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Initial characterization of transposable elements in the pseudo-tetraploid genome of the rainbow trout

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Transposable elements (TEs) are mobile genetic elements able to move into new location within genomes. As consequence, they can strongly affect and shape host genomes (Feschotte, 2008). They were discovered in the fifties by Barbara McClintock. For a long time, they were considered as junk and selfish DNA. Nowadays, sequencing helps us to better understand structure and composition of genome, and their TEs. They have been found in almost all eukaryotic genomes (Pace *et al.*, 2008) Here, TEs were annotated in the genome of the rainbow trout (*Oncorhynchus mykiss*), one of the most widely introduced fish species with a major aquaculture interest. The annotation was done on 46 fully sequenced genomic Bacterial Artificial Chromosomes (BAC) clones, representing a total length of 5.4 Mb (0.23% of the genome). Both classes (retrotransposons and DNA transposons) were found, including 24 different families. TEs represent 12% of the rainbow trout sequences, with a majority of LINE retrotransposons. Some elements, as Tc1-transposase, seem to be recently active in the genome. Moreover, the presence of endogenous retroviruses reflects past infections.

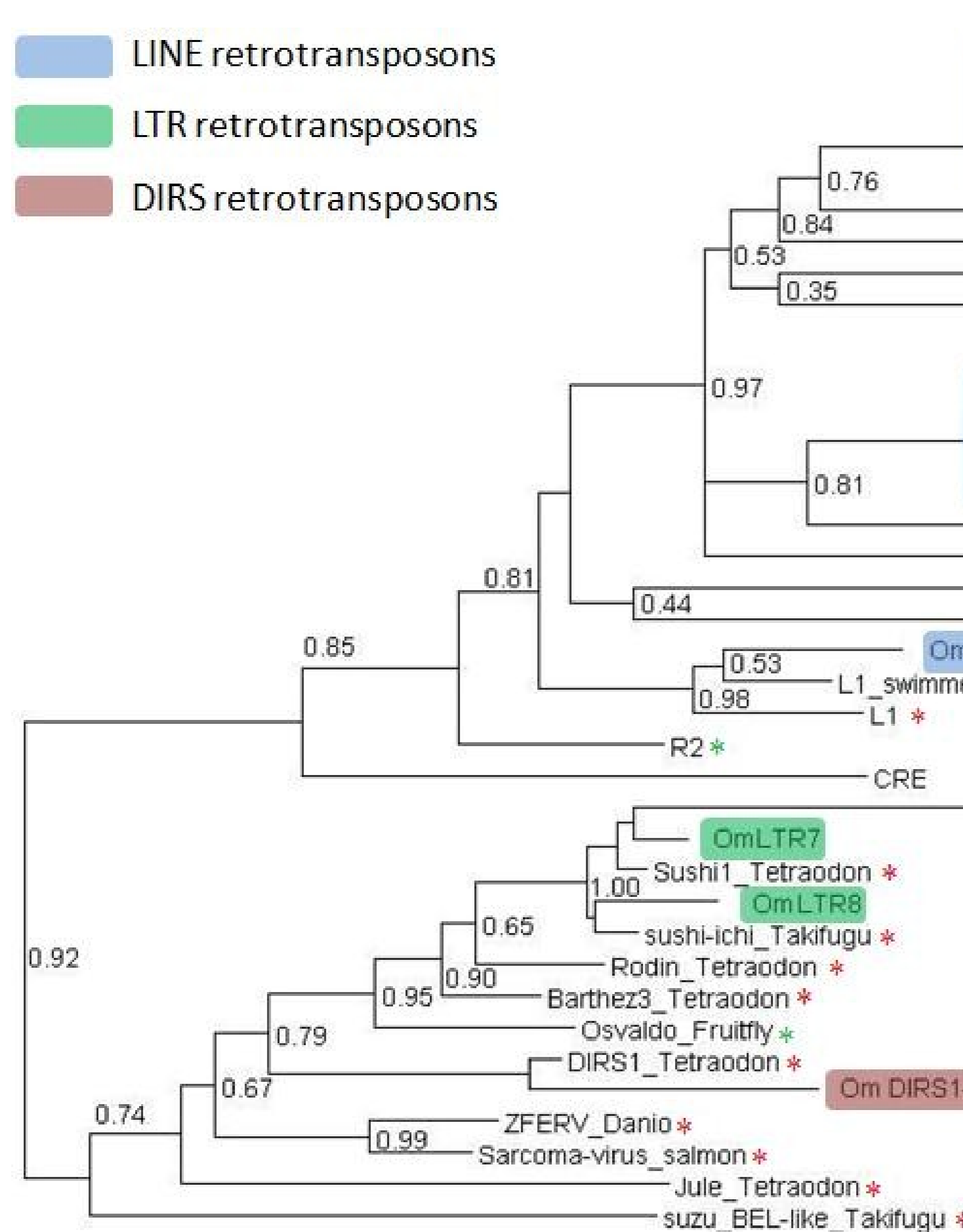


Figure 1: Phylogenetic analysis of retrotransposons-encoded reverse transcriptases identified in the genome of the rainbow trout. Rainbow trout elements are highlighted in blue (LINE order), green (LTR order) and red (DIRS1 order). Already annotated elements found in vertebrates are marked by a red star, in arthropods by a green star. Elements without a star are found in other lineages as fungi, nematodes and trypanosomes.

