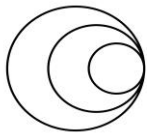


**Hybrid Conference Programme**

Start (GMT)	Finish (GMT)	Presenter details
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**Wednesday, 30 November 2022**

<b>11:30</b>	<b>12:50</b>	<b>Registration, lunch and networking</b>
12:30	12:45	<i>Briefing for Keynote &amp; Session 1 speakers, chair, moderator &amp; committee - Auditorium</i>
<b>12:50</b>	<b>13:00</b>	<b>Welcome</b>
		<p><b>Scientific Programme Committee:</b>  <a href="#">Federica Di Palma, Genome British Colombia, Canada</a>  <a href="#">Klaus-Peter Koepfli, Smithsonian Conservation Biology Institute, USA</a>  <a href="#">Beth Shapiro, UCSC, USA</a>  <a href="#">Dario Valenzano, Leibniz Institute on Aging, Germany</a></p>
<b>13:00</b>	<b>14:00</b>	<b>Keynote 1</b>
		<p><i>Chair: Beth Shapiro</i>  <i>Moderator: Dario Valenzano</i></p> <p>Conservation Genomics: innovations, applications &amp; where to next?  <a href="#">Carolyn Hogg, University of Sydney, Australia</a></p>
14:00	14:10	Comfort break
<b>14:10</b>	<b>15:40</b>	<b>Session 1: New technologies for applying genomic to biodiversity conservation</b>
		<p><i>Chair: Beth Shapiro</i>  <i>Moderator: Dario Valenzano</i></p>
14:10	14:40	Why control grey squirrel numbers through gene drive technology <a href="#">Bruce Whitelaw, University of Edinburgh, UK</a>
14:40	14:55	Benchmarking relatedness estimates and SNP panel design for conservation toolkits <i>Ellie Armstrong, Washington State University, USA</i>
14:55	15:10	New opportunities offered by genomics for the conservation of the Asian elephant: from captivity to the wild <i>Mirte Bosse, VU Amsterdam &amp; Wageningen University, The Netherlands</i>
15:10	15:25	Investigating hybridisation between living and extinct Galapagos giant tortoises to inform a unique captive breeding programme <i>Rachel Gray, Newcastle University, UK</i>
15:25	15:40	Implications For conservation: A population genomic study of short-finned pilot whales ( <i>Globicephala macrorhynchus</i> ) in the Caribbean Sea <i>Nicolas Restrepo Garzon, Universidad de los Andes, Colombia - <u>VIRTUAL</u></i>
15:40	16:10	Refreshment break



15:50 16:05 Briefing for Session 2 speakers, chair & moderator - Auditorium

**16:10 18:10 Session 2: Detecting adaptation in populations**

*Chair: Klaus-Peter Koepfli*

*Moderator: Beth Shapiro*

16:10 16:40 Genomic signals of adaptation after a population range expansion

[Laurent Excoffier, University of Bern, Switzerland](#)

16:40 17:10 Evolution of regulatory networks associated with traits of cichlid phenotypic diversity

[Federica Di Palma, University of East Anglia, UK -VIRTUAL](#)

17:10 17:40 Conservation genomics and the role of museums

[Jan Barnes, Natural History Museum, UK](#)

17:40 17:55 Local genetic adaptation in chimpanzees

*Harrison Ostridge, University College London, UK*

17:55 18:10 Resilience and adaptation of grey wolves over 100,000 years

*Anders Bergström, The Francis Crick Institute, UK*

18:15 21:00 Dinner

18:15 Bar open (card payments only)

**Thursday, 1 December 2022**

07:30 09:00 Breakfast

09:15 09:30 Briefing for Session 3 speakers, chair & moderator - Auditorium

**09:30 11:15 Session 3: New Technologies - eDNA**

*Chair: Beth Shapiro*

*Moderator: Dario Valenzano*

09:30 10:00 eDNA sampling and analysis as a tool for population genetics and genomics in conservation

[Marta de Barba, University of Ljubljana, Slovenia](#)

10:00 10:30 Uncovering Population Information from Environmental DNA

[Kristy Deiner, ETH Zurich, Switzerland](#)

10:30 11:00 Ancient environmental DNA to track the history of ecosystems and populations

