

Appendix S1. List of the publications matching a population genetics context using microsatellite markers with (a) butterflies (Scopus database, 50 articles: keywords butterfly* AND microsatellite*), (b) mammals (Scopus database, 10 most recent articles: keywords mammal* AND microsatellite*), and (c) birds (Scopus database, 10 most recent articles: keywords bird* AND microsatellite*).

a. Butterflies

Albuquerque de Moura, P., Quek, S.-P., Cardoso, M.Z. & Kronforst, M.R. (2011). Comparative population genetics of mimetic *Heliconius* butterflies in an endangered habitat. *BMC genetics*, **12**, 9.

Anton, C., Zeisset, I., Musche, M., Durka, W., Boomsma, J.J. & Settele, J. (2007). Population structure of a large blue butterfly and its specialist parasitoid in a fragmented landscape. *Molecular Ecology*, **16**, 3828–3838.

Caplins, S.A., Gilbert, K.J., Ciotir, C., Roland, J., Matter, S.F. & Keyghobadi, N. (2014). Landscape structure and the genetic effects of a population collapse. *Proceedings of the Royal Society B: Biological Sciences*, **281**, 20141798–20141798.

Couchoux, C., Seppä, P. & van Nouhuys, S. (2016). Strong dispersal in a parasitoid wasp overwhelms habitat fragmentation and host population dynamics. *Molecular Ecology*, **25**, 3344–3355.

Fauvelot, C., Cleary, D.F.R. & Menken, S.B.J. (2006). Short-Term Impact of 1997/1998 ENSO-induced disturbance on abundance and genetic variation in a tropical butterfly. *Journal of Heredity*, **97**, 367–380.

Finger, A., Schmitt, T., Zachos, F.E., Meyer, M., Assmann, T. & Habel, J.C. (2009). The genetic status of the violet copper *Lycaena helle* - a relict of the cold past in times of global warming. *Ecography*, **32**, 382–390.

Habel, J.C., Brückmann, S.V., Krauss, J., Schwarzer, J., Weig, A., Husemann, M. & Steffan-Dewenter, I. (2015). Fragmentation genetics of the grassland butterfly *Polyommatus coridon*: Stable genetic diversity or extinction debt? *Conservation Genetics*, **16**, 549–558.

Habel, J.C., Finger, A., Schmitt, T. & Nève, G. (2011a). Survival of the endangered butterfly *Lycaena helle* in a fragmented environment: genetic analyses over 15 years. *Journal of Zoological Systematics and Evolutionary Research*, **49**, 25–31.

Habel, J.C., Husemann, M., Schmitt, T., Dapporto, L., Rodder, D. & Vandewoestijne, S. (2013). A forest butterfly in Sahara Desert oases: isolation does not matter. *Journal of Heredity*, **104**, 234–247.

Habel, J.C., Ivinskis, P. & Schmitt, T. (2010a). On the limit of latitudinal range shifts - population genetics of relict butterfly populations. *Acta Zoologica Academiae Scientiarum Hungaricae*, **56**, 383–393.

Habel, J.C., Rödder, D., Schmitt, T. & Nève, G. (2011b). Global warming will affect the genetic diversity and uniqueness of *Lycaena helle* populations. *Global Change Biology*, **17**, 194–205.

Habel, J.C., Schmitt, T., Meyer, M., Finger, A., Rödder, D., Assmann, T. & Zachos, F.E. (2010b). Biogeography meets conservation: the genetic structure of the endangered lycaenid butterfly *Lycaena helle* (Denis & Schiffermüller, 1775). *Biological Journal of the Linnean Society*, **101**, 155–168.

