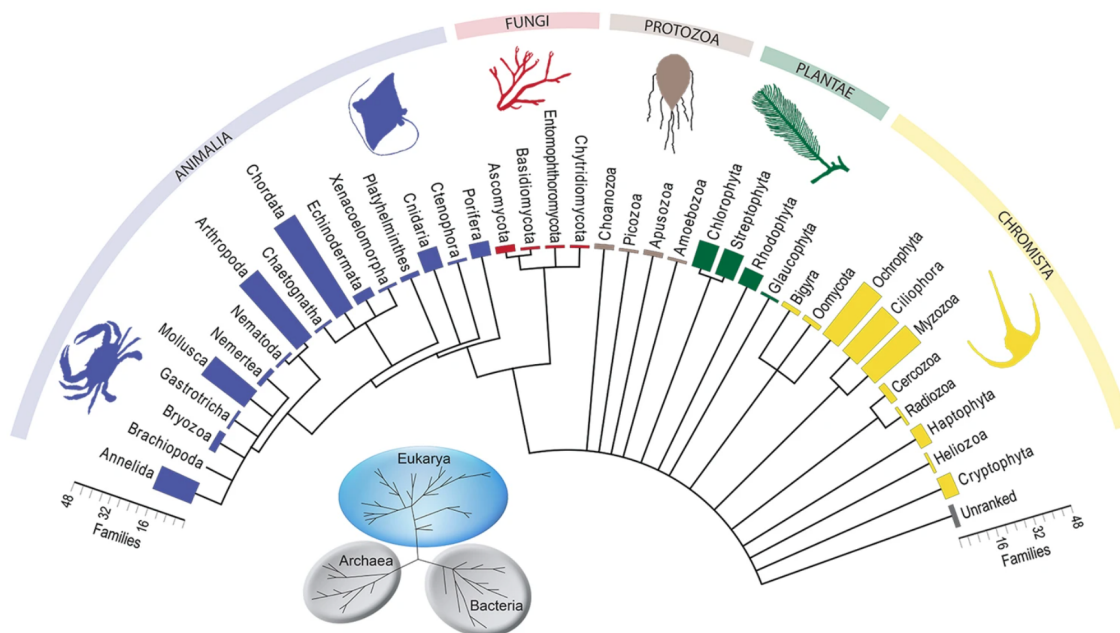


eDNA ecology affects population inferences. **a** eDNA from reproduction and decomposition could produce similar temporal patterns despite different origins. **b** Different filter types could yield different eDNA concentrations that reflect particle size classes rather than population size differences. **c** Resuspension of old sedimentary eDNA could produce false inferences of presence after organisms are gone. **d** Different environmentally-mediated eDNA decay rates could confound inferences about population size or biomass from eDNA concentration

Extra Citations

- Andruszkiewicz, E. A., Starks, H. A., Chavez, F. P., Sassoubre, L. M., Block, B. A., & Boehm, A. B. (2017). Biomonitoring of marine vertebrates in Monterey Bay using eDNA metabarcoding. *PLOS ONE*, 12(4), e0176343.
- Barnes, M. A., & Turner, C. R. (2016). The ecology of environmental DNA and implications for conservation genetics. *Conservation Genetics*, 17(1), 1–17. <https://doi.org/10.1007/s10592-015-0775-4>
- Ficetola, G. F., Miaud, C., Pompanon, F., & Taberlet, P. (2008). Species detection using environmental DNA from water samples. *Biology Letters*, 4(4), 423–425. <https://doi.org/10.1098/rsbl.2008.0118>
- Ragot, R., & Villemur, R. (2022). eDNA profiling of mammals, birds, and fish of surface waters by mitochondrial metagenomics: Application for source tracking of fecal contamination in surface waters. *Environmental Monitoring and Assessment*, 194(2), 72. <https://doi.org/10.1007/s10661-021-09668-w>
- Stat, M., Huggett, M. J., Bernasconi, R., DiBattista, J. D., Berry, T. E., Newman, S. J., Harvey, E. S., & Bunce, M. (2017). Ecosystem biomonitoring with eDNA: Metabarcoding across the tree of life in a tropical marine environment. *Scientific Reports*, 7(1), 12240. <https://doi.org/10.1038/s41598-017-12501-5>
- Sepulveda, A. J., Birch, J. M., Barnhart, E. P., Merkes, C. M., Yamahara, K. M., Marin, R., Kinsey, S. M., Wright, P. R., & Schmidt, C. (2020). Robotic environmental DNA bio-surveillance of freshwater health. *Scientific Reports*, 10(1), 14389. <https://doi.org/10.1038/s41598-020-71304-3>

Extra Image from- Stat paper (ToL= Tree of life metabarcoding)



Taxonomic phylogram of eukaryotic diversity at Coral Bay in west Australia derived from ToL-metabarcoding. Bar graphs indicate the number of families in each phyla characterised at Coral Bay, and are coloured according to kingdom.

Fecal-DNA Diet Analysis for Conservation

Ando, H., Mukai, H., Komura, T., Dewi, T., Ando, M., & Isagi, Y. (2020). Methodological trends and perspectives of animal dietary studies by noninvasive fecal DNA metabarcoding. *Environmental DNA*, 2(4), 391–406. <https://doi.org/10.1002/edn3.117>

Roffler, G. H., Allen, J. M., Massey, A., & Levi, T. (2021). Metabarcoding of fecal DNA shows dietary diversification in wolves substitutes for ungulates in an island archipelago. *Ecosphere*, 12(1). <https://doi.org/10.1002/ecs2.3297>

Extra Readings

Alberdi, A., Aizpurua, O., Gilbert, M. T. P., & Bohmann, K. (2017). Scrutinizing key steps for reliable metabarcoding of environmental samples. *Methods in Ecology and Evolution*, 9(1), 134–147. <https://doi.org/10.1111/2041-210x.12849>

Deagle, B. E., Thomas, A. C., McInnes, J. C., Clarke, L. J., Vesterinen, E. J., Clare, E. L., Kartzinel, T. R., & Eveson, J. P. (2018). Counting with DNA in metabarcoding studies: How should we convert sequence reads to dietary data? *Molecular Ecology*, 28(2), 391–406. <https://doi.org/10.1111/mec.14734>

Deiner, K., Bik, H. M., Mächler, E., Seymour, M., Lacoursière-Roussel, A., Altermatt, F., Creer, S., Bista, I., Lodge, D. M., Vere, N., Pfrender, M. E., & Bernatchez, L. (2017). Environmental DNA metabarcoding: Transforming how we survey animal and plant communities. *Molecular Ecology*, 26(21), 5872–5895. <https://doi.org/10.1111/mec.14350>

Massey, A. L., Roffler, G. H., Vermeul, T., Allen, J. M., & Levi, T. (2021). Comparison of mechanical sorting and DNA metabarcoding for diet analysis with fresh and degraded wolf scats. *Ecosphere*, 12(6). <https://doi.org/10.1002/ecs2.3557>

Sousa, L. L., Silva, S. M., & Xavier, R. (2019). DNA metabarcoding in diet studies: Unveiling ecological aspects in aquatic and terrestrial ecosystems. *Environmental DNA*, 1(3), 199–214. <https://doi.org/10.1002/edn3.27>

Schematic from Alberdi:

