



Daniel W. Förster

CURRICULUM VITAE

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Research fields and interests

My research interests are mainly focused on genome evolution, molecular ecology, and conservation. My work involves a diverse range of study species, including felids, canids, ursids, ungulates, rodents, and amphibians; using ancient and archival specimens I am able to incorporate data about populations that are now extinct in the wild.

Research Experience and Education

Since 2018	Head of Carnivore Conservation Genomics (Evolutionary Genetics Dept) <i>Leibniz Institute for Zoo and Wildlife Research (IZW), Berlin, Germany</i>
2016-2017	Carnivore Genomics (Postdoc) <i>Leibniz Institute for Zoo and Wildlife Research (IZW), Berlin, Germany</i>
2011-2015	Developing and genotyping SNPs in rare European carnivores (Postdoc) <i>Leibniz Institute for Zoo and Wildlife Research (IZW), Berlin, Germany</i>
2009-2011	Chromosome Evolution and Speciation (Postdoc) <i>University of York, Biology Department, UK</i>
2002-2008	PhD in Genetics and Molecular Evolution <i>University of York, Biology Department, UK</i>
1998-2001	BSc in Genetics <i>University of York, Biology Department, UK</i>

Recent publications

◆ 2021 ◆

Paijmans JLA, Barlow A, Becker MS, Cahill JA, Fickel J, **Förster DW**, Gries K, Hartmann S, Havmøller RW, Henneberger K, Kern C, Kitchener AC, Lorenzen ED, Westbury MV, Mayer F, Obrien SJ, von Seth J, Sinding MHS, Spong G, Uphyrkina O, Wachter B, Dalén L, Bhak J, Manica A, Hofreiter M (accepted): African and Asian leopards are highly differentiated at the genomic level. CURR BIOL

◆ 2020 ◆

Kunde MN, Martins RF, Premier J, Fickel J, **Förster DW** (2019): Population and landscape genetic analysis of the Malayan sun bear *Helarctos malayanus*. CONSERV GENET. Epub ahead of print. doi:10.1007/s10592-019-01233-w

Derežanin L, Fickel J, **Förster DW** (2020): The complete mitochondrial genome of the meerkat (*Suricata suricatta*) and its phylogenetic relationship with other feliform species. MITOCHOND DNA Part B5, 1100-1101. doi:10.1080/23802359.2020.1726221

Kunde MN, Martins RF, Premier J, Fickel J, **Förster DW** (2020): Population and landscape genetic analysis of the Malayan sun bear *Helarctos malayanus*. CONSERV GENET **21**, 123-135. doi:10.1007/s10592-019-01233-w

◆ 2019 ◆

Seeber PA, McEwen GK, Löber U, **Förster DW**, East ML, Melzheimer J, Greenwood AD (2019), Terrestrial mammal surveillance using hybridization capture of environmental DNA from African waterholes. Mol Ecol Resour. 2019 doi:10.1111/1755-0998.13069

Stöck M, Fakharzadeh F, Kuhl H, Rozenblut-Kościsty B, Leinweber S, Patel R, Ebrahimi M, Voitel S, Schmidtler JF, Kami HG, Ogielska M, **Förster DW** (2019): Shedding Light on a Secretive Tertiary urodelean Relict: Hynobiid salamanders (*Paradactylodon persicus sl*) from Iran, Illuminated by Phylogeographic, Developmental and Transcriptomic Data. Genes 10(4), 306.

Mengülluoğlu D, Fickel J, Hofer H, **Förster DW** (2019): Non-invasive faecal sampling reveals spatial organization and improves measures of genetic diversity for the conservation assessment of territorial species: Caucasian lynx as a case species. PLoS ONE 14(5), e0216549.

Paijmans JLA, Fortes GG, **Förster DW** (2019): Application of solid-state capture for the retrieval of small-to-medium sized target loci from ancient DNA. In: Ancient DNA: Methods and Protocols (Second Edition). Methods in Molecular Biology, vol 1963. B. Shapiro, Hofreiter M, Soares AER, Heintzman P, Paijmans JLA, Barlow A (eds). Humana Press, USA, 129-139.

Martins RF, Kampmann ML, **Förster DW** (2019): Sequencing Library Preparation from Degraded Samples for Non-illumina Sequencing Platforms. In: Ancient DNA: Methods and Protocols (Second Edition). Methods in Molecular Biology, vol 1963. Shapiro B, Hofreiter M, Soares AER, Heintzman P, Paijmans JLA, Barlow A (eds). Humana Press, USA, 85-92.

◆ 2018 ◆

Ambarl H, Mengülluoğlu D, Fickel J and **Förster DW** (2018): Population genetics of the main population of brown bears in southwest Asia. PeerJ. doi: 10.7717/peerj.5660

Förster DW, Bull JK, Lenz D, Autenrieth M, Pajmans LAJ, Kraus RHS, Nowak JC, Bayerl H, Kuehn R, Saveljev AP, Sindičić M, Hofreiter M, Schmidt K, Fickel J (2018): Targeted resequencing of coding DNA sequences for SNP discovery in nonmodel species. *Mol Ecol Resour.*18(6), 1356–1373.