- Habel, J.C., Zachos, F.E., Finger, A., Meyer, M., Louy, D., Assmann, T. & Schmitt, T. (2009). Unprecedented long-term genetic monomorphism in an endangered relict butterfly species. *Conservation Genetics*, **10**, 1659–1665.
- Harper, G.L., Maclean, N. & Goulson, D. (2006). Analysis of museum specimens suggests extreme genetic drift in the adonis blue butterfly (*Polyommatus bellargus*). *Biological Journal of the Linnean Society*, **88**, 447–452.
- Harper, G.L., Maclean, N. & Goulson, D. (2003). Microsatellite markers to assess the influence of population size, isolation and demographic change on the genetic structure of the UK butterfly *Polyommatus bellargus*. *Molecular Ecology*, **12**, 3349–3357.
- Keyghobadi, N., Roland, J., Matter, S.F. & Strobeck, C. (2005a). Among- and within-patch components of genetic diversity respond at different rates to habitat fragmentation: an empirical demonstration. *Proceedings of the Royal Society B: Biological Sciences*, **272**, 553–560.
- Keyghobadi, N., Roland, J. & Strobeck, C. (2005b). Genetic differentiation and gene flow among populations of the alpine butterfly, *Parnassius smintheus*, vary with landscape connectivity. *Molecular Ecology*, **14**, 1897–1909.
- Keyghobadi, N., Roland, J. & Strobeck, C. (1999). Influence of landscape on the population genetic structure of the alpine butterfly *Parnassius smintheus* (Papilionidae). *Molecular Ecology*, **8**, 1481–1495.
- Keyghobadi, N., Unger, K.P., Weintraub, J.D. & Fonseca, D.M. (2006). Remnant populations of the regal fritillary (*Speyeria idalia*) in Pennsylvania: local genetic structure in a high gene flow species. *Conservation Genetics*, **7**, 309–313.
- Kodandaramaiah, U., Weingartner, E., Janz, N., DaléN, L. & Nylin, S. (2011). Population structure in relation to host-plant ecology and *Wolbachia* infestation in the comma butterfly. *Journal of Evolutionary Biology*, **24**, 2173–2185.
- Kodandaramaiah, U., Weingartner, E., Janz, N., Leski, M., Slove, J., Warren, A. & Nylin, S. (2012). Investigating concordance among genetic data, subspecies circumscriptions and hostplant use in the nymphalid butterfly *Polygonia faunus* (D.A. Filatov, Ed.). *PLoS ONE*, **7**, e41058.
- Lyons, J.I., Pierce, A.A., Barribeau, S.M., Sternberg, E.D., Mongue, A.J. & de Roode, J.C. (2012). Lack of genetic differentiation between monarch butterflies with divergent migration destinations. *Molecular Ecology*, **21**, 3433–3444.
- Mattila, A.L.K., Duploux, A., Kirjokangas, M., Lehtonen, R., Rastas, P. & Hanski, I. (2012). High genetic load in an old isolated butterfly population. *Proceedings of the National Academy of Sciences*, **109**, E2496–E2505.
- Mikheyev, A.S., McBride, C.S., Mueller, U.G., Parmesan, C., Smee, M.R., Stefanescu, C., Wee, B. & Singer, M.C. (2013). Host-associated genomic differentiation in congeneric butterflies: now you see it, now you do not. *Molecular Ecology*, **22**, 4753–4766.