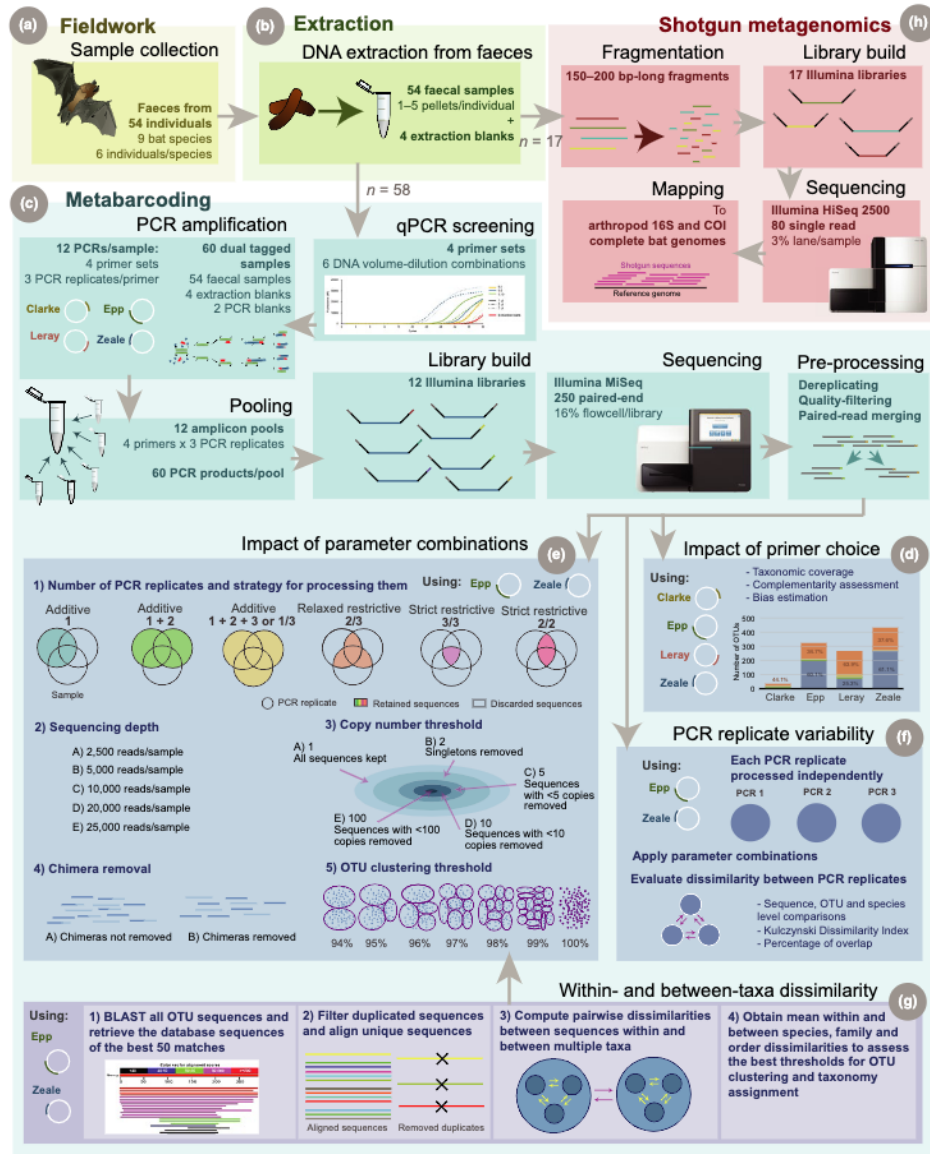


FIGURE 1 Study overview. (a) Faecal samples were obtained from wild bats captured in cave entrances. (b) DNA was extracted from the bat faecal samples in a dedicated pre-PCR laboratory. (c) The 54 samples and six extraction blanks were processed as described in Appendix S1 to obtain amplicon libraries. (d) After applying a common bioinformatic pipeline (also described in Appendix S1), we compared the diversity detected by each of the four primer sets and assessed their complementarity and taxonomic biases. (e) We evaluated the impact of different parameters on the detected diversity by comparing 2,100 parameter combinations. (f) We evaluated the effect of parameter combinations on the dissimilarity between PCR replicates. (g) Dissimilarity between and within taxonomic groups was measured using sequences from reference databases in order to assess the optimal thresholds for Operational Taxonomic Unit (OTU) clustering and taxonomy assignment. (h) Finally, we estimated the relative amount of target DNA in the faecal extracts by shotgun sequencing 17 bat faecal extracts

Terms:

Metabarcoding: Taxonomic identification of multiple species extracted from a mixed sample PCR-amplified and sequenced on a high-throughput platform (Deiner et al., 2017)

Ungulate: Any hoofed mammal, they make up the majority of wolf diets

Forensic Conservation Genetics

- Reading: Ogden, R, N Dawnay, & R McEwing. 2009. Wildlife DNA forensics - bridging the gap between conservation genetics and law enforcement. **Endangered Species Research** 9: 179-195..
- Padilla-Jacobo, G, TC Monterrubio-Rico, H Cano-Camacho & MG Zavala-Páramo. 2021. Genealogical relationship inference to identify areas of intensive poaching of the Orange-fronted Parakeet (*Eupsittula canicularis*). **BMC Zoology** 6: 14..

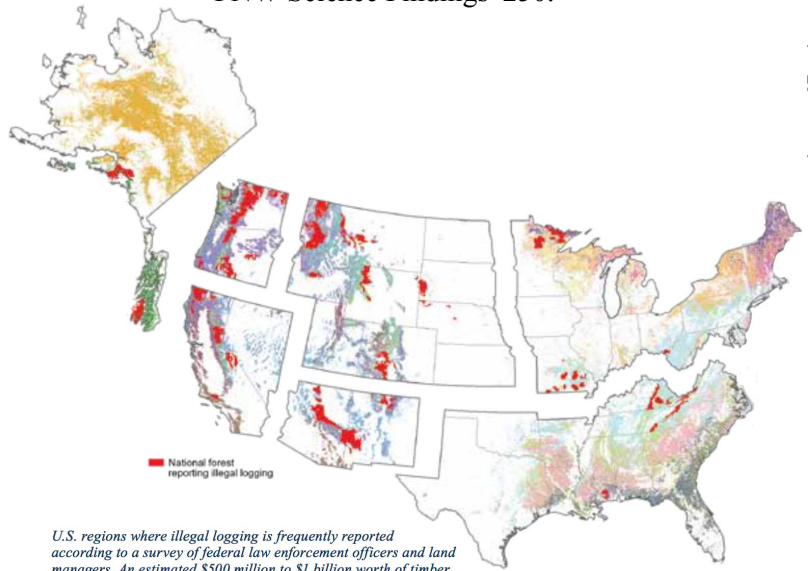
Additional Papers

- Cronn, RC, KN Finch, L Hauck, M Parker-Forneyc, BG Milligand, J Dowling & Adventure Scientists. 2021. Range-wide assessment of a SNP panel for individualization and geolocalization of bigleaf maple (*Acer macrophyllum* Pursh). *Forensic Science International: Animals and Environments* 1 (2021): 100033.
- Eaton, MJ, GJ Meyers; S-O Kolokotronis, MS Leslie, AP Martin, & G Amato. 2010. Barcoding bushmeat: molecular identification of Central African and South American harvested vertebrates. USGS Staff -- Published Research. 1127.
- Ewart, KM, AL Lightson, FT Sitam, J Rovie-Ryan, SG.Nguyen, KI Morgan, A Luczon, EMS Anadon. M De Bruyn, S Bourgeois, K Ouitavon, A Kotze, MSA Bakar, M Salgado-Lynn, & R McEwing. 2021. DNA analyses of large pangolin scale seizures: Species identification validation and case studies. *Forensic Science International: Animals and Environments* 1 (2021): 100014.
- Finch, KN, RC Cronn, A Richter, C Blanc-Jolivet, MCA Guerrero, LDS Beltrán, CRGarcía-Dávila, ENH Coronado, S Palacios-Ramos, K Paredes-Villanueva & FA Jones. 2020. Predicting the geographic origin of Spanish cedar (*Cedrela odorata* L) based on DNA variation. *Conservation Genetics* 21: 625–639.
- Pérez-Espona, S. 2021. Conservation-focused biobanks: A valuable resource for wildlife DNA forensics. *Forensic Science International: Animals and Environments* 1 (2021): 100017,.
- Schroeder, H, R Cronn, Y Yanbaev, T Jennings, M Mader, B Degen, & B Kersten 2016. Development of molecular markers for determining continental origin of wood from white oaks (*Quercus* L. sect. *Quercus*). *PLoS ONE* 11(6): e0158221.
- Tang, K, J Ren, R Cronn, DL Erickson, BG Milligan, M Parker-Forney, JL Spouge & F Sun. 2018. Alignment-free genome comparison enables accurate geographic sourcing of white oak DNA. *BMC Genomics* 19: 896.
- Wang, Z-F, H-L Cao, C-X Cai, & Z-M Wang. 2020. Using genetic markers to identify the origin of illegally traded agarwood-producing *Aquilaria sinensis* trees. *Global Ecology and Conservation* 22: e00958.
- Wasser, SK, L Brown, C Mailand, S Mondol, W Clark, C Laurie & BS Weir. 2015. Genetic assignment of large seizures of elephant ivory reveals Africa's major poaching hotspots. *Science* 349: 84 -87

