Artemia: from the southern biogeographic reality (Chile) to global trends



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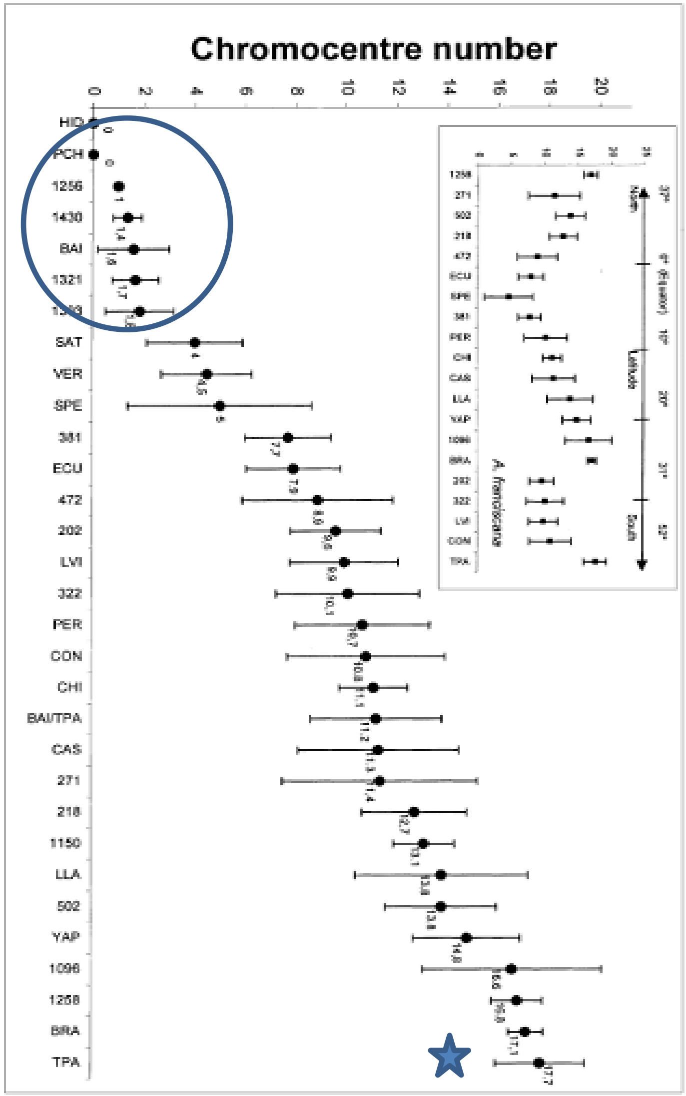
A glimpse (9 minutes) to:
1.the importance of non-coding , highly repetitive AluI sequences;
2. from the edge of *A. franciscana* distribution

- A significant part of the genome? There are about 6 x 10^{5} copies per haploid genome.
- Probably regulating the about 21,000 genes?
- need to be physically mapped.
- A vision from the southern edge (Chile) of *A. franciscana,* very likely a source of novelty regarding this marker.
- Chile harbors the New World species, *A. franciscana* and *A. persimilis*, two highly divergent species, differing in AluI (and heterochromatin) quantity, separated by a latitudinal barrier, inhabit contrasting habitats and/or climatic conditions.
- Alu I sequences (high in A-T content) have to do with genomic amplification, gene expression and adaptation.
- Alu I sequences vary in quantity and distribution at different taxonomic levels (species, pops.), in spite of being highly conserved

The southern (Chile)biogeographic reality

Saltworks (semi-artificial habitat),
a probable hybridization zone (*A. franciscana* – *A. persimilis*)

North-South latitudinal change in heterochromatin content in *A. franciscana*: adaptive?



