



Genome size estimation in amphibians through Real-Time PCR

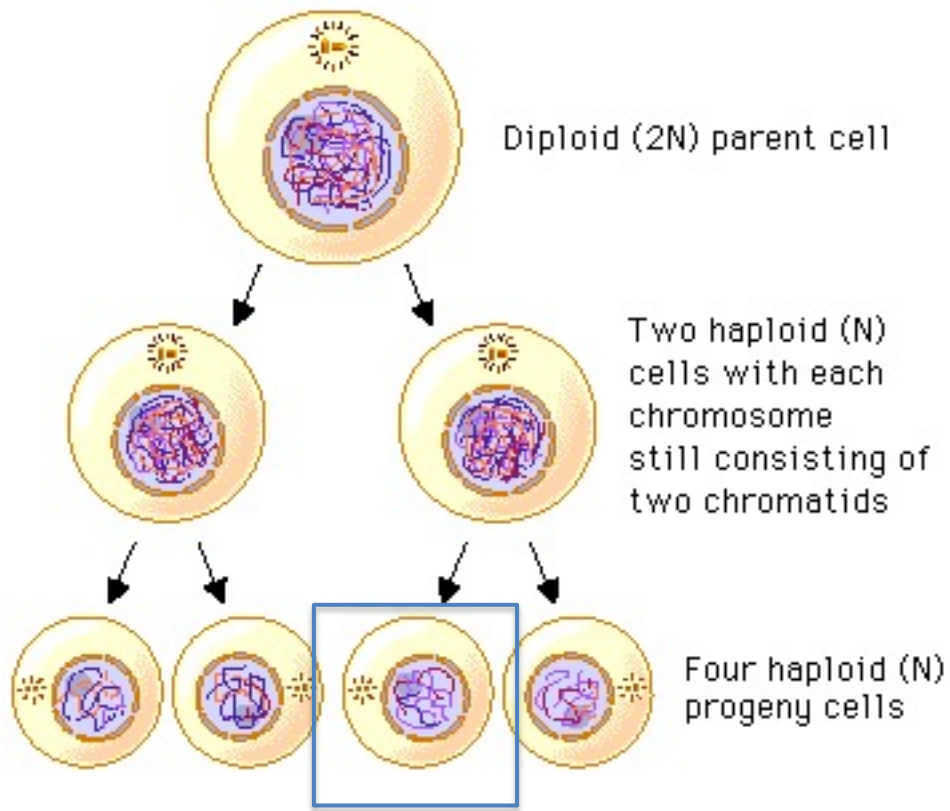
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SEVINOMICS Spring Meeting



March 16th 2016

The Basis of Genome Size



Genome size is the total amount of DNA contained within one copy of a single genome



C-value: mass (in picograms) of DNA per haploid nucleus

Why should anyone care about genome size?

Genome size is a major consideration when choosing targets for complete genome sequencing projects