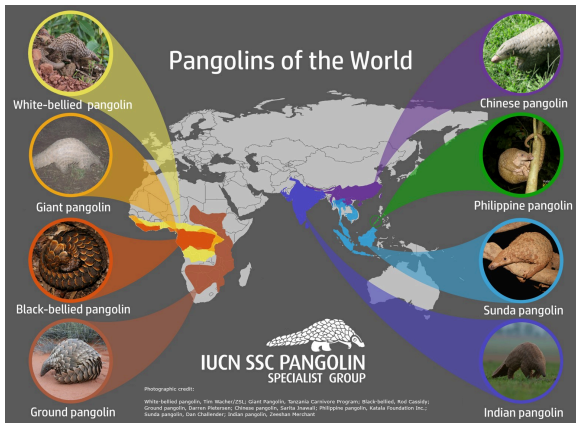


Orange-fronted parakeet (wikimedia.org)
Eupsittula canicularis

Watts, A, R. Cronn, & L Hauck. 2022. Decoding the fingerprints of trees through their DNA. PNW Science Findings 250.



U.S. regions where illegal logging is frequently reported according to a survey of federal law enforcement officers and land managers. An estimated \$500 million to \$1 billion worth of timber is stolen through illegal logging in the United States each year.



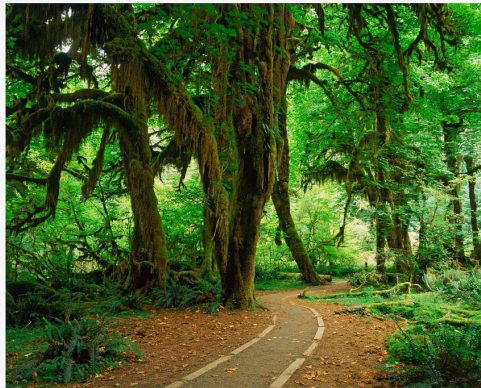
<https://www.pangolins.org/>

"Pangolins are the most trafficked mammal in the world, and all eight species are listed under CITES Appendix I." (Ewart et al., 2021)

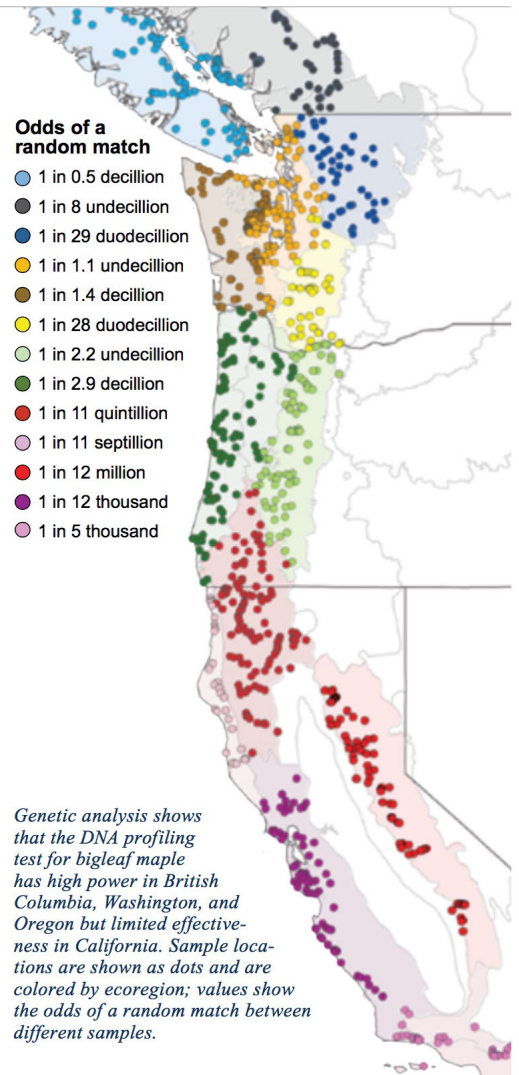
Trees fight back: First-ever use of tree DNA in prosecution sends poacher to prison

By Adelia Sullivan
 November 11, 2021 at 8:57 a.m. EST

The Washington Post
 Democracy Dies in Darkness



USA, Washington, Olympic National Park, Hoh Rainforest, Trail of Mosses (James Rankley/Getty Images)



Genetic analysis shows that the DNA profiling test for bigleaf maple has high power in British Columbia, Washington, and Oregon but limited effectiveness in California. Sample locations are shown as dots and are colored by ecoregion; values show the odds of a random match between different samples.

Bio 431: Section F02

Conservation Genetics

October 25, 2022

Identifying Evolutionarily Significant Units for conservation

Crandall, KA, OR Bininda-Emonds, GM Mace, & RK Wayne. 2000. Considering evolutionary processes in conservation biology. *Trends in Ecology & Evolution* 15: 290–295.

<https://reed.idm.oclc.org/login?url=https://www.sciencedirect.com/science/article/pii/S0169534700018760>

Posso-Terranova, A, & J Andrés. 2018. Multivariate species boundaries and conservation of harlequin poison frogs. *Molecular Ecology* 27: 3432–3451.

<https://reed.idm.oclc.org/login?url=https://onlinelibrary-wiley-com.reed.idm.oclc.org/doi/10.1111/mec.14803>

Additional Reading

Hausdorf, B., & Hennig, C. (2010). Species delimitation using dominant and codominant multilocus markers. *Systematic Biology*, 59(5), 491–503. <https://doi.org/10.1093/sysbio/syq039>

Hedrick, P. W. (1995). Gene flow and genetic restoration: The Florida panther as a case study.

Conservation Biology, 9(5), 996–1007. <https://doi.org/10.1046/j.1523-1739.1995.9050988.x-i1>