- Milko, L.V., Haddad, N.M. & Lance, S.L. (2012). Dispersal via stream corridors structures populations of the endangered St. Francis' satyr butterfly (*Neonympha mitchellii francisci*). *Journal of Insect Conservation*, **16**, 263–273.
- Miller, M.P., Pratt, G.F., Mullins, T.D. & Haig, S.M. (2014). Comparisons of genetic diversity in captive versus wild populations of the federally endangered Quino checkerspot butterfly (*Euphydryas editha quino* Behr; Lepidoptera: Nymphalidae). *Proceedings of the Entomological Society of Washington*, **116**, 80–90.
- Monroe, E.M., Alexander, K.D. & Britten, H.B. (2016). Still here after all these years: the persistence of the Uncompahgre fritillary butterfly. *Journal of Insect Conservation*, **20**, 305–313.
- Nair, A., Fountain, T., Ikonen, S., Ojanen, S.P. & van Nouhuys, S. (2016). Spatial and temporal genetic structure at the fourth trophic level in a fragmented landscape. *Proceedings of the Royal Society B: Biological Sciences*, **283**, 20160668.
- Orsini, L., Corander, J., Alasentie, A. & Hanski, I. (2008). Genetic spatial structure in a butterfly metapopulation correlates better with past than present demographic structure. *Molecular Ecology*, **17**, 2629–2642.
- Pierce, A.A., de Roode, J.C., Altizer, S. & Bartel, R.A. (2014). Extreme heterogeneity in parasitism despite low population genetic structure among monarch butterflies inhabiting the Hawaiian islands (P. O'Grady, Ed.). *PLoS ONE*, **9**, e100061.
- Proshok, B., Crawford, L.A., Davis, C.S., Desjardins, S., Henderson, A.E. & Sperling, F.A.H. (2013). *Apodemia mormo* in Canada: population genetic data support prior conservation ranking. *Journal of Insect Conservation*, **17**, 155–170.
- Proshok, B., Dupuis, J.R., Engberg, A., Davenport, K., Opler, P.A., Powell, J.A. & Sperling, F.A. (2015). Genetic evaluation of the evolutionary distinctness of a federally endangered butterfly, Lange's Metalmark. *BMC Evolutionary Biology*, **15**.
- Ritter, S., Michalski, S.G., Settele, J., Wiemers, M., Fric, Z.F., Sielezniew, M., Šašić, M., Rozier, Y. & Durka, W. (2013). *Wolbachia* infections mimic cryptic speciation in two parasitic butterfly species, *Phengaris teleius* and *P. nausithous* (Lepidoptera: Lycaenidae) (B.J. Mans, Ed.). *PLoS ONE*, **8**, e78107.
- Rutkowski, R., Sielezniew, M. & Szostak, A. (2009). Contrasting levels of polymorphism in cross-amplified microsatellites in two endangered xerothermophilous, obligatorily myrmecophilous, butterflies of the genus *Phengaris* (*Maculinea*) (Lepidoptera: Lycaenidae). *Eur J Entomol*, **106**, 457–469.
- Saarinen, E.V., Austin, J.D. & Daniels, J.C. (2010). Genetic estimates of contemporary effective population size in an endangered butterfly indicate a possible role for genetic compensation. *Evolutionary Applications*, **3**, 28–39.
- Saarinen, E.V. & Daniels, J.C. (2012). Using museum specimens to assess historical distribution and genetic diversity in an endangered butterfly. *Animal Biology*, **62**, 337–350.

