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Can telomere length be estimated from fish scales to inform on individual stress?

Gaëlle Brahy | Aurélie Manicki | Maïka Minjou | François Guéraud | Sylvie Oddou-Muratorio | Jacques Labonne
 UMR ECOBIOP 1224, EDENE, Université de Pau et des Pays de l'Adour. 64310, Saint-Pée-sur-Nivelle, France

Telomeres are non coding repetitive sequences of TTAGGG, between 1000 and 30 000 base pairs. They are expectedly shortening with each cell division, individual age and oxidative stress. Relative telomere length (RTL) is hence used as an indicator of stress in many taxa.

Various types of fish tissues have been used to carry out telomere length analysis, but not yet fish scales. Scale sampling is low invasive, cost and storage-effective, and scale collections are widely available databanks. Here we explore the potential for scale collections to provide (1) estimation of RTL, and (2) information on stress.

1. Samples and data

INRAE-GISED
Salmo trutta
 3 populations
 3 age classes
 198 individuals

PRELEVEMENT D'ÉCAILLES

INRAE-GISED
 S.M.A. Hydrobiologie
 S.M.A. Pisciculture
 Écologie - Pisciculture

ESPÈCE: *Salmo trutta* DATE: 12/01/2024
 LIEU DE CAPTURE: *147*
 LONGUEUR FOURCHE: *147*
 PÈSE: *147*
 SEXE (Mâle ou femelle): *SMAS*
 MARQUE: *SMAS*
 ANNEE: *SMAS*
 AGE: *SMAS*

2. Fish scale sampling: optimization for DNA extraction

Mucus
 Scales
 Scales + Mucus
 Half (Scales + Mucus)

Test a: type of material
 Test b: amount of material

3. Individual RTL estimation through qPCR

Principle

2 ng of purified DNA material is used for qPCR

Long telomeres → qPCR Time → Low C_t value
 Short telomeres → ++qPCR Time → High C_t value

Threshold fluorescence

Formula

$$RTL = \frac{E_{telo} \Delta C_{t_{telo}}}{E_{ref} \Delta C_{t_{ref}}}$$

Where $E =$ qPCR efficiency value
 $\Delta C_t = C_{t_{calibrator}} - C_{t_{focal}}$
 Ref = reference gene (here, β -actin)

Cawthon, 2002; Naslund et al., 2015

4. Results

Fish scale collection: most efficient approach

Test a: type of material
 Test b: amount of material

Heterogeneous relationship between amount of material and [DNA] obtained

5. Take home message

- Greater DNA concentrations are obtained when both **mucus and scales** are used
- Amount of available material does not limit DNA extraction
- **RTL can be estimated through qPCR from scale material**
- Intra-individual variability in RTL estimation calls for tailored statistical approach
- Our results open a new opportunity to **valorise scale collections**
- There is a **potential to understand RTL variation with stress**

RTL in 3 populations, 3 age classes

Chateau Nord Studer

n = number of individuals.

Population: Chateau Nord Studer

2 replicates per individual
 106 (53%) individuals with a C_t difference between replicates < 0,5
 165 (83%) individuals with a C_t difference between replicates < 1

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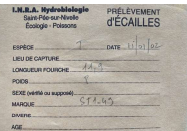
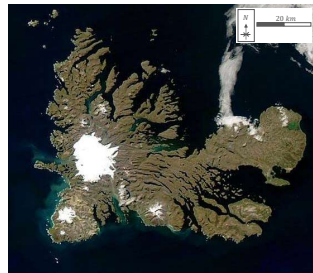
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1. Samples and data



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4. Individual RTL estimation through qPCR: formula

$$RTL = \frac{E_{telo} \Delta C_{t_{telo}}}{E_{ref} \Delta C_{t_{ref}}}$$

Where

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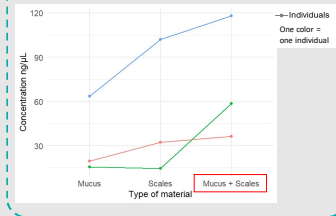
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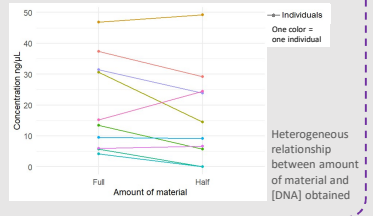
5. Results