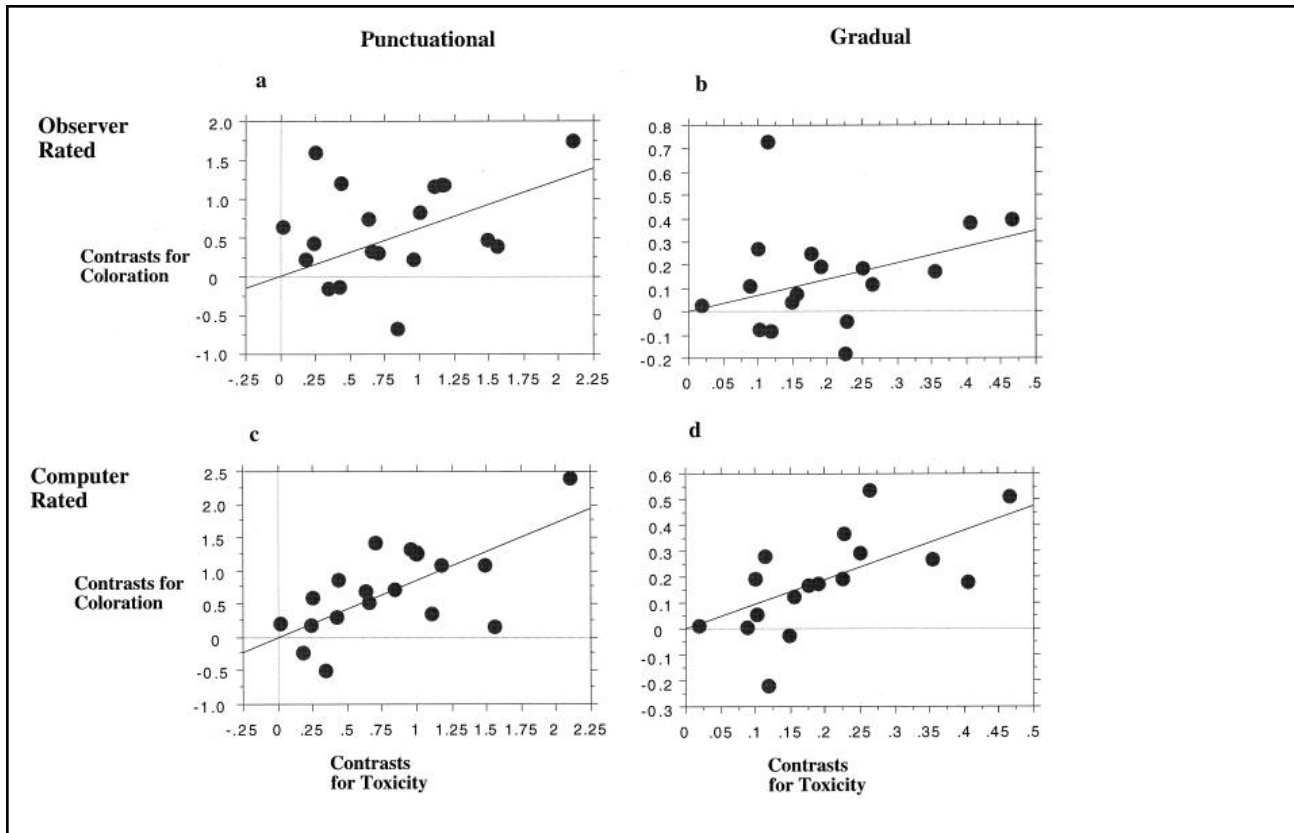
Lynch, J. D., & Arroyo, S. B. (2009). Risks to Colombian amphibian fauna from cultivation of coca (*Erythroxylum coca*): A geographical analysis. *Journal of Toxicology and Environmental Health, Part A*, 72(15–16), 974–985. <https://doi.org/10.1080/15287390902929733>

Malin C. Rivers, Neil A. Brummitt, Eimear Nic Lughadha, Thomas R. Meagher, Do species conservation assessments capture genetic diversity?, *Global Ecology and Conservation*, Volume 2, 2014, Pages 81-87, ISSN 2351-9894,

Myers, C. W., & Daly, J. W. (1976). Preliminary evaluation of skin toxins and vocalizations in taxonomic and evolutionary studies of poison- dart frogs (Dendrobatidae). *Bulletin of the American Museum of Natural History*, 157, 175–262.

Negret, P. J., Allan, J., Braczkowski, A., Maron, M., & Watson, J. E. (2017). Need for conservation planning in postconflict Colombia. *Conservation Biology*, 31(3), 499–500, <https://doi.org/10.1111/cobi.12902>

Summers, K., & Clough, M. E. (2001). The evolution of coloration and toxicity in the poison frog family (Dendrobatidae). *Proceedings of the National Academy of Sciences of the United States of America*, 98(11), 6227–6232. <https://doi.org/10.1073/pnas.10113489>



Summers, K., & Clough, M. E. (2001): Regressions of standardized contrasts for coloration on standardized contrasts for toxicity across the poison frogs: (a) Coloration as measured by human rates vs. toxicity, using a punctuational model of evolutionary change in each character. (b) Coloration as measured by human raters vs. toxicity, using a gradual model of evolutionary change. (c) Coloration as measured with a computer-based analysis vs. toxicity, using a punctuational model of evolutionary change. (d) Coloration as measured with a computer-based analysis vs. toxicity, using a gradual model of evolutionary change.



Herbert the Poison Dart Frog
Phylllobates terribilis 'Mint'
 (captive bred)

Conservation Epigenetics

Rey, O, C Eizaguirre, B Angers, M Baltazar-Soares, K Sagonas, JG Prunier, & S Blanchet. 2020. Linking epigenetics and biological conservation: Towards a conservation epigenetics perspective. *Functional Ecology* 34: 414– 427.

Kitavi, M, R Cashell, M Ferguson, J Lorenzen, M Nyine, PC McKeown & C Spillane. 2020. Heritable epigenetic diversity for conservation and utilization of epigenetic germplasm resources of clonal East African Highland banana (EAHB) accessions. *Theoretical and Applied Genetics* 133: 2605–2625.

Additional Papers

Herrel, A, Joly, D, Danchin, E. Epigenetics in ecology and evolution. *Funct Ecol.* 2020; 34: 381–384. <https://doi.org/10.1111/1365-2435.13494> -**Useful review with more details on epigenetics**

Leitwein, M, Laporte, M, Le Luyer, J, et al. Epigenomic modifications induced by hatchery rearing persist in germ line cells of adult salmon after their oceanic migration. *Evol Appl.* 2021; 14: 2402– 2413. <https://doi.org/10.1111/eva.13235> -**Salmon, whole genome bisulfite sequencing (WGBS), DNA methylation in multiple environments**

Le Luyer J, Laporte M, Beacham TD, Kaukinen KH, Withler RE, Leong JS, Rondeau EB, Koop BF, Bernatchez L. Parallel epigenetic modifications induced by hatchery rearing in a Pacific salmon. *Proc Natl Acad Sci U S A.* 2017 Dec 5;114(49):12964-12969. doi: 10.1073/pnas.1711229114. Epub 2017 Nov 21. PMID: 29162695; PMCID: PMC5724268. -**Salmon, DNA methylation wild vs hatchery**

Vergeer P, Wagemaker NC, Ouborg NJ. Evidence for an epigenetic role in inbreeding depression. *Biol Lett.* 2012 Oct 23;8(5):798-801. doi: 10.1098/rsbl.2012.0494. Epub 2012 Jul 11. PMID: 22791708; PMCID: PMC3441007. -**Evidence of DNA methylation in inbreeding depression and how we can alter it**

Zheng X, Chen L, Xia H, Wei H, Lou Q, Li M, Li T, Luo L. Transgenerational epimutations induced by multi-generation drought imposition mediate rice plant's adaptation to drought condition. *Sci Rep.* 2017 Jan 4;7:39843. doi: 10.1038/srep39843. PMID: 28051176; PMCID: PMC5209664.- **Rice, transgenerational DNA methylation**

Zeng, T., Yin, J., Feng, P. *et al.* Analysis of genome and methylation changes in Chinese indigenous chickens over time provides insight into species conservation. *Commun Biol* 5, 952 (2022). <https://doi.org/10.1038/s42003-022-03907-7> -**Chickens, DNA methylation level differences based on conservation programs**

