

## **DNA Working Group Meeting**

16 & 17 November 2016

## South Hall Complex, Pollock Halls University of Edinburgh, Holyrood Park Road, Edinburgh <u>EH16 5AY</u>

Hosted by the Scottish Environment Protection Agency

Agenda – day 1				
11:00	Registration opens			
12:00-12:45	Lunch			
12:45-12:55	Welcome & introduction	Willie Duncan		
	Session Chair: Bernd Hänfling, University of Hull			
12:55-13:40	International cooperation & collaboration			
12:55-13:20	<ul> <li>Biomonitoring 2.0: implementing DNA meta-barcoding as a tool for research and monitoring in river ecosystems in Canada</li> </ul>	Donald Baird		
13:20-13:40	The EU COST Action DNAqua-Net: aims, scope, participation	Florian Leese		
13:40-14:40	Operational role out			
13:40-13:55	Developing protocols and standards - what are our options?	Willie Duncan		
13:55-14:10	Towards a global biodiversity monitoring using eDNA in aquatic ecosystems	Alice Valentini		
14:10-14:25	<ul> <li>Comparison of capture and storage methods for aqueous macrobial eDNA - advantage of enclosed filters</li> </ul>	Micaela Hellström		
14:25-14:40	Discussion - operational deployment challenges and priorities			
14:40-15:05	Coffee			

Session Chair tbc				
15:05-15:35	NERC highlight projects - an overview and early findings			
15:05-15:20	LOFRESH- Understanding the ecological relevance of eDNA in freshwater lotic ecosystems	Si Creer		
15:20-15:35	SeaDNA - Assessing marine biodiversity and structure using environmental DNA: from ground truthing to food web structure and stability	Stefano Mariani		
15:35-17:20	Method development - aquatic.  Speed talks (10 minute presentations, 2 minutes of questions)  Fate, transportation and application of eDNA in aquatic ecosystems	Elvira Mächler		
	<ul> <li>Development of DNA-based metagenomic methodologies for seabed monitoring and aquaculture management</li> </ul>	Tom Wilding		
	<ul> <li>Primers for detecting marine fish using eDNA metabarcoding</li> </ul>	Owen Wangensteen		
	eDNA - detection of non-native and invasive alien species	Rosetta Blackman		
	<ul> <li>An environmental DNA approach for elasmobranch assessment and monitoring</li> </ul>	Judith Bakker		
	<ul> <li>Using DNA metabarcoding to model trophic interactions of the Dikerogammarus villosus and Harmonia axyridis in the UK</li> </ul>	Marco Benucci		
	Development of eDNA techniques for management and conservation of Irish freshwater animal species	Luca Mirimin		
	Great Crested Newt Detectives project; Detection of Great Crested Newts in Scotland by eDNA sampling	Peter Minting		
17:20 - 17:30	Discussion			
17:30	Close - day 1			
19:30 for 20:00	Dinner - Mercure Hotel Princes Street, Edinburgh			

Agenda – day 2  Session Chair: Si Creer University of Bangor Method Developments - Non-Aquatic				
	A toe in the water- conservation agency applications	Keith Porter		
	Pollinator research in Wales	Andrew Lucas		
	<ul> <li>Metabarcoding of soil mesofauna across a soil chronosequence</li> </ul>	Daniel Read		
	<ul> <li>Using molecular genetics to understand grass species pollen deposition</li> </ul>	Georgina Brennan		
	Next Generation Pollinator Monitoring	Cuong Tang		
10:00-10:50	Quantification and Understanding Error and Sampling Bias  Speed talks (10 minute presentations, 2 minutes of questions)			
10:00-10:50	Speed talks (10 minute presentations, 2 minutes of questions)  • A comparison of uncertainty in light microscope and NGS	Martyn Kelly		
	analyses of benthic diatoms	Wateyii Keny		
	<ul> <li>Fishing for traces: the efficiency of metabarcoding in detecting and quantifying freshwater fish species in still and running waters</li> </ul>	Rein Brys		
	Influences on seasonal changes in eDNA concentration	Andrew Buxton		
	The effect of environment DNA capture method on aquaculture fish ponds quantification via meta-barcoding analysis	Joe, Jianlong Li		
10:50-11:15	Coffee	,		
Quantification	and Understanding Error and Sampling Bias (continued)			
11:15-12:15	Speed talks (10 minute presentations, 2 minutes of questions)			
	Temporal eDNA analyses of fish community composition in Lake Windermere	Lori Lawson- Handley		
	<ul> <li>Evaluating metagenomics vs. metabarcoding for diversity and biomass estimations in environmental samples of macroinvertebrates</li> </ul>	Iliana Bista		
	Fish metabarcoding from eDNA of lake water samples: developments in laboratory methods and data analysis	Harriet Johnson		

	Persistence of environmental DNA in experimental river systems: implications for molecular biodiversity assessment	Mat Seymour
	<ul> <li>UK freshwater pond monitoring: an evaluation of eDNA metabarcoding for detection of vertebrate communities using great crested newt (Triturus cristatus) eDNA</li> </ul>	Lynsey Harper
	Session Chair: Willie Duncan, SEPA Technological Advances	
12:15-12:45		
12:15-12:30	Onsite DNA sequencing and automated species classification for environmental studies	Tomas Fitzgerald
12:30-12:45	Defining "rare" in Environmental DNA: an approach to evaluate mock community sensitivity using Oxford Nanopore and Illumina technology	Peter Schum
12:45-13:30	Lunch	
	Session Chair: Doug Wilson, Environment Agency Open Discussion	
13:30-14:30	Questions and issues from the morning sessions	
	Priorities for action	
	Moving towards operational delivery and development challenges	
	Introducing Standards- Good Idea/Bad Idea	
	Improving current applications	
	Identifying new applications	
	Quantification/understanding error	
	Technological advances	
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