

detection of degraded eDNA:

qPCR **vs** metabarcoding **vs** metagenomic

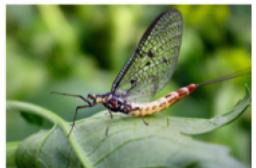
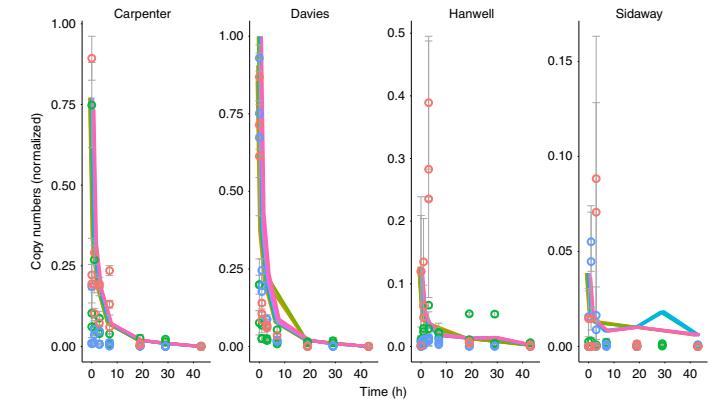
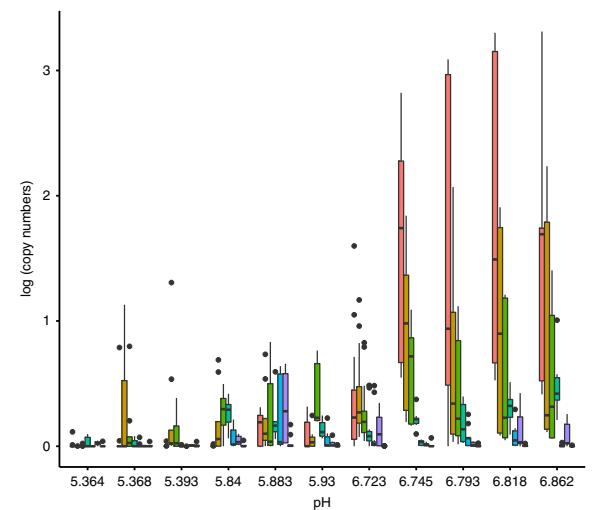
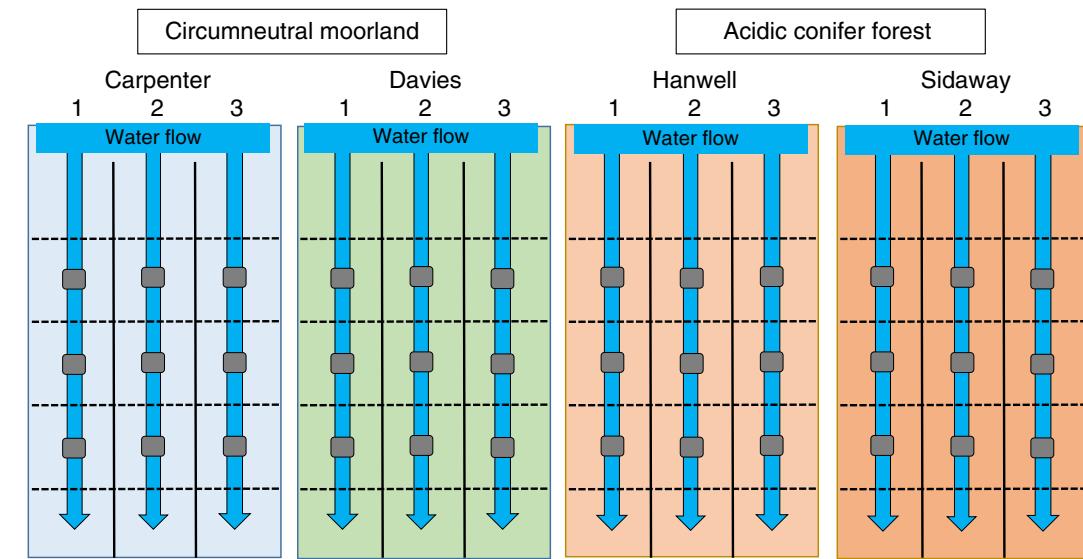
ARTICLE