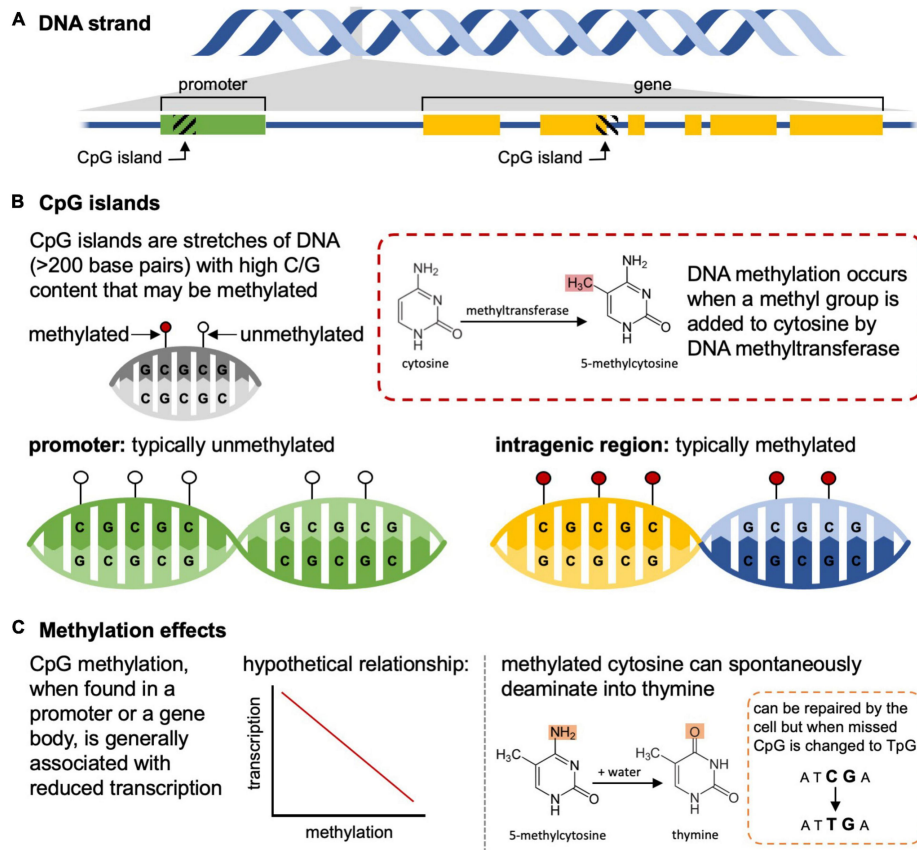


FIGURE 1. Methylation of cytosine-phosphate-guanine (CpG) islands influences transcription and can result in spontaneous mutations. (A) CpG islands can be found within promoters (left) or in coding and non-coding regions (right). (B) In mammals, the CpG islands in promoters of genes that are transcriptionally active are unmethylated, while those in gene bodies are often methylated. (C) Methylation of CpG islands in promoters is generally associated with reduced transcription relative to unmethylated regions, and methylated cytosines can spontaneously deaminate into thymine resulting in changes to the underlying DNA sequence. (taken from Herrel et al., 2020)

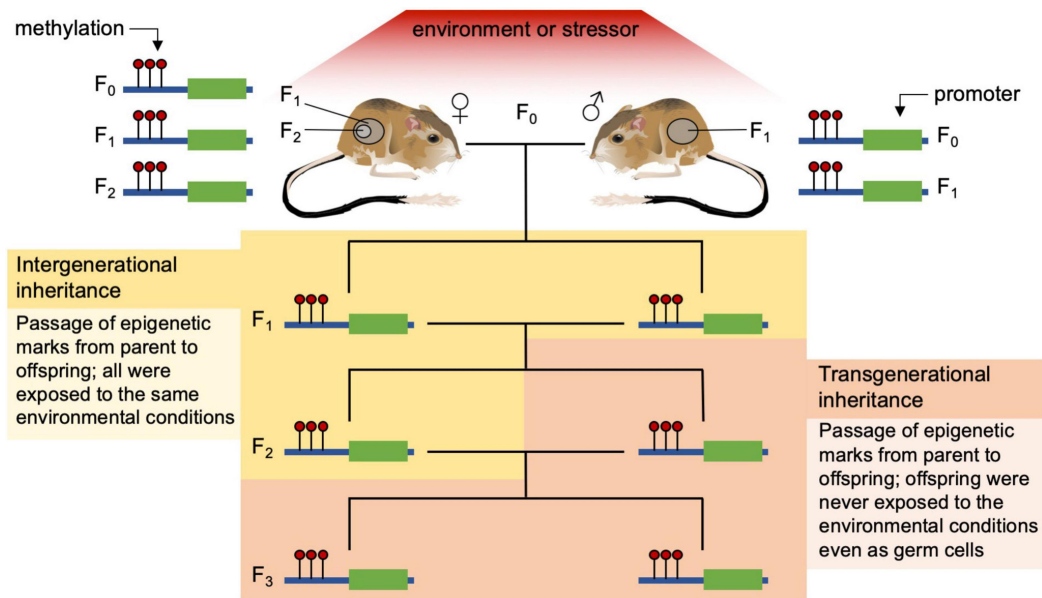


FIGURE 2. Examples of intergenerational and transgenerational inheritance of epigenetic marks (methylation) in a vertebrate. Intergenerational inheritance tracks epigenetic modifications through parent and offspring that were all exposed to the same environment or stressor. On the left a female kangaroo rat (F₀), her developing embryo (F₁), and the embryo's germ cells (F₂) are all exposed to the current environmental stressor that can alter the epigenome directly; on the right the male rat (F₀) and his germ cells (sperm, F₁) are being exposed to the same stressor. Transgenerational inheritance occurs when offspring (F₃ from females, and F₂ from males) never exposed to the stressor (even as germ cells) have the same methylation pattern as their parents that were exposed to the stressful environment. (taken from Herrel et al., 2020)

Ex-Situ Collections & Conservation Genetics

Abeli, Thomas, et al. “Ex Situ Collections and Their Potential for the Restoration of Extinct Plants.” *Conservation Biology*, vol. 34, no. 2, 2019, pp. 303–313., <https://doi.org/10.1111/cobi.13391>.

Clugston, James A., et al. “Conservation Genomics of an Australian Cycad *Cycas Callicola*, and the Absence of Key Genotypes in Botanic Gardens.” *Conservation Genetics*, vol. 23, no. 3, 2022, pp. 449–465., <https://doi.org/10.1007/s10592-022-01428-8>.

Additional Papers

Cibrian-Jaramillo A, Hird A, Oleas N, Ma H, Meerow AW, Francisco-Ortega J, Griffith MP (2013) What is the conservation value of a plant in a botanic garden? Using indicators to improve management of ex situ collections. *Bot Rev* 79(4):559–577 —> **Measuring allelic richness in botanical gardens**

Enßlin A, Sandner TM, Matthies D (2011) Consequences of ex situ cultivation of plants: genetic diversity, fitness and adaptation of the monocarpic *Cynoglossum officinale* L. in botanic gardens. *Biol Conserv* 144(1):272–278 —> **effects of cultivation on genetic diversity / fitness of ex situ populations**

Fant JB, Havens K, Kramer AT, Walsh SK, Callicrate T, Lacy RC, Smith PP (2016) What to do when we can't bank on seeds: what botanic gardens can learn from the zoo community about conserving plants in living collections. *Am J Bot* 103:1541–1543 —> **Zoological protocols for minimizing genetic / demographic decline in ex situ populations**

Nadarajan J, Benson EE, Xaba P, Harding K, Lindstrom A, Donaldson J, King E (2018) Comparative biology of cycad pollen, seed and tissue-A plant conservation perspective. *Bot Rev* 84(3):295–314 —> **Cycad horticultural practices, phytosanitary control in cycad germplasm**