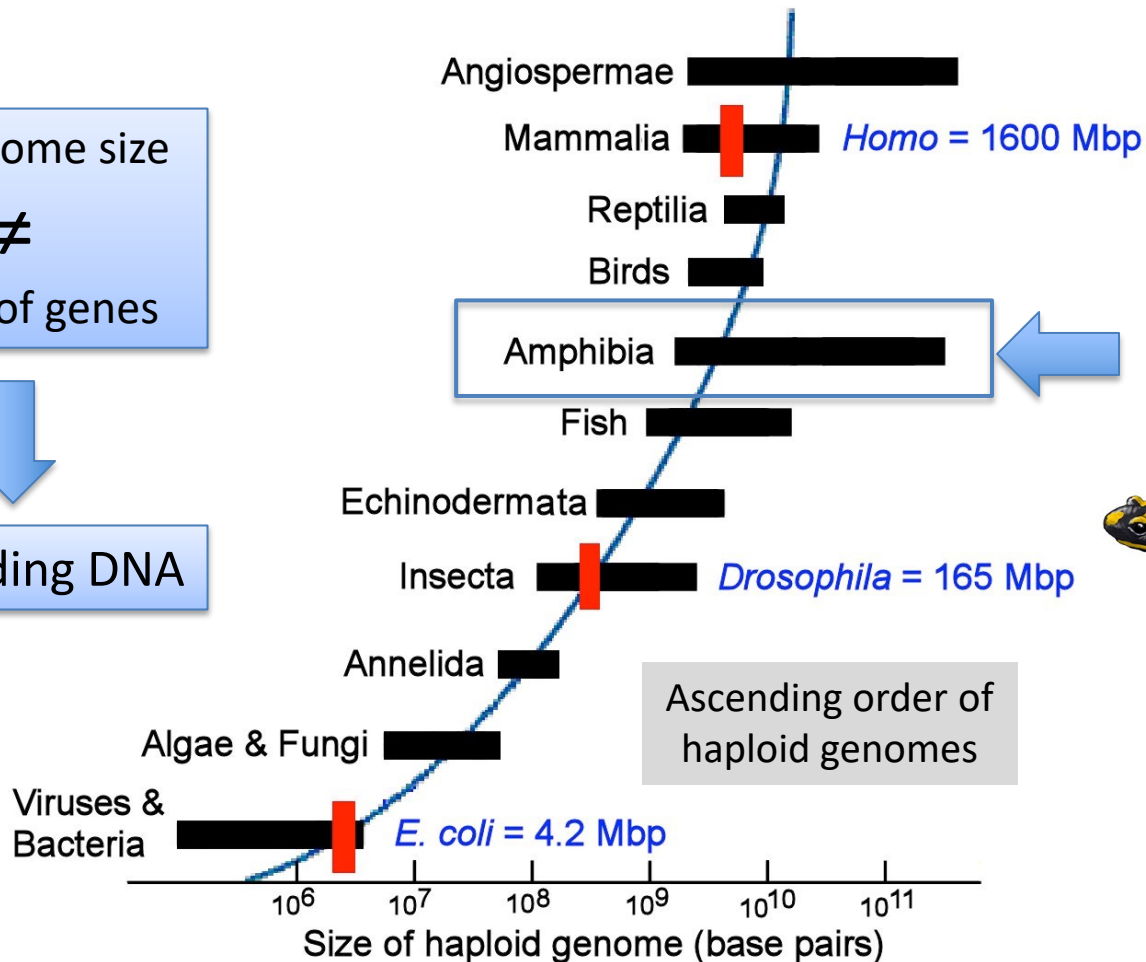
- Mapping
- Construction libraries
- Reading the sequence of nucleotides
- Reassembling the individual sequenced fragments