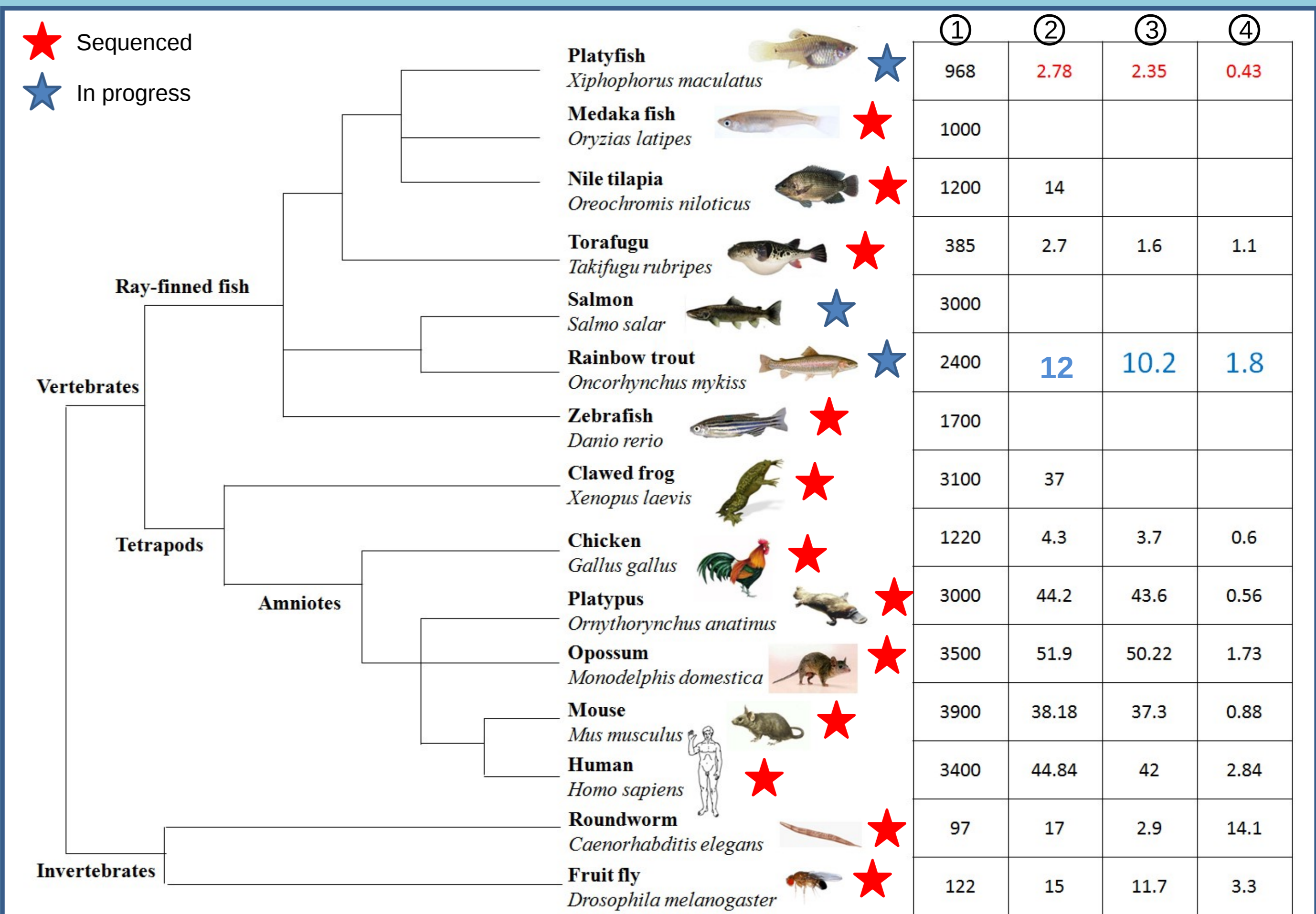


Figure 2: Genome size and proportion of TEs in genomes of different vertebrates and invertebrates. Column 1 indicates the genome sizes in Megabases (Mb), column 2 indicates the percentage of TEs in genomes. The column 3 and 4 indicate the percentage of the genome constituted by retrotransposons and DNA transposons, respectively.

ORDERS	ELEMENTS	STRUCTURE
Class I Retrotransposons		
LTR	OmLTR1	→ GAG PR RT INT CHR →
	OmLTR7	→ PR RT INT →
	OmLTR8	→ GAG PR RT RH INT CHR →
	OmLTR9	→ RT →
	OmERV1	→ INT ENV →
	OmERV2	→ INT ENV →
DIRS	OmDIRS1-1	→ GAG RT RH λ rec →
	OmDIRS1-2	λ rec
LINE	OmLINE1,13,15,16,17	APE endo RT
	OmLINE3,7,8,14	APE endo RT
	OmLINE2,5,6,9,10,11,12,18,19	APE endo RT
	OmLINE4	RT
SINE	MIR	—
	Mermaid	—
	5S	—
	Rsa	—
	Hpa	—
	Sma	—
	Ssa	—
Class II DNA transposons		
TIR	Tc1	→ Tpmse ←
	Tsn1-3	→ Tpmse ←
	Tc1-like salmon	→ Tpmse ←
	Tcb1	→ Tpmse ←
	Tcb2	→ Tpmse ←
	Tc5/pogo	→ Tpmse ←
	Harbinger	→ Tpmse ←
	MavericksHASI-like	→ INT ←

Sushi family

BEL family

Endogenous retroviruses reflect past infection. OmERV1 shares similarities (91% on 360bp) with a VHSV-induced mRNA of the rainbow trout.

Structural features

- Long Terminal Repeat
- Terminal Inverted Repeat
- Non-coding region
- GAG
- λ rec
- ENV
- POL (PR, RT, RH, INT, CHR)
- APE endo
- Tpmse
- INT (DNA transposon)
- RT (LINE)

Protein coding domains (abbreviations)

- GAG: Capsid protein
- PR: Protease
- RT: Reverse Transcriptase
- INT: Integrase
- CHR: Chromodomain
- RH: Ribonuclease H
- ENV: Envelope protein
- λ rec: Lambda recombinase
- APE endo: Apurinic/apyrimidic endonuclease
- Tpmse: Transposase

Figure 3: Structure of the transposable elements in the rainbow trout genome. The elements are classified according to their class and families. Sizes of predicted coding region boxes are not representative of TE sizes. 24 families are identified including 16 non-annotated in the rainbow trout genome.