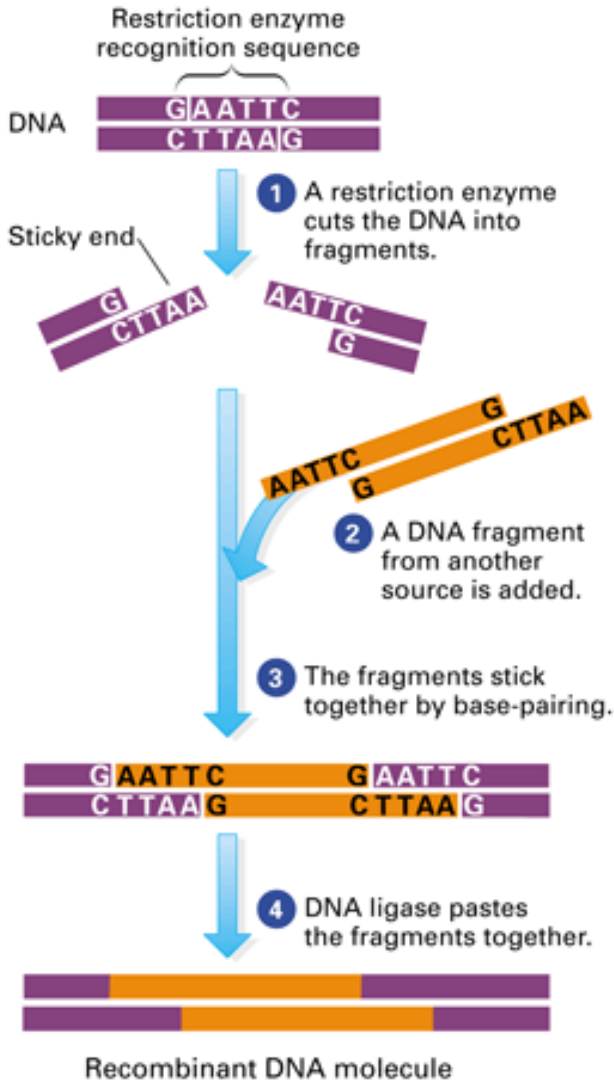
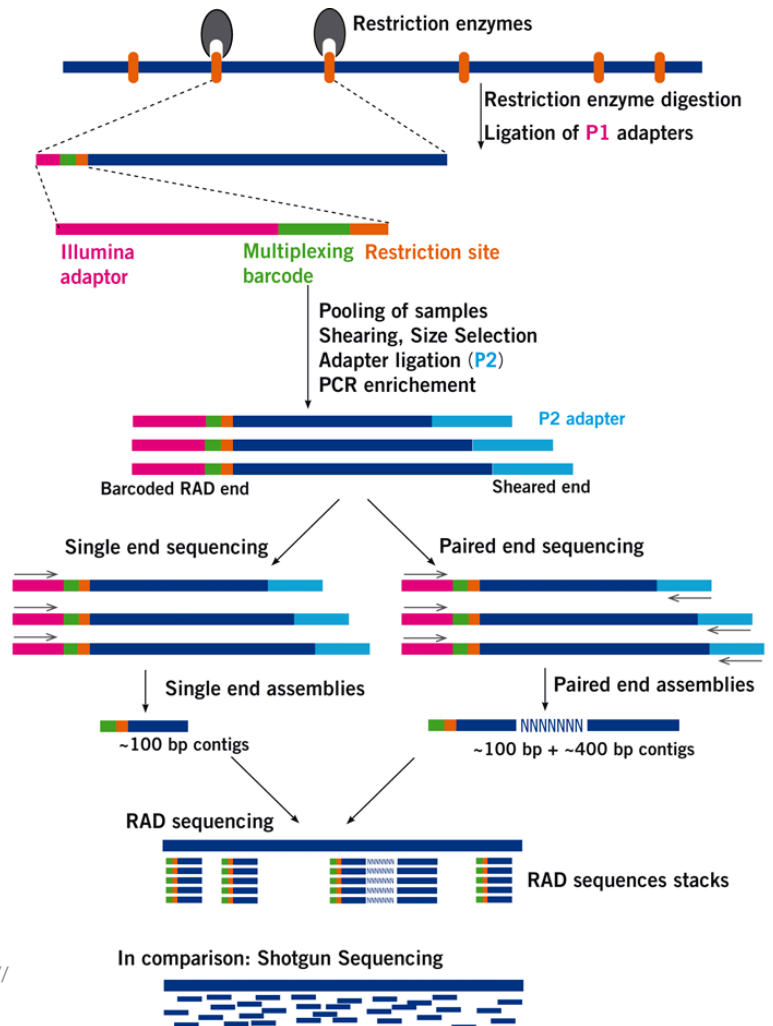


Figure 1: The process of Restriction Enzyme cutting. Taken from <https://www.mathwizurd.com/bio/2016/4/13/recombinant-dna>



Royal Botanic Gardens in London. Taken from <https://www.zmescience.com/science/biology/botanic-garden-endangered-plants-26092017/>

Figure 2: RadSeq explained. Taken from <https://www.floragenex.com/rad-seq>

Genome editing applications to conservation biology

Phelps MP, LW Seeb, & JE Seeb. 2020. Transforming ecology and conservation biology through genome editing. *Conservation Biology* 34: 54-65.

Kosch, TA, CNS Silva, LA Brannelly, AA Roberts, Q Lau, G Marantelli, L Berger & LF Skerratt. 2019. Genetic potential for disease resistance in critically endangered amphibians decimated by chytridiomycosis. *Animal Conservation* 22: 238–250.

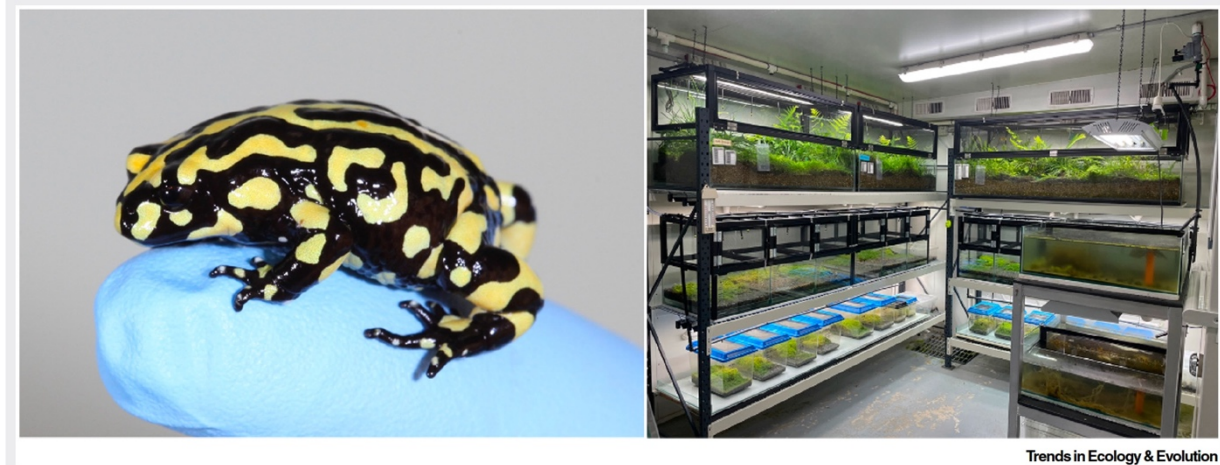


Figure 1. The Australian southern corroboree frog (*Pseudophryne corroboree*) has been driven to functional extinction in the wild by Bd and is dependent on CBPs for its continued survival (*P. corroboree* photograph by C. Doughty; *P. corroboree* breeding facility at Melbourne Zoo by M. Davidson). **from Kosch, et al., 2022.**