The C-value Enigma

(+) Genome size
 \neq
(+) N^o of genes



Noncoding DNA

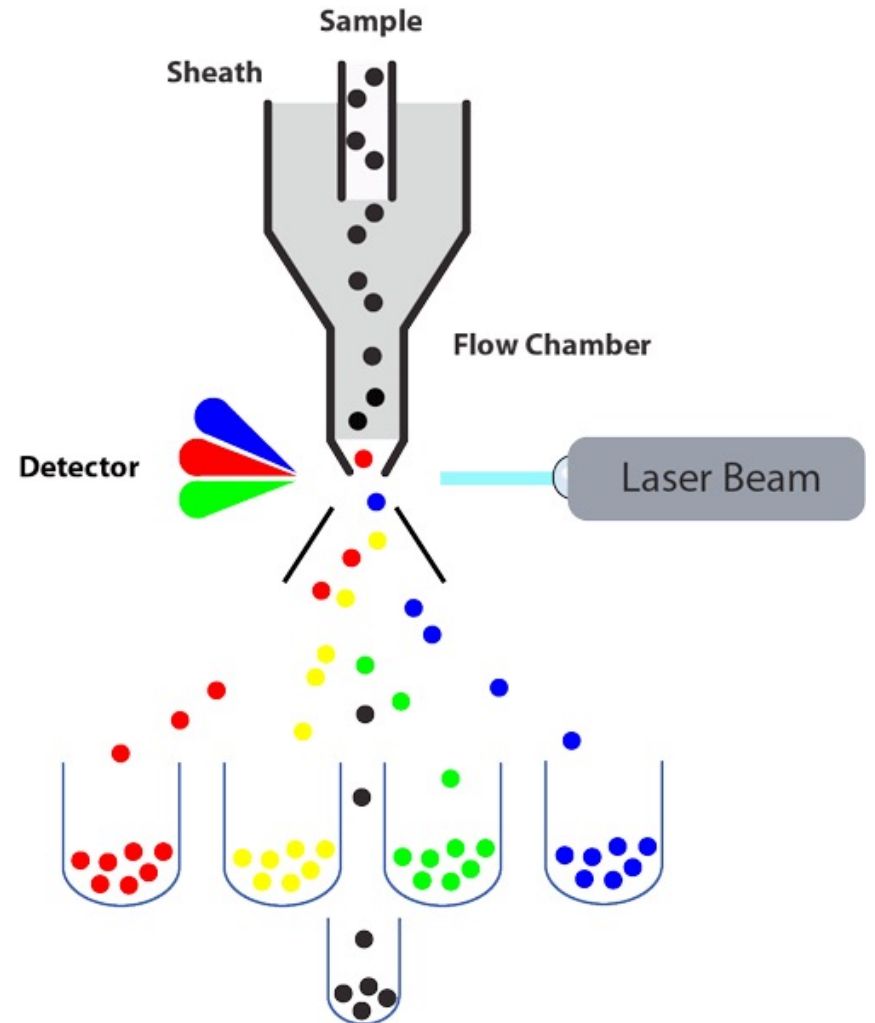


WHY?



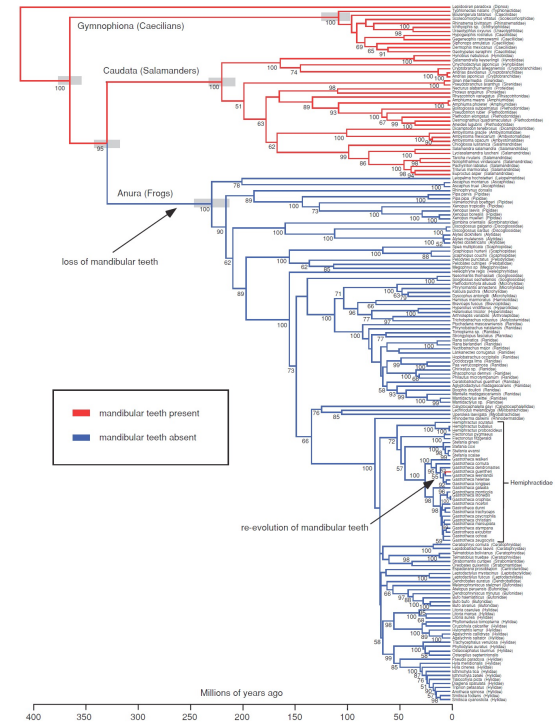
Classical Methods for Estimating the C-value

- Measuring the phosphate content
- Reassociation kinetics
- Flow cytometry
- Image analysis
- Absorption cytometry



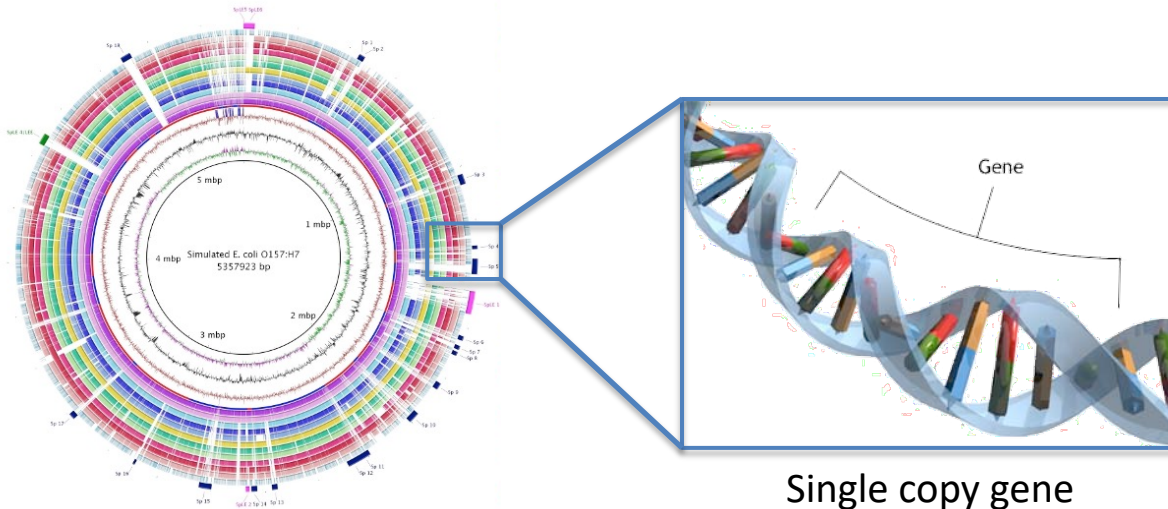
Issues and Challenges

Classical methods require the use of fresh non-processed tissues. This means genome size **can't be estimated** on museum samples