- Saarinen, E.V., Daniels, J.C. & Maruniak, J.E. (2014). Local extinction event despite high levels of gene flow and genetic diversity in the federally-endangered Miami blue butterfly. *Conservation Genetics*, **15**, 811–821.
- Seraphim, N., Barreto, M.A., Almeida, G.S.S., Esperanço, A.P., Monteiro, R.F., Souza, A.P., Freitas, A.V.L. & Silva-Brandão, K.L. (2016). Genetic diversity of *Parides ascanius* (Lepidoptera: Papilionidae: Troidini): implications for the conservation of Brazil's most iconic endangered invertebrate species. *Conservation Genetics*, **17**, 533–546.
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- Sielezniew, M. & Rutkowski, R. (2012). Population isolation rather than ecological variation explains the genetic structure of endangered myrmecophilous butterfly *Phengaris* (= *Maculinea*) *arion*. *Journal of Insect Conservation*, **16**, 39–50.
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- Tartally, A., Kelager, A., Fürst, M.A. & Nash, D.R. (2016). Host plant use drives genetic differentiation in syntopic populations of *Maculinea alcon*. *PeerJ*, **4**, e1865.
- Tison, J.-L., Edmark, V.N., Sandoval-Castellanos, E., Van Dyck, H., Tammaru, T., Välimäki, P., Dalen, L. & Gotthard, K. (2014). Signature of post-glacial expansion and genetic structure at the northern range limit of the speckled wood butterfly. *Biological Journal of the Linnean Society*, **113**, 136–148.
- Turlure, C., Vandewoestijne, S. & Baguette, M. (2014). Conservation genetics of a threatened butterfly: comparison of allozymes, RAPDs and microsatellites. *BMC Genetics*, **15**.
- Ugelvig, L.V., Andersen, A., Boomsma, J.J. & Nash, D.R. (2012). Dispersal and gene flow in the rare, parasitic Large Blue butterfly *Maculinea arion*. *Molecular Ecology*, **21**, 3224–3236.
- Ugelvig, L.V., Nielsen, P.S., Boomsma, J.J. & Nash, D.R. (2011). Reconstructing eight decades of genetic variation in an isolated Danish population of the large blue butterfly *Maculinea arion*. *BMC evolutionary biology*, **11**, 201.
- Vandewoestijne, S. & Van Dyck, H. (2010). Population genetic differences along a latitudinal cline between original and recently colonized habitat in a butterfly. *PLoS ONE*, **5**, e13810.
- Vila, M., Lundhagen, A.C., Thuman, K.A., Stone, J.R. & Björklund, M. (2006). A new conservation unit in the butterfly *Erebia triaria* (Nymphalidae) as revealed by nuclear and mitochondrial markers. *Annales Zoologici Fennici*, **43**, 72–79.

Williams, B.L., Brawn, J.D. & Paige, K.N. (2003). Landscape scale genetic effects of habitat fragmentation on a high gene flow species: *Speyeria idalia* (Nymphalidae). *Molecular Ecology*, **12**, 11–20.

Zakharov, E.V. & Hellmann, J.J. (2008). Genetic differentiation across a latitudinal gradient in two co-occurring butterfly species: revealing population differences in a context of climate change. *Molecular Ecology*, **17**, 189–208.

b. Mammals

Bani, L., Orioli, V., Pisa, G., Fagiani, S., Dondina, O., Fabbri, E., Randi, E., Sozio, G. & Mortelliti, A. (2017). Population genetic structure and sex-biased dispersal of the hazel dormouse (*Muscardinus avellanarius*) in a continuous and in a fragmented landscape in central Italy. *Conservation Genetics*, **18**, 261–274.

Braaker, S., Kormann, U., Bontadina, F. & Obrist, M.K. (2017). Prediction of genetic connectivity in urban ecosystems by combining detailed movement data, genetic data and multi-path modelling. *Landscape and Urban Planning*, **160**, 107–114.

Brüniche-Olsen, A., Hazlitt, S.L. & Eldridge, M.D.B. (2017). Genetic evidence of range-wide population declines in an Australian marsupial prior to European settlement. *Conservation Genetics*.

Cypriano-Souza, A.L., Engel, M.H., Caballero, S., Olavarria, C., Flórez-González, L., Capella, J., Steel, D., Sremba, A., Aguayo, A., Thiele, D., Baker, C.S. & Bonatto, S.L. (2017). Genetic differentiation between humpback whales (*Megaptera novaeangliae*) from Atlantic and Pacific breeding grounds of South America. *Marine Mammal Science*, **33**, 457–479.

Del Real-Monroy, M. & Ortega, J. (2017). Spatial distribution of microsatellite and MHC-DRB exon 2 gene variability in the Jamaican fruit bat (*Artibeus jamaicensis*) in Mexico. *Mammalian Biology*, **84**, 1–11.

Lagerholm, V.K., Norén, K., Ehrlich, D., Ims, R.A., Killengreen, S.T., Abramson, N.I., Niemimaa, J., Angerbjörn, A., Henttonen, H. & Dalén, L. (2017). Run to the hills: gene flow among mountain areas leads to low genetic differentiation in the Norwegian lemming. *Biological Journal of the Linnean Society*, **121**, 1–14.