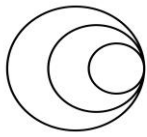
[Laura Epp, Konstanz, Germany](#)

11:00 11:15 A genome-wide analysis of Late Pleistocene black bears using environmental genomics

*Bianca De Sanctis, University of Cambridge, UK*

11:15 11:45 Refreshment break

11:30 11:45 Briefing for Session 4 speakers, chair & moderator - Auditorium



**11:45 13:15 Session 4: Linking genotypes to phenotypes for conservation**

*Chair: Dario Valenzano*

*Moderator: Beth Shapiro*

- 11:45 12:15 Quantitative traits, genomics and conservation  
[\*Josephine Pemberton, Unniversity of Edinburgh, UK\*](#)
- 12:15 12:45 Understanding the impact of mutational load in ex-situ populations of a threatened species  
[\*Klaus-Peter Koepfli, Smithsonian Conservation Biology Institute, USA\*](#)
- 12:45 13:00 Decomposing Phenotypes via Probabilistic Programming in Kākāpō  
*Joseph Guhlin, Genomics Aotearoa / University of Otago, New Zealand - **VIRTUAL***
- 13:00 13:15 What does the occurrence of rare variants mean for the well-being of populations?  
*Vinay Sagar, National Centre for Biological Sciences (TIFR), India*

13:15 14:30 Lunch

14:15 14:30 *Briefing for Session 5 speakers, chair & moderator - Auditorium*

**14:30 16:00 Panel Discussion - Translating research into conservation efforts**

*Chair: Beth Shapiro*

*Mark Blaxter, Wellcome Sanger Institute, UK*

*Carolyn Hogg, University of Sydney, Australia*

*Klaus-Peter Koepfli, Smithsonian Conservation Biology Institute, USA*

*Dario Valenzano, Leibniz Institute on Aging, Germany*

16:00 16:30 Refreshment break

**16:30 17:00 Lightning talks for posters**

*Chair: Klaus-Peter Koepfli*

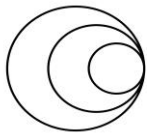
**17:00 18:30 Poster session**

*17:00-17:45 - odd numbered posters*

*17:45-18:30 - even numbered posters*

18:30 21:00 Dinner

18:30 Bar open (card payments only)



**Friday, 2 December 2022**

07:30 09:00 Breakfast

09:15 09:30 Briefing for Session 6 speakers, chair & moderator

**09:30 11:15 Session 5: Detecting and understanding the effects of deleterious variation**

*Chair: Klaus-Peter Koepfli*

*Moderator: Dario Valenzano*

09:30 10:00 Quantifying dominance of deleterious mutations & implications for conservation biology  
[Kirk Lohmueller, UCLA, USA](#)

10:00 10:30 Genetic load in the age of genomics  
[Lukas Keller, University of Zurich, Switzerland](#)

10:30 10:45 Genetic load in the Apennine brown bear: testing deleterious variants in cell cultures  
*Roberto Biello, University of Ferrara, Italy*

10:45 11:00 Uncovering deleterious mutations in the non-coding genome of the Black-footed ferret, a severely endangered species  
*Rebecca Shaw, Earlham Institute, UK*

11:00 11:15 High realized genetic load in the Scandinavian wolf population  
*Linnéa Smeds, Uppsala University, Sweden*

11:15 11:45 Refreshment break

11:30 11:45 Briefing for Keynote, chair, moderator & committee

**11:45 12:45 Keynote 2**

*Chair: Klaus-Peter Koepfli*

*Moderator: Beth Shapiro*

Conservation genomics of wild carnivorans

[Eduardo Eizirik, Pontifical Catholic University of Rio Grande do Sul, Brazil](#)

**12:45 13:00 Closing remarks and prize presentation**

**Scientific Programme Committee:**

[Federica Di Palma, Genome British Columbia, Canada](#)

[Klaus-Peter Koepfli, Smithsonian Conservation Biology Institute, USA](#)

[Beth Shapiro, UCSC, USA](#)

[Dario Valenzano, Leibniz Institute on Aging, Germany](#)

13:00 13:50 Lunch

13:50 Coach departures for Stansted and Heathrow airports

14:00 Coach departures for Cambridge train station and city centre