GOAL: to develop a method to estimate genome size across all amphibians (frogs, newts, salamanders and caecilians)

The Idea Behind



Absolute quantification
of a single copy gene in
a genomic DNA sample
by real-time PCR

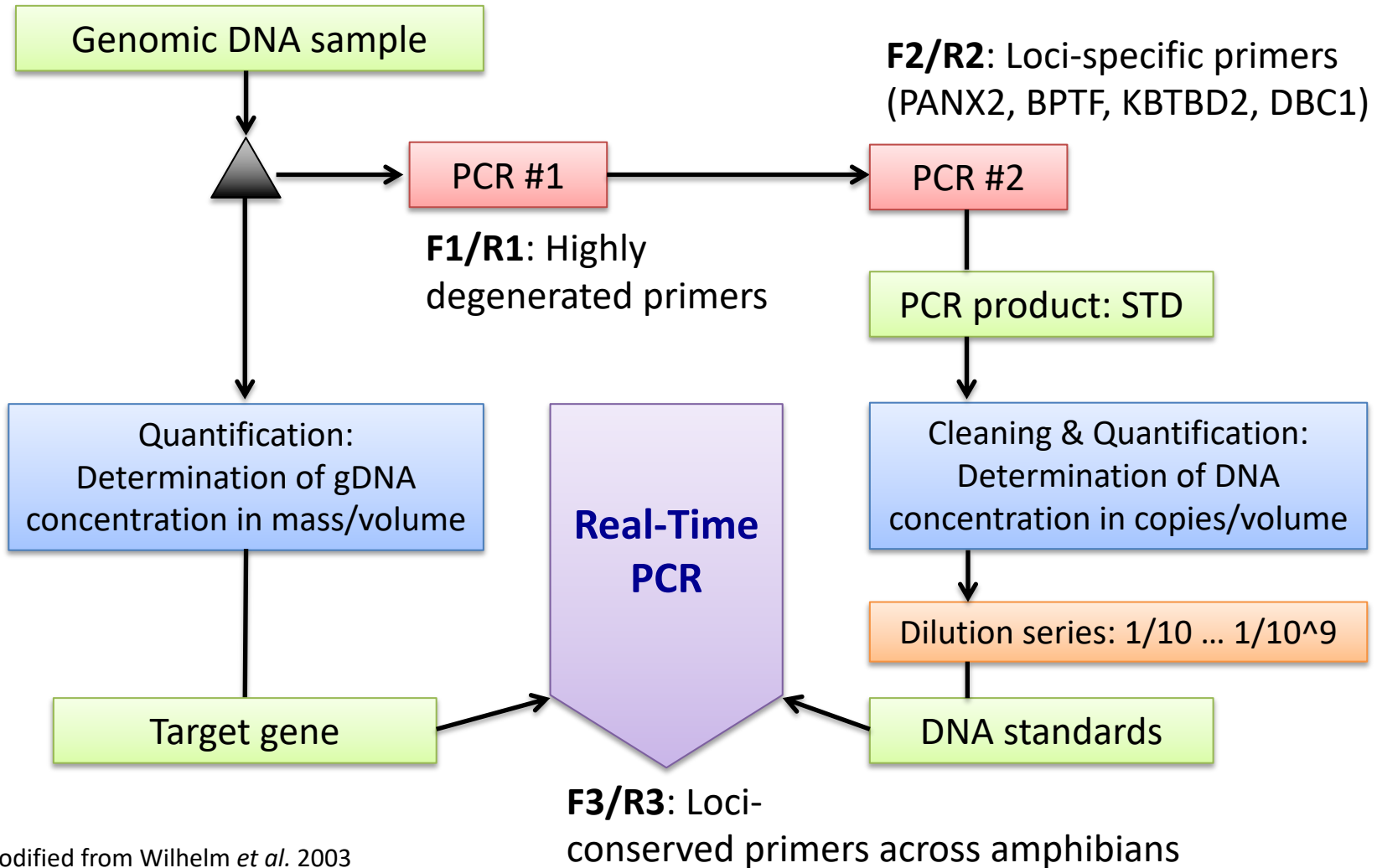
$$C = \frac{m}{N}$$

C = Mass of DNA per haploid nucleus (ng)

m = Total mass of template DNA (ng / uL)