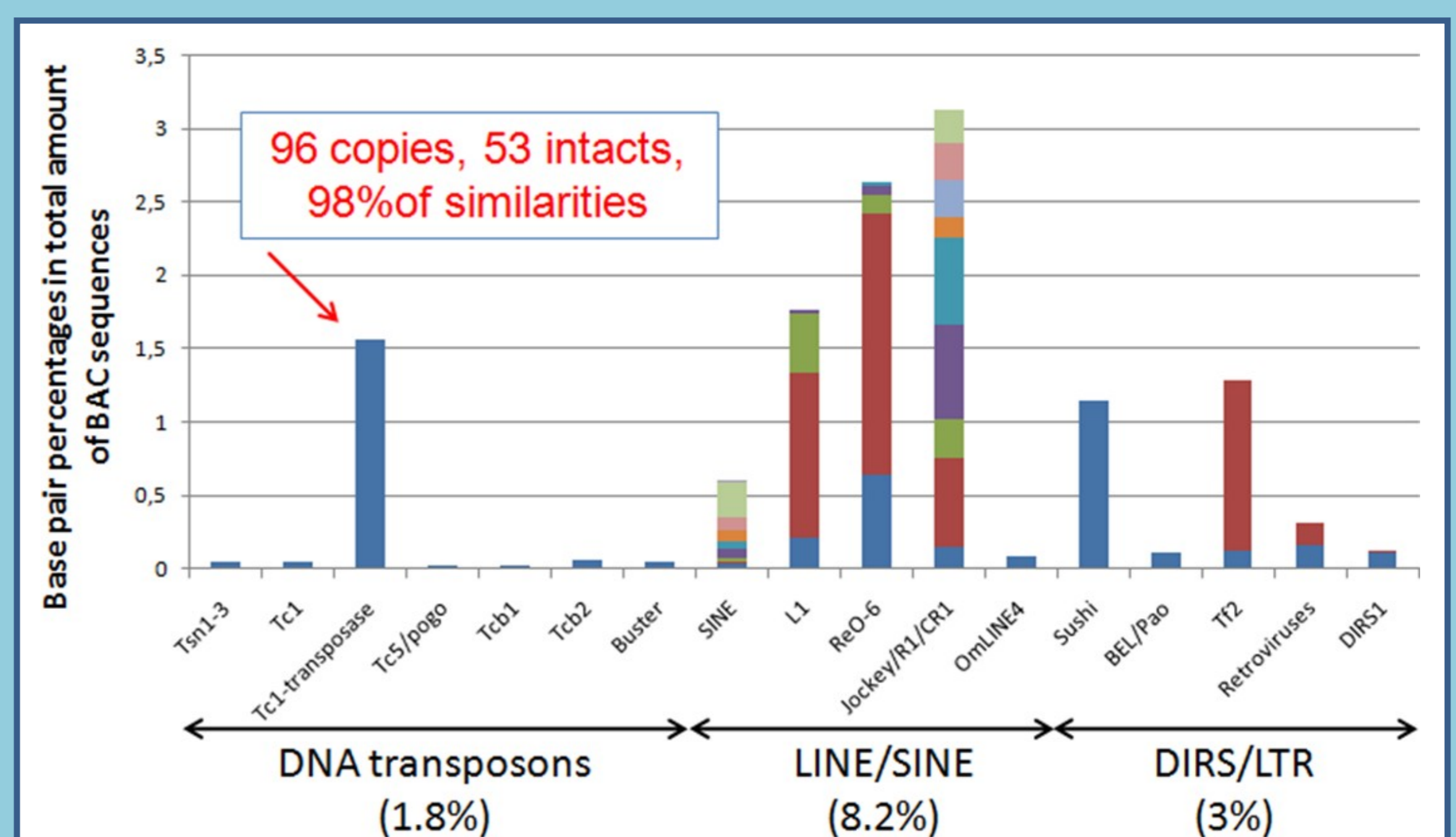


Figure 4: Transposable elements proportion in rainbow trout sequences. Nucleotide coverage of each element among the total BAC sequences, expressed in percentage of total BAC sequences.

Conclusion: this work shows that both classes of TEs (retrotransposons and DNA transposons) are present in the rainbow trout genome. Retrotransposons and particularly LINE elements are the main TEs. The Tc1-transposase family seems to be highly active: many intact copies have been identified. Diversity among retrotransposons and DNA transposons is relatively poor: few families have been found in the different orders. This preliminary study will be completed with the first draft of the complete genome. Moreover, further comparative genomic analyses will be important to better understand the evolutionary fate of TEs among teleosts and among vertebrates, but also to study the impact of tetraploidization and rediploidization on their evolution.