MacDonald, A.J. (2008). *Sex chromosome microsatellite markers from an Australian marsupial: development, application and evolution*. University of Canberra, Institute for Applied Ecology Division of Health, Design and Science.

Polfus, J.L., Manseau, M., Klitzsch, C.F.C., Simmons, D. & Wilson, P.J. (2017). Ancient diversification in glacial refugia leads to intraspecific diversity in a Holarctic mammal. *Journal of Biogeography*, **44**, 386–396.

Rodrigues, M., Bos, A.R., Schembri, P.J., de Lima, R.F., Lymberakis, P., Parpal, L., Cento, M., Ruetter, S., Ozkurt, S.O., Santos-Reis, M., Merilä, J. & Fernandes, C. (2017). Origin and introduction history of the least weasel (*Mustela nivalis*) on Mediterranean and Atlantic islands inferred from genetic data. *Biological Invasions*, **19**, 399–421.

Rosel, P., Wilcox, L., Sinclair, C., Speakman, T., Tumlin, M., Litz, J. & Zolman, E. (2017). Genetic assignment to stock of stranded common bottlenose dolphins in southeastern Louisiana after the Deepwater Horizon oil spill. *Endangered Species Research*, **33**, 221–234.

Stillfried, M., Fickel, J., Börner, K., Wittstatt, U., Heddergott, M., Ortmann, S., Kramer-Schadt, S. & Frantz, A.C. (2017). Do cities represent sources, sinks or isolated islands for urban wild boar population structure? (J. Frair, Ed.). *Journal of Applied Ecology*, **54**, 272–281.

c. Birds

Abou-Emera, O.K., Ali, U., Galal, A., El-Safty, S., Abdel-Hame, E.F. & Fathi, M.M. (2017). Evaluation of genetic diversity of naked neck and frizzle genotypes based on microsatellite markers. *International Journal of Poultry Science*, **16**, 118–124.

Canal, D., Roques, S., Negro, J.J. & Sarasola, J.H. (2017). Population genetics of the endangered Crowned Solitary Eagle (*Buteogallus coronatus*) in South America. *Conservation Genetics*, **18**, 235–240.

Chetverikova, R., Babushkina, O., Galkina, S., Shokhrin, V. & Bojarinova, J. (2017). Special case among passerine birds: long-tailed tits keep family bonds during migration. *Behavioral Ecology and Sociobiology*, **71**.

Domínguez, M., Tiedemann, R., Reboreda, J.C., Segura, L., Tittarelli, F. & Mahler, B. (2017). Genetic structure reveals management units for the yellow cardinal (*Gubernatrix cristata*), endangered by habitat loss and illegal trapping. *Conservation Genetics*.

Ely, C.R., Wilson, R.E. & Talbot, S.L. (2017). Genetic structure among greater white-fronted goose populations of the Pacific Flyway. *Ecology and Evolution*, **7**, 2956–2968.

He, K., Liu, H.-Y., Ge, Y.-F., Wu, S.-Y. & Wan, Q.-H. (2017). Historical gene flow and profound spatial genetic structure among golden pheasant populations suggested by multi-locus analysis. *Molecular Phylogenetics and Evolution*, **110**, 93–103.

LeBlanc, N.M., Stewart, D.T., Pálsson, S., Elderkin, M.F., Mittelhauser, G., Mockford, S., Paquet, J., Robertson, G.J., Summers, R.W., Tudor, L. & Mallory, M.L. (2017). Population structure of Purple Sandpipers (*Calidris maritima*) as revealed by mitochondrial DNA and microsatellites. *Ecology and Evolution*, **7**, 3225–3242.

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Szczys, P., Lamothe, K.A., Druzyaka, A., Poot, M.J.M., Siokhin, V. & van der Winden, J. (2017). Range-wide patterns of population differentiation of Eurasian Black Terns (*Chlidonias niger niger*) related to use of discrete post-nuptial staging sites. *Journal of Ornithology*, **158**, 365–378.