Additional Reviews

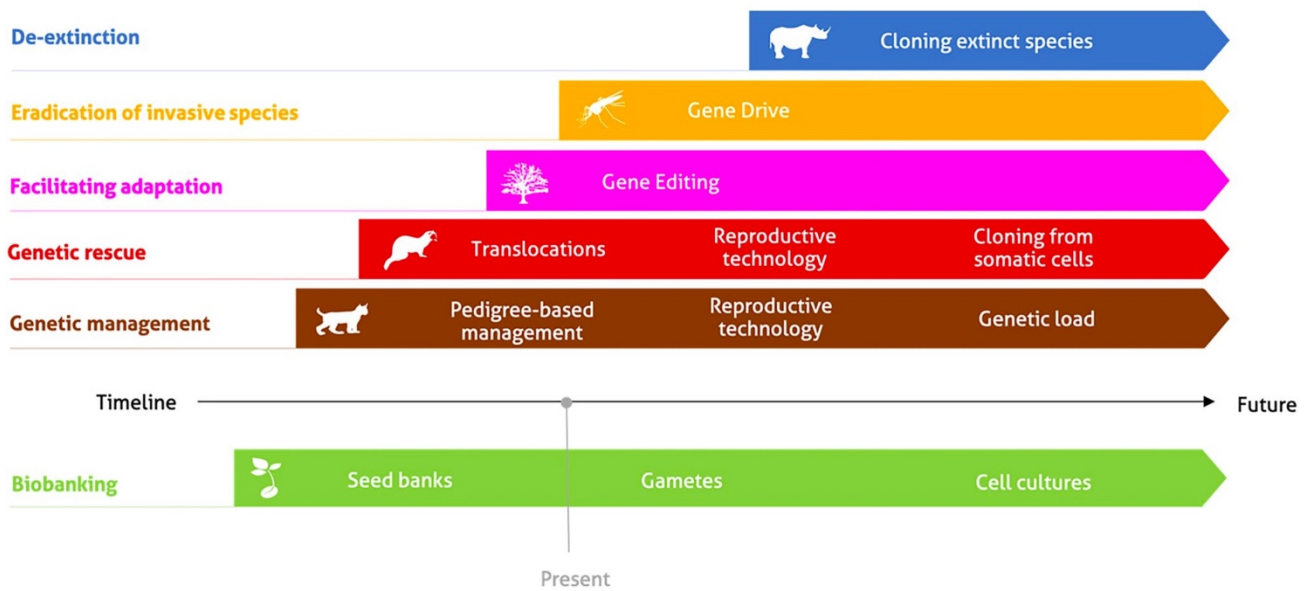
Kosch, TA, AW Waddle, CA Cooper, KR Zenger, DJ Garrick, L Berger, & LF Skerratt. 2022. Genetic approaches for increasing fitness in endangered species. *Trends in Ecology & Evolution* 37: 332-345.

Macfarlane, NBW, J Adams, EL Bennett, TM Brooks, JA Delborne, H Eggermont, D Endy, KM Esvelt, B Kolodziejczyk, T Kuiken, MJ Oliva, S Peña Moreno, L Slobodian, RB Smith, D Thizy, DM Tompkins, W Wei, & KH Redford. **2022.** Direct and indirect impacts of synthetic biology on biodiversity conservation. *iScience* 25: 105423.

Piaggio AJ, G Segelbacher, PJ Seddon, L Alphey, EL Bennett, RH Carlson, RM Friedman, D Kanavy, R Phelan, KH Redford, M Rosales, L Slobodian, & K Wheeler. 2017. Is it time for synthetic biodiversity conservation? *Trends in Ecology & Evolution* 32: 97-107.

Reynolds, JL. 2021. Engineering biological diversity: the international governance of synthetic biology, gene drives, and de-extinction for conservation. *Current Opinion in Environmental Sustainability* 49: 1–6.

Segelbacher, G, M Bosse, P Burger, P Galbusera, JA Godoy, P Helsen, C Hvilsom, L Iacolina, A Kahric, C Manfrin, M Nonic, D Thizy, I Tsvetkov, N Veličković, C Vilà, SM Wisely & E Buzan. 2022. New developments in the field of genomic technologies and their relevance to conservation management. *Conservation Genetics* 23: 217–242.



Feasibility of conservation areas and the different genomic and biotechnological tools. from Segelbacher et al., 2022.

Table 2. Examples of conservation projects using synthetic biology for genetic modification^a

from Kosch, et al., 2022.

| Species | Trait(s) | Method | Stage | Refs |
|--|------------------------------------|---|--|----------|
| American chestnut trees (<i>Castanea dentata</i>) | Chestnut blight resistance | <i>Agrobacterium</i> -mediated transformation | Restoration planting pending regulatory approval | [73,74] |
| American elm trees (<i>Ulmus americana</i>) | Dutch elm resistance | <i>Agrobacterium</i> -mediated transformation | Field testing ongoing | [147] |
| Branching corals (<i>Acropora millepora</i>) | Thermal tolerance | CRISPR-Cas9 | First proof of concept complete | [76] |
| Invasive cane toads (<i>Rhinella marina</i>) | Toxicity via bufotoxin hydrolase | Sperm transfection with CRISPR-Cas9 | First proof of concept complete | [148] |
| Black-footed ferrets (<i>Mustela nigripes</i>) | Sylvatic plague resistance | Vectored immunoprophylaxis (VIP) | Proof of concept underway | [59,85] |
| Southern corroboree frogs (<i>Pseudophryne corroboree</i>) | Chytridiomycosis resistance | CRISPR-Cas9 | In development | [36] |
| Invasive rodents | Male fertility, sex determination | CRISPR gene drive | In development | [79,149] |
| Hawaiian amakihi (<i>Chlorodrepanis virens</i>) | Avian malaria resistance | Undetermined | In development | [37,150] |
| Invasive mosquitos (<i>Culex quinquefasciatus</i>) | Male fertility, disease resistance | Various | In development | [81] |

^aAbbreviation: CRISPR, clustered regularly interspaced short palindromic repeats.

organism examples:

Adams, WM, & KH Redford. 2021. Fix that genome? *Oryx*, 2021, 55: 481–482. [short piece about cloning of a black-footed ferret].

Cleves PA, AI Tinoco, J Bradford, D Perrin, LK Bay, & JR Pringle. 2020. Reduced thermal tolerance in a coral carrying CRISPR-induced mutations in the gene for a heat-shock transcription factor. *Proceedings of the National Academy of Sciences, U S A.* 117: 28899-28905.

Snow, AA. 2019. Genetically engineering wild mice to combat Lyme disease: an ecological perspective. *BioScience* 69: 746–756.

Movie: Genesis 2.0

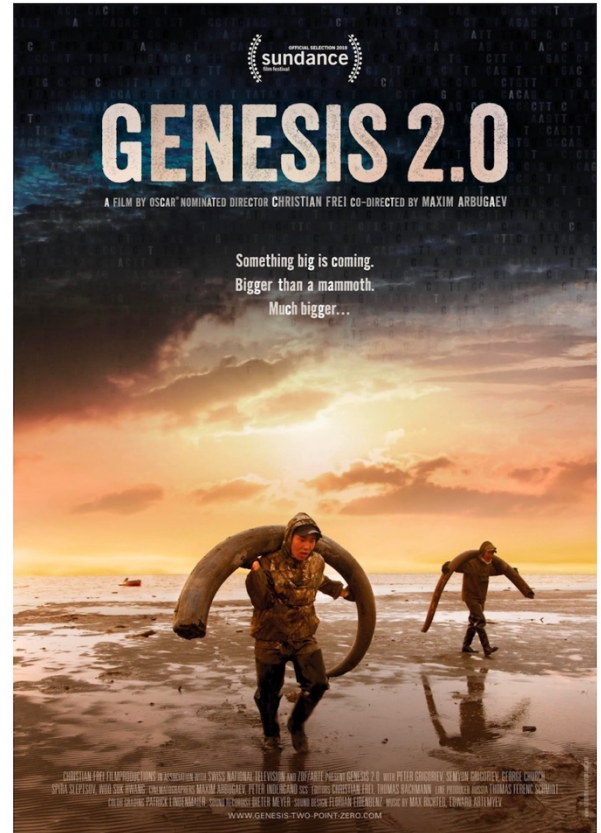
LONG SYNOPSIS (from press kit: <https://genesis-two-point-zero.com/mediafiles/genesis-presskit-en.pdf>)

The film observes the harsh and dangerous life of so-called mammoth hunters on the remote New Siberian Islands in the far north of Siberia. The archaic landscape in which these people are looking for the tusks of extinct mammoths looks like primordial earth. There is a kind of gold rush fever in the air, because the prices for this white gold have never been so high. But the thawing permafrost unveils more than just precious ivory. Sometimes the hunters find an almost completely preserved mammoth carcass with fur, liquid blood and muscle tissue on which arctic foxes gnaw.