DOI: 10.1038/s42003-017-0005-3

OPEN

Acidity promotes degradation of multi-species environmental DNA in lotic mesocosms

Mathew Seymour¹, Isabelle Durance², Bernard J. Cosby³, Emma Ransom-Jones⁴, Kristy Deiner⁵, Steve J. Ormerod^{1,6}, John K. Colbourne⁶, Gregory Wilgar¹, Gary R. Carvalho¹, Mark de Bruyn^{1,7}, François Edwards^{1,8}, Bridget A. Emmett³, Holly M. Bik^{1,9} & Simon Creer¹

*Ephemera danica**Daphnia magna**Anguilla anguilla*

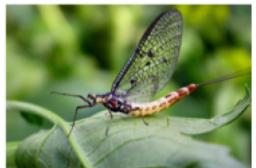
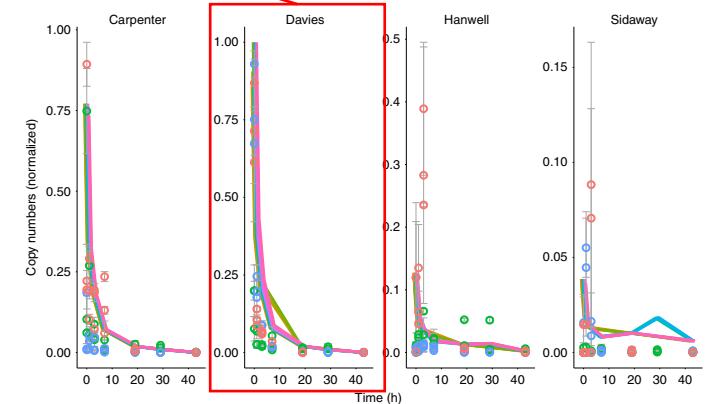
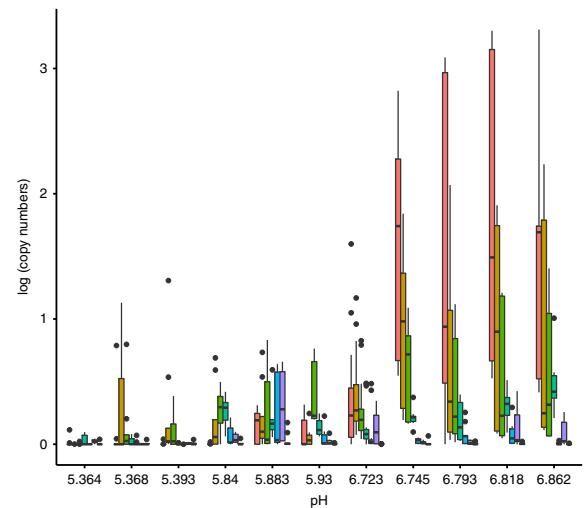
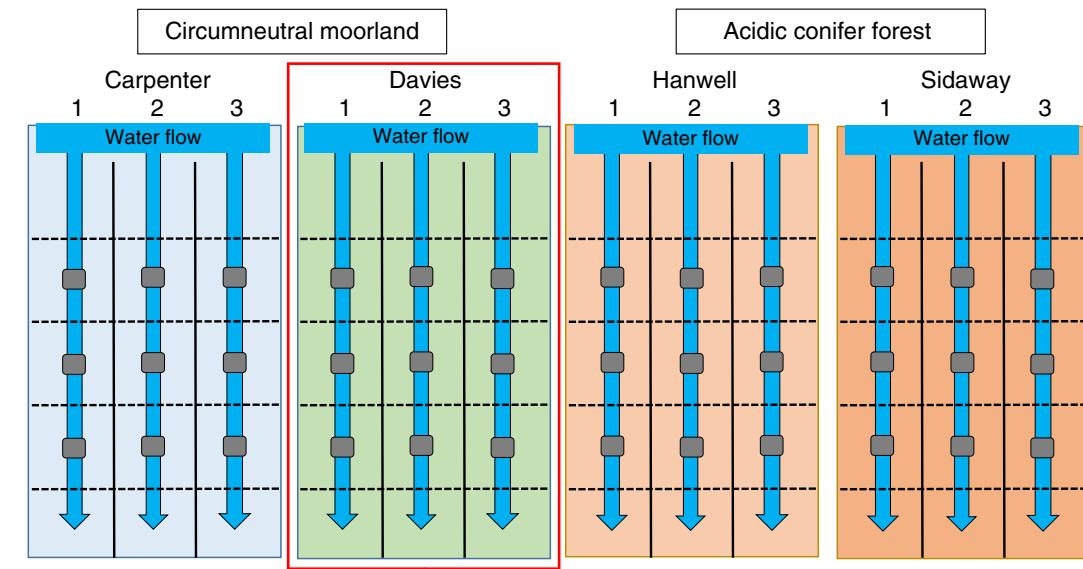
ARTICLE