Fish scale collection: most efficient approach

Test a: type of material

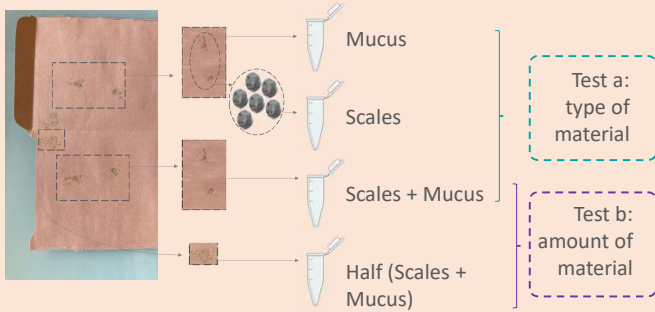


Test b: amount of material



Heterogeneous relationship between amount of material and [DNA] obtained

2. Fish scale sampling: optimization for DNA extraction

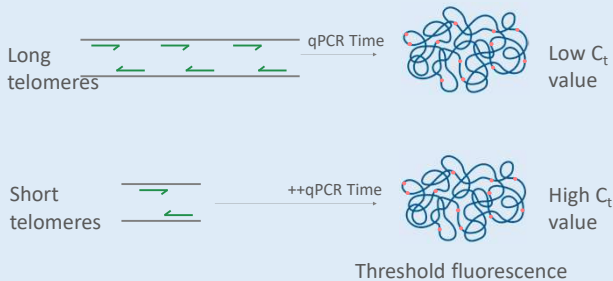


Test a: type of material

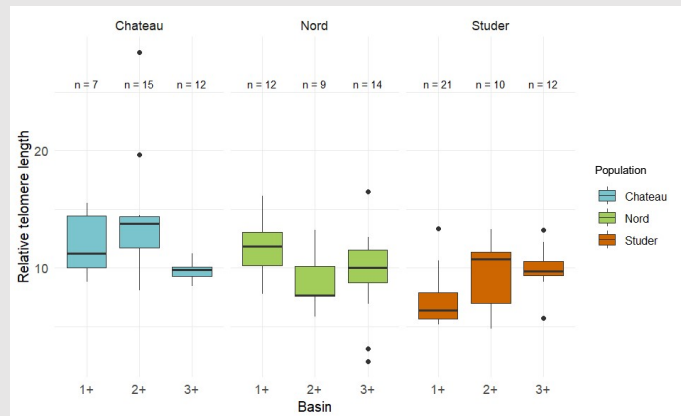
Test b: amount of material

3. Individual RTL estimation through qPCR: principle

2 ng of purified DNA material is used for qPCR



RTL in 3 populations, 3 age classes



2 replicates per individual

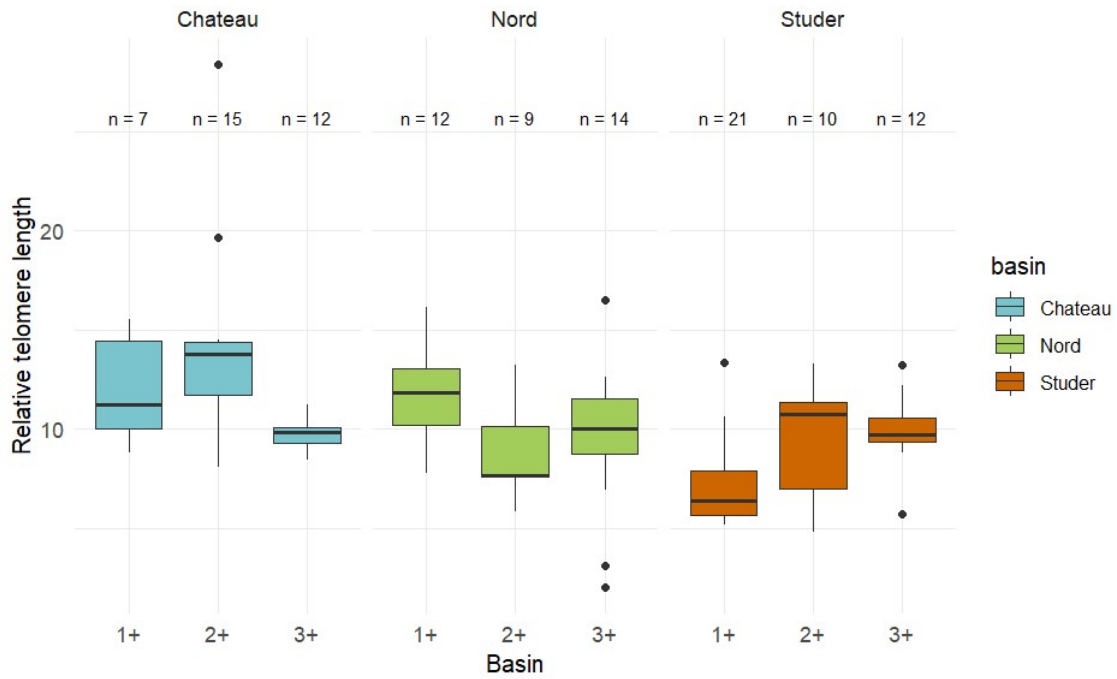
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diff entre réplcats <0.5



diff entre réplcats <1