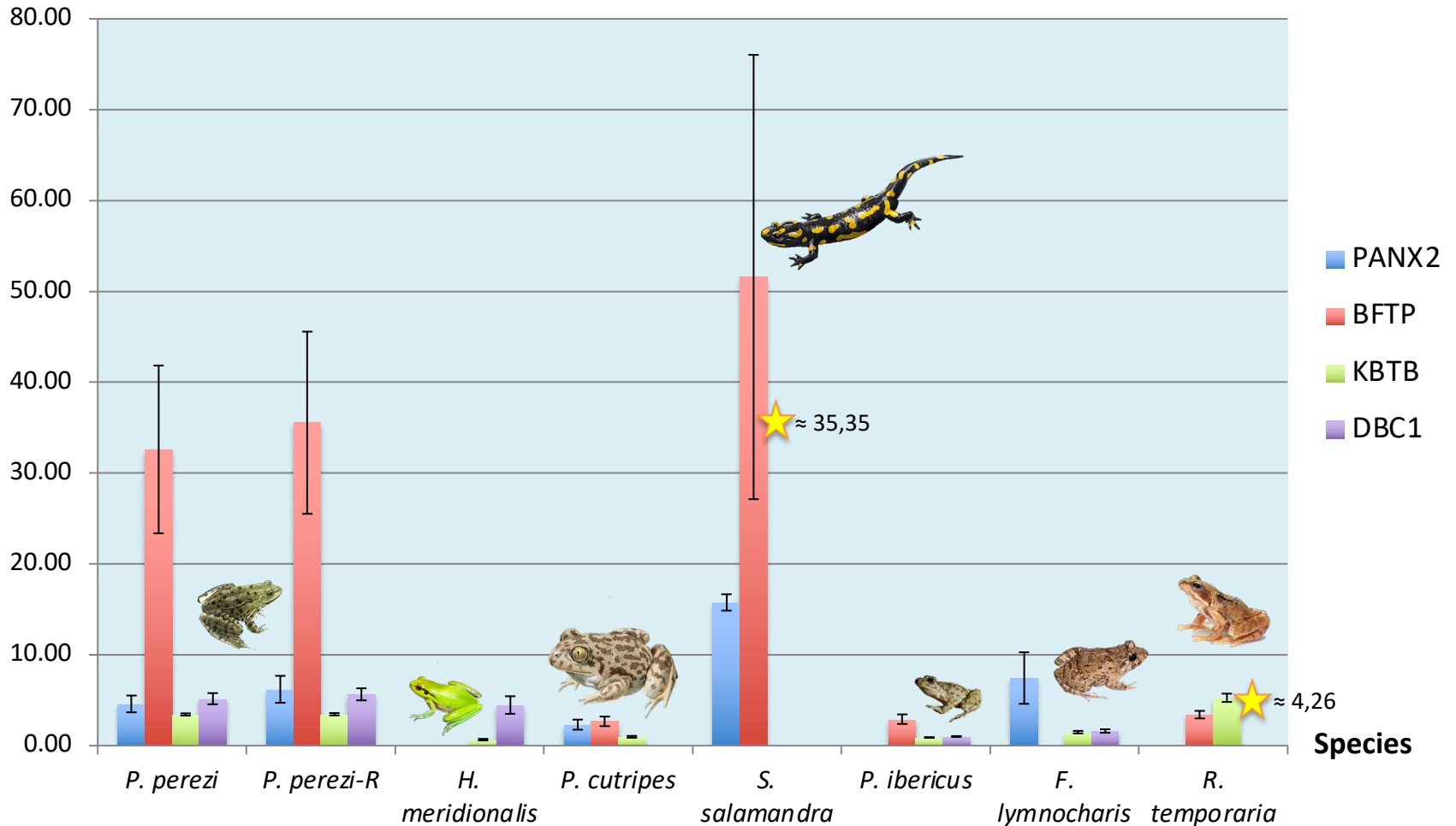
N = Copy number of the target sequence (copies / uL)

The approach



Results to date

C-value (pg)



Conclusions and Future Perspectives

- **Positive part:** Estimations seem accordant with published data
- **Negative part:** High variation within technical replicates



Validation of the method

- ✧ To use more loci / markers
- ✧ To use biological replicates
- ✧ To use different DNA extraction methodologies



Rana temporaria C-value \approx 4,26

Acknowledgments

Carles Vilà



Jennifer Leonard



Ivan Gómez



Miguel Camacho



SMM is funded by an FPI grant from the Ministerio de Economía y Competitividad, Spain (BES-2014-069006).