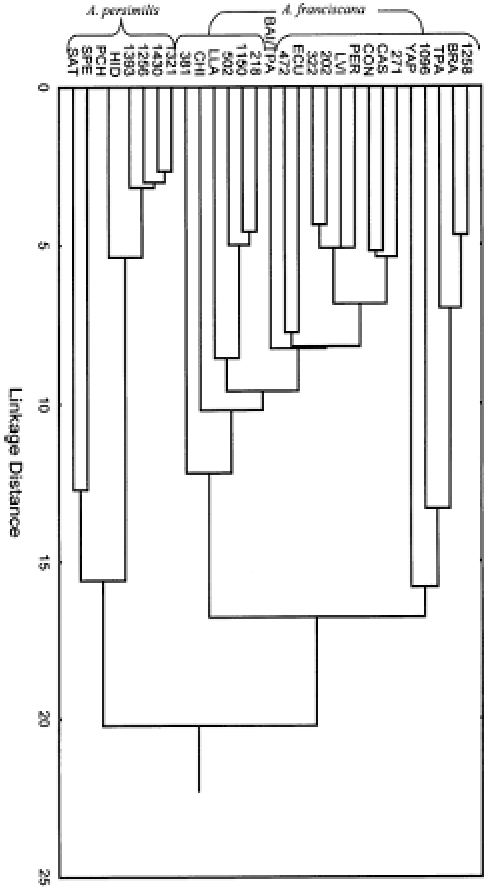
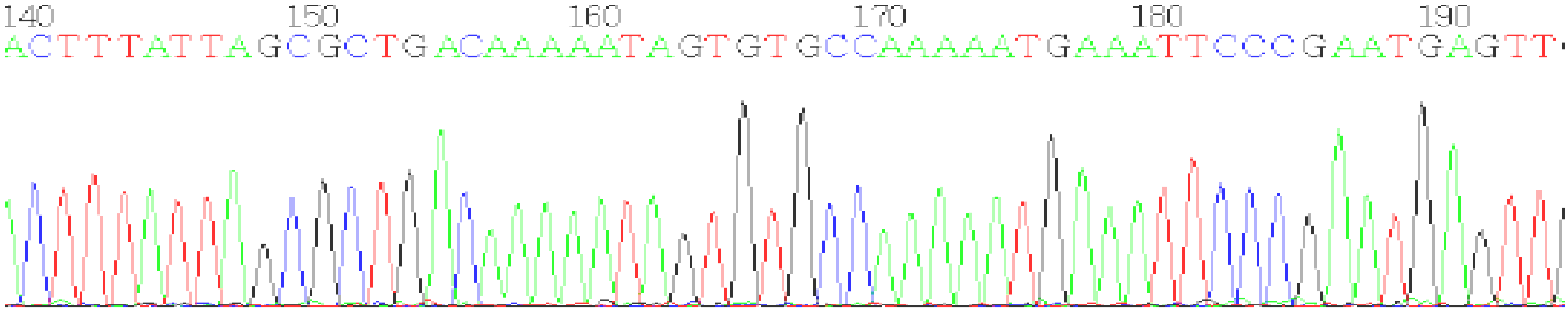