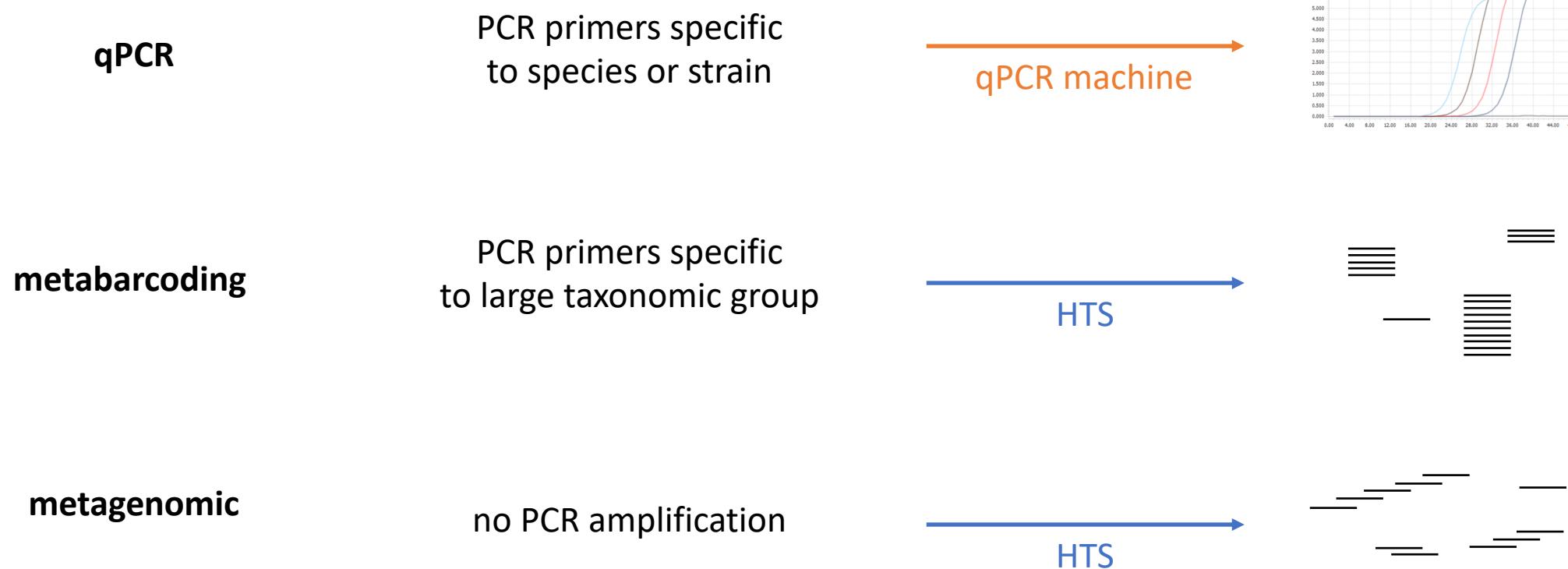
DOI: 10.1038/s42003-017-0005-3

OPEN

Acidity promotes degradation of multi-species environmental DNA in lotic mesocosms

