

The *let-7* micro RNA Family

Deuterostome Evolution from Acon worm to Human

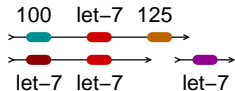
Jana Hertel

Bioinformatics Group of Peter F. Stadler,
Department of Computer Science,
University Leipzig

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The *let-7* miRNA family

- 1st known miRNA in human
- control timing of stem cell division & differentiation
- misregulation → development of cell-based diseases (e.g. cancer)
- family members conserved throughout Metazoa
- 14 copies in human vs. 1 in basal Deuterostomes
- organised in gene clusters:



Why analysing this special family?

- NOBODY did it so far
- one of the largest miRNA families
- bad/wrong and incomplete annotation in the miRBase 16.0
- high number of copies in human *can* be evolutionarily explained
- orthologs *can* be assigned correctly

Study based on the bioinformatics computer lab in January 2011

Databasis & Aim

- ~ 400 *let-7*, *mir-100* and *mir-125* pre-miRNA sequences
- annotated in **28** Deuterostome species
→ genomes of **59** Deuterostome species available!

Aim:

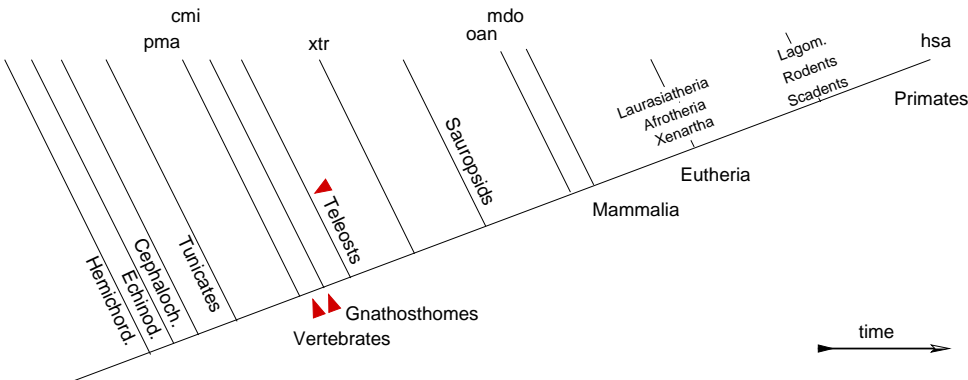
- (Re-)detect **ALL** query miRNAs in **ALL** available Deuterostome species
- *correctly* assign **ALL** hits to their respective ortholog in human
- find ancestral Deuterostome state of *let-7* miRNAs
- follow their duplication history up to human

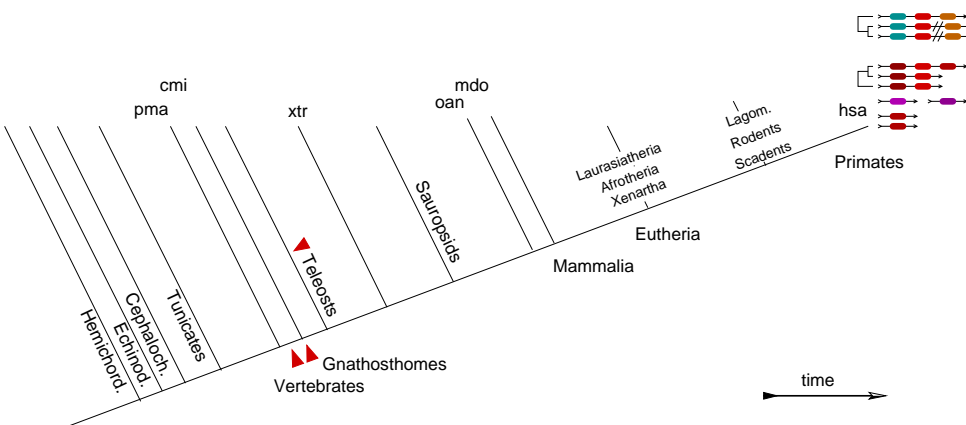
Method

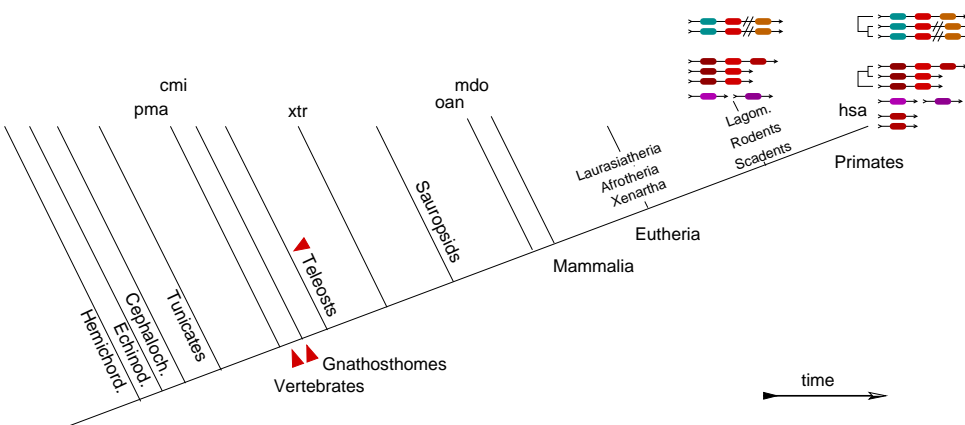
- Blast all query miRNAs against all genomes
- additional sytheny information via UCSC browser
- seq./str. conservation + genomic location + sytheny
→ correct orthologs
- cut sequence + add to the alignment → re-check sequence similarity
- log presence of orthologs for each species

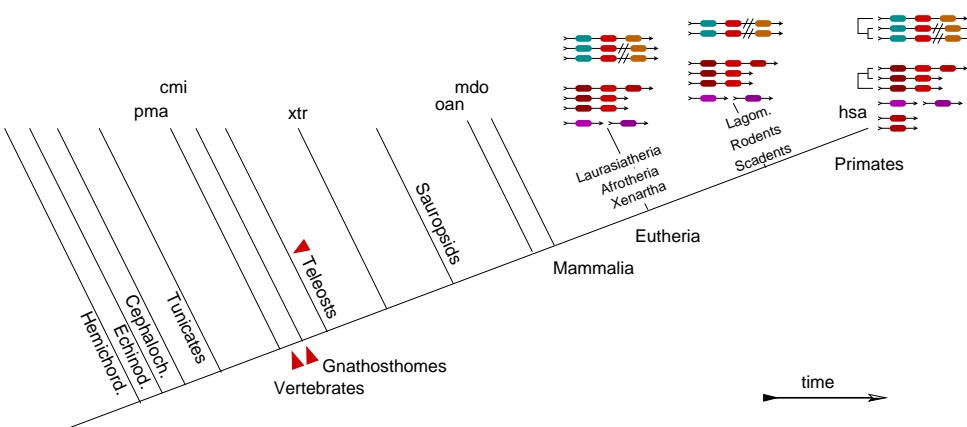
Results in numbers

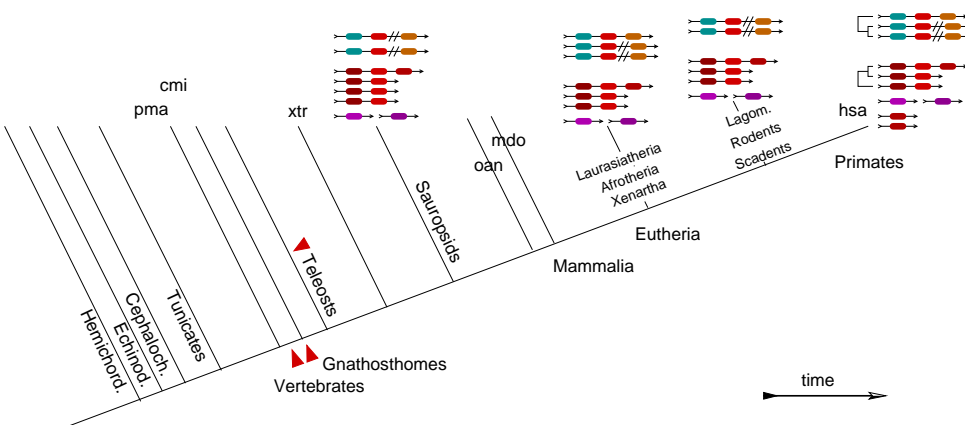
- 781 members in 59 species
- 33 additional members to already annotated species
- 2 additional members found in primates
- many clustered miRNAs are scattered over several scaffolds in low coverage assemblies
- origin/relationship of 11/14 members solved

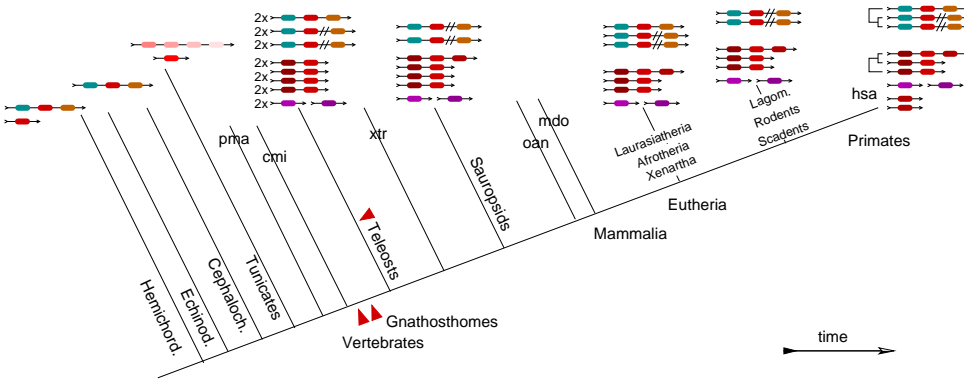












What to do next?

- more detailed analysis in teleosts
- alignments & sequence logos for each ortholog
- determine distances of sequence logos → tree

Tell it to the world!