Pajmans JLA, Barlow A, **Förster DW**, Henneberger K, Meyer M, Nickel B, Nagel D, Worsøe Havmøller R, Baryshnikov GF, Joger U, Rosendahl W, Hofreiter M (2018): Historical biogeography of the leopard (*Panthera pardus*) and its extinct Eurasian populations. *BMC Evolutionary Biology*, 18-156.

◆ 2017 ◆

Bayerl H, Kraus RHS, Nowak C, **Förster DW**, Fickel J, Kuehn R (2017): Fast and cost-effective single nucleotide polymorphism (SNP) detection in the absence of a reference genome using semideep next generation Random Amplicon Sequencing (RAMseq). *Molecular Ecology Resources* 18: 107-117.

Patel RP, Wutke S, Lenz D, Mukherjee S, Ramakrishnan U, Veron G, Fickel J, Wilting A, **Förster DW** (2017): Genetic structure and phylogeography of the Leopard Cat (*Prionailurus bengalensis*) inferred from mitochondrial genomes. *Journal of Heredity* 108: 349-360.

Giménez MD, **Förster DW**, Jones EP, Jóhannesdóttir F, Gabriel SI, Panithanarak T, Scascitelli M, Merico V, Garagna S, Searle JB, Hauffe HC (2017): A half-century of studies on a chromosomal hybrid zone of the house mouse. *Journal of Heredity* 108: 25-35.

Martins RF, Fickel J, Le M, Nguyen T, Nguyen HM, Timmins R, Gan HM, Rovie-Ryan JJ, Lenz D, **Förster DW**, Wilting A (2017): Phylogeography of red muntjacs reveals three distinct mitochondrial lineages. *BMC Evolutionary Biology* 17:34.

Patel RP, Lenz D, Kitchener AC, Fickel J, **Förster DW**, Wilting A (2017): Threatened but understudied – supporting conservation by understanding the genetic structure of the flat-headed cat. *Conservation Genetics* 18: 1423-1433.

◆ 2016 ◆

Bull JK, Heurich M, Saveljev AP, Schmidt K, Fickel J, **Förster DW** (2016): The effect of reintroductions on the genetic variability in Eurasian lynx populations: the cases of Bohemian–Bavarian and Vosges–Palatinian populations. *Conservation Genetics* 17: 1229-1234.

Förster DW, Jones EP, Jóhannesdóttir F, Gabriel SI, Giménez MD, Panithanarak T, Hauffe HC, Searle JB (2016): Genetic differentiation within and away from the chromosomal rearrangements characterising hybridising chromosomal races of the western house mouse (*Mus musculus domesticus*). *Chromosome Research* 24: 271-280.

Pajmans JLA, Fickel J, Courtiol A, Hofreiter M, **Förster DW** (2016): Impact of enrichment conditions on cross-species capture of fresh and degraded DNA. *Molecular Ecology Resources* 16: 42-55.

Patel RP, **Förster DW**, Kitchener AC, Rayan MD, Mohamed SW, Werner L, Lenz D, Pfestorf H, Kramer-Schadt S, Radchuk V, Fickel J, Wilting A (2016): Two species of Southeast Asian cats in the genus *Catopuma* with diverging histories: an island endemic forest specialist and a widespread habitat generalist. *Royal Society Open Science* 3: 160350

Wilting A, Patel RP, Pfestorf H, Kern C, Sultan K, Ario A, Penaloza F, Kramer-Schadt S, Radchuk V, **Förster DW**, Fickel J (2016): Evolutionary history and conservation significance of the Javan leopard *Panthera pardus melas*. *Journal of Zoology* 299: 239-250.

Didion JP, Morgan AP, Yadgary L, Bell TA, McMullan RC, Solorzano LO, Britton-Davidian J, Bult CJ, Campbell KJ, Castiglia R, Ching YH, Chunco AJ, Crowley JJ, Chesler EJ, **Förster DW**, French JE, Gabriel SI, Gatti DM, Garland T, Giagia-Athanasopoulou EB, Giménez MD, Grize SA, Gündüz İ, Holmes A, Hauffe HC, Herman JS, Holt JM, Hua K, Jolley WJ, Lindholm AK, López-Fuster MJ, Mitsainas G, Mathias ML, McMillan L, Ramalhinho MG, Rehermann B, Rosshart SP, Searle JB, Shiao MS, Solano E, Svenson KL, Thomas-Laemont P, Threadgill DW, Ventura J, Weinstock GM, Pomp D, Churchill GA, Pardo-Manuel de Villena F (2016): R2d2 drives selfish sweeps in the house mouse. *Molecular Biology and Evolution* 33: 1381-1395.

Kraus RHS, VonHoldt B, Cocchiararo B, Harms V, Bayerl H, Kühn R, **Förster DW**, Fickel J, Roos C, Nowak C (2015): A single-nucleotide polymorphism-based approach for rapid and cost-effective genetic wolf monitoring in Europe based on noninvasively collected samples. *Molecular Ecology Resources* 15: 295-305.

Stakeholder Publications

Heurich M, Magg N, Fickel J, **Förster DW**, Müller J (2016): Gründe für die Stagnation der Luchspopulation. *Forst Praxis* **2/16**, 19-21.

Fickel J, **Förster DW** (2016): Langfristige Perspektiven für den Luchs. *ÖKOJAGD* **3/16**. 62-63.