Mathew Seymour¹, Isabelle Durance², Bernard J. Cosby³, Emma Ransom-Jones⁴, Kristy Deiner⁵, Steve J. Ormerod^{1,6}, John K. Colbourne⁶, Gregory Wilgar¹, Gary R. Carvalho¹, Mark de Bruyn^{1,7}, François Edwards^{1,8}, Bridget A. Emmett³, Holly M. Bik^{1,9} & Simon Creer¹

*Ephemera danica**Daphnia magna**Anguilla anguilla*



qPCR

- _ 7 time points (0h -> 29h)
- _ 27 replicates per time point

metabarcoding

- _ 3 time points (1, 7 and 29h)
- _ 9 replicates per time point
- _ COI and 18S

metagenomic

- _ 3 time points (1, 7 and 29h)
- _ 3 replicates per time point



	μ	σ	μ	σ	μ	σ
T 1 (n = 27)	1	0.3	6.3	5.2	54.4	17
T 7 (n = 27)	0.4	0.4	4	5.4	5	1.3
T 29 (n = 27)	0.2	0.8	1.6	2.8	0.3	0.1

- clustering at 97% similarity
- samples rarefied at 45,000 reads



	μ	σ	μ	σ	μ	σ
T 1 (n = 4)	2.3	2.9	0	0	0	0
T 7 (n = 7)	0	0	0	0	0	0
T 29 (n = 6)	0	0	0	0	0	0

- clustering at 97% similarity
- samples rarefied at 65,000 reads



	μ	σ	μ	σ	μ	σ
T 1 (n = 9)	15.5	12.6	26.1	22.4	1365.4	753.9
T 7 (n = 9)	0	0	10.6	17.1	156.4	37
T 29 (n = 9)	0	0	0.1	2.2	3.3	2.6

- read mapping using Bowtie2
- out of 30,000,000 reads



	μ	σ	μ	σ	μ	σ
T 1 (n = 3)	3.7	1.2	21.7	27.1	144	21.2
T 7 (n = 3)	0	0	26	27.7	17	9.4
T 29 (n = 3)	0	0	439.3	565.6	1.7	1.2
Neg CT (n = 3)	0	0	40.3	26.7	0	0

- read mapping using Bowtie2
- out of 30,000,000 reads



	μ	σ	μ	σ	μ	σ
T 1 (n = 3)	1193.3		757.3		71135.7	
T 7 (n = 3)	709		2148.7		59074.7	
T 29 (n = 3)	1447		47247.3		161420	
Neg CT (n = 3)	40.7		3010.7		182.7	

- read mapping using Bowtie2
- out of 30,000,000 reads



all CDS
(n = 19,557)

	μ	σ
T 1 (n = 3)	16461.3	2595.6
T 7 (n = 3)	13670.7	3447.3
T 29 (n = 3)	18146.7	12507.2
Neg CT (n = 3)	30	20.1

EDAN018988-RA	18956	eukaryote (?)
EDAN011676-RA	14878	bacteria
EDAN019233-RA	7007	algae
EDAN018842-RA	5302	algae
EDAN011677-RA	4826	eukaryote (?)

- read mapping using Bowtie2
- out of 30,000,000 reads



	all CDS (n = 19,557)		filtered CDS (n = 12,259)	
	μ	σ	μ	σ
T 1 (n = 3)	16461.3	2595.6	146.3	184.3
T 7 (n = 3)	13670.7	3447.3	3.3	1.9
T 29 (n = 3)	18146.7	12507.2	3.3	2.4
Neg CT (n = 3)	30	20.1	0	0

detection of degraded eDNA:

metabarcoding

qPCR = COI >> 18S = metagenomic

	metabarcoding	qPCR	18S	metagenomic
1 h	✓	✓	✗	✗
7 h	✓	✓	✗	✗
29 h	✓	✗	✗	✗

-> the most specific approaches are the most sensitive ones