Such finds are magnets for high-tech Russian and South Korean clone researchers in search of mammoth cells with the greatest possible degree of intact DNA. Their mission could be part of a science-fiction plot. They want to bring the extinct woolly mammoth back to life à la “Jurassic Park”, and resurrect it as a species. And that’s just the beginning. Worldwide, biologists are working on re-inventing life. They want to learn the language of nature and create life following the Lego principle¹². The goal of synthetic biology is to produce complete artificial biological systems. Man becomes the Creator.

The resurrection of the mammoth is a first track and manifestation of this next great technological revolution. An exercise. A multi-million dollar game. The new technology may well turn the world as we know it completely on its head...and all of this has its origin in the unstoppably thawing permafrost at the extreme edge of Siberia.

Genesis two point zero.



Further reading on the intersection of Conservation Biology and film:

Silk, MJ, SL Crowley, AJ Woodhead, & A Nuno. 2018. Considering connections between Hollywood and biodiversity conservation. Conservation Biology 32: 597-606.

Bio 431, Section F02
Keith Karoly
Fall 2022

Conservation Genetics

We will be surveying issues of current controversy and active research in conservation biology, highlighting places where molecular genetic techniques and data are providing new insights for classical problems in the management and conservation of rare and threatened species.

Meeting place and time will be: **B200A, Tuesdays, 6:10-8:00pm**

prerequisites: Biology 101/102, two additional units of biology with laboratory, and junior or senior standing.

course web page: <http://academic.reed.edu/biology/courses/BIO431/congen/index.html>

Instructor: **Keith Karoly**, x7846. Office hours: W/Th 10:30-11:30am. (Office B238A/Lab B238),

Course Requirements

Everyone taking part in the seminar is expected to:

- 1) **read the assigned material each week.** The reading will consist of 2 or 3 research articles and/or book chapters from the primary research and review literature. The reading assignment for each meeting will be provided the preceding week. We will primarily make use of e-journals and e-reserves, linked to the course web page. If the articles are not available through Reed electronic resources, PDFs of the assigned reading will be available using the Biology Department Resources shared google drive (not Moodle). The articles or chapters may provide opposing opinions or evidence on a subject, and should always be read critically.

Note: access to Library resources from off-campus may require use of the Library's proxy so you can authenticate as a Reed user. From the library's off-campus access page (<https://library.reed.edu/help/off-campus.html>): "*Add this prefix to the article's URL: <https://reed.idm.oclc.org/login?url=> (Note: the prefix is only necessary for accessing subscription resources.)*"

- 2) **participate in the seminar discussion. I expect everyone in this class to participate in all discussions.** The topics we will address should lend themselves to lively discussion. It will be important for our discussions to have all participants contributing their views on the reading. **Everyone should come to seminar prepared to briefly summarize the assigned reading for the group.** Each week, a randomly chosen person **may** be asked to provide a brief (maximum of 5 minutes) description for each of the papers.

Note: I would like our discussion to cover both positive and negative aspects of the papers.

- 3) **assume the role of Discussion Leader in turn.** Your primary responsibilities in this role will be to choose a topic for discussion, identify papers for the class to read (in consultation with Keith), and facilitate discussion during the seminar meeting. This will require assessing the available literature on your chosen topic as a means for you to identify the papers we will read for class. Your review of the broader literature on your subject should help you to place the assigned reading into a larger context. You are not expected to prepare (nor will you be allowed to present) a two-hour lecture on your topic.

On the day we discuss your reading, please bring:

- a) **a brief bibliography of the related papers and background information you have found**, along with any additional information (diagrams, pictures, maps, etc) from other sources (not the papers the class will read) that may help to put the reading in context. ***This handout will be provided to the class.*** Please provide an electronic copy of this document to me prior to class, and I will print enough copies for everyone (and print in color if warranted)
- b) **a cartoon/schematic/sketch of the methods** for the (or one of the) empirical paper we will discuss. This will be turned in to Keith and need not be shared with the class.

[depending on the number of enrolled students in the class, we may add some part or all of these additional assignments]

- 4) **complete a review of a recent research papers investigating a question related to the general topics covered by our seminar.** This is expected to be a short review (a **maximum** of 3 pages, double-spaced). Select a paper from a topic that differs from the topic you selected as Discussion Leader. The article you review should be reporting new research (i.e. do not use review articles) and should be from the **current periodicals reading room** (i.e. unbound). If you use electronic journals, please focus on articles from the **past 12 months**.

Some appropriate journals to search include: *Conservation Biology, Conservation Genetics, Biological Conservation, Molecular Ecology, Journal of Wildlife Management, Economic Botany, American Journal of Botany, Ecology, Evolution, Oecologia, Botanical Journal of the Linnaean Society, Journal of Ecology, Canadian Journal of Botany, and American Naturalist.*

- 5) **complete a brief research proposal for one of the topics covered in class** (this may be completed in assigned pairs). You will revisit one of the papers we discussed for seminar this term, and identify a follow-up question for additional research. You will then write a 2 to 3 page description of a research project that will build upon the report we read. More details will be provided towards the end of the term.

SEPT 6 **Introduction to conservation genetics**

Reading: Ouborg, NJ, P Vergeer, & C Mix. 2006. The rough edges of the conservation genetics paradigm for plants. *Journal of Ecology* 94: 1233–1248.
<https://reed.idm.oclc.org/login?url=https://besjournals.onlinelibrary.wiley.com/doi/10.1111/j.1365-2745.2006.01167.x>

Frankham, R. 2010. Challenges and opportunities of genetic approaches to biological conservation. *Biological Conservation* 143: 1919-1927.
<https://reed.idm.oclc.org/login?url=https://www.sciencedirect.com/science/article/abs/pii/S000632071000234X>

For Sept. 6, bring to class a list of terms and concepts about which you are unsure of their meaning and/or application

Examples of potential topics for the weekly reading/discussion

- Conservation analyses for neutral v. functional genetic variation
- Conservation genomics
- Conservation of crop genetic research
- eDNA methods for population/community monitoring
- *Ex situ* management of captive/zoo/garden/seed-bank populations
- Genetic approaches to defining conservation units (species)
- Genetic perspectives on assisted migration
- Genetic rescue/exchange for endangered species
- Genetics as a tool for restoration
- Hybridization and conservation
- Monitoring gene expression as a tool in conservation
- Wildlife forensics and resource conservation

Course Information

Course Number: BIO431F02
Title: Conservation Genetics
Instructor: Keith Karoly
Day & Time: Tu 18:10-20:00
Room(s): Bio 200A

Instructor Information

Office: B238A
Office Hours: W, Th 10:30am-11:30am
Contact information: kkaroly@reed.edu

Course Description:

One-half course for one semester. An examination of current topics and areas in biology with an emphasis on primary literature. Participants will lead group discussions and/or make oral presentations. Prerequisites: Biology 101 and 102, two additional units of biology with laboratory, and junior or senior standing. Conference. Not all topics offered every year. May be repeated for credit.

Conservation Genetics. An exploration of issues of current controversy and active research in conservation biology, highlighting places where molecular genetic techniques and data are providing new insights for classical problems in the management and conservation of rare and threatened species.

Learning Outcomes:

At the end of this seminar style course with a writing component, students will be able to:

- 1) Critically read and interpret the current primary scientific literature where genetic approaches are used to investigate applied questions in conservation biology.
- 2) Interpret and evaluate scientific data presented in the form of figures, tables, and graphs.
- 3) Understand how elements of experimental design affect the analysis and interpretation of the data collected.
- 4) Participate in and lead a discussion around a specific scientific finding or set of findings.
- 5) Summarize and evaluate, in writing, the goals, methods, results and interpretations found in scientific articles that are reporting primary research results.

Distribution Requirements: This course can be used towards your Group III, “Natural, Mathematical, and Psychological Science,” requirement. It accomplishes the following learning goals for the group (indicate as appropriate):

- Evaluate quantitative data that are presented in support of scientific statements
- Given a question, formulate a hypothesis
- Interpret data

This course **does not** satisfy the “primary data collection and analysis” requirement.