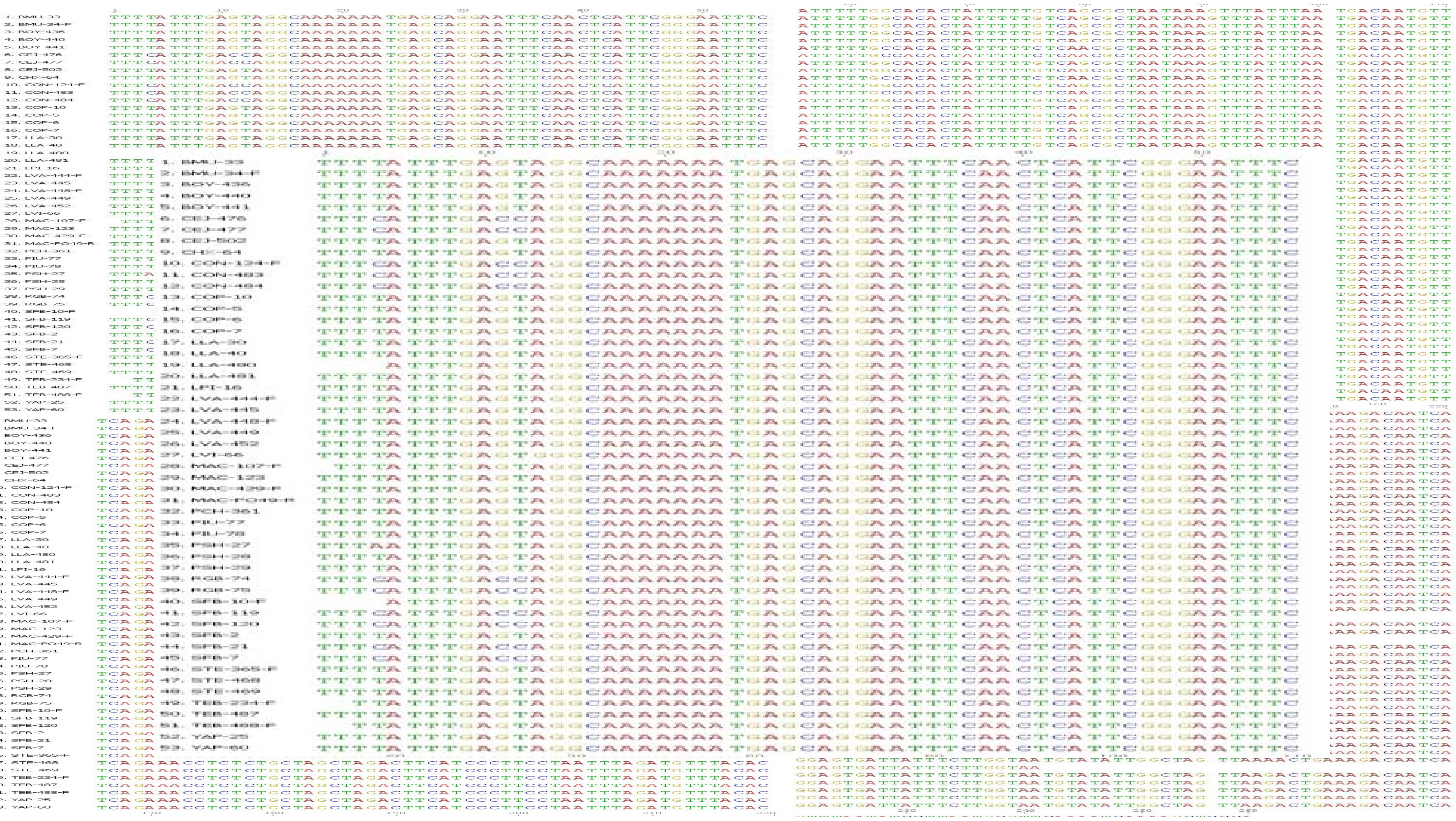
Fig. 2 Clustering of 29 *Artemia* populations based on the Euclidean distance (raw data) between mean chromocentre numbers.

Gajardo, Beardmore & Sorgeloos, 2001

Alu I sequences: inter (3 species) and intra-specific differences (*A. franciscana*)

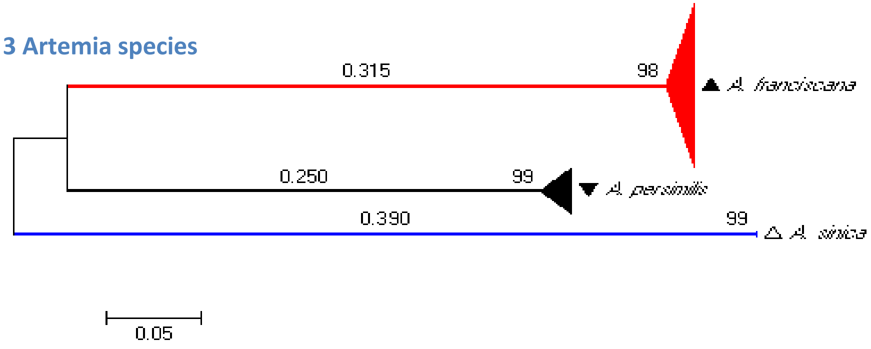


Alu sequences of *Artemia* populations (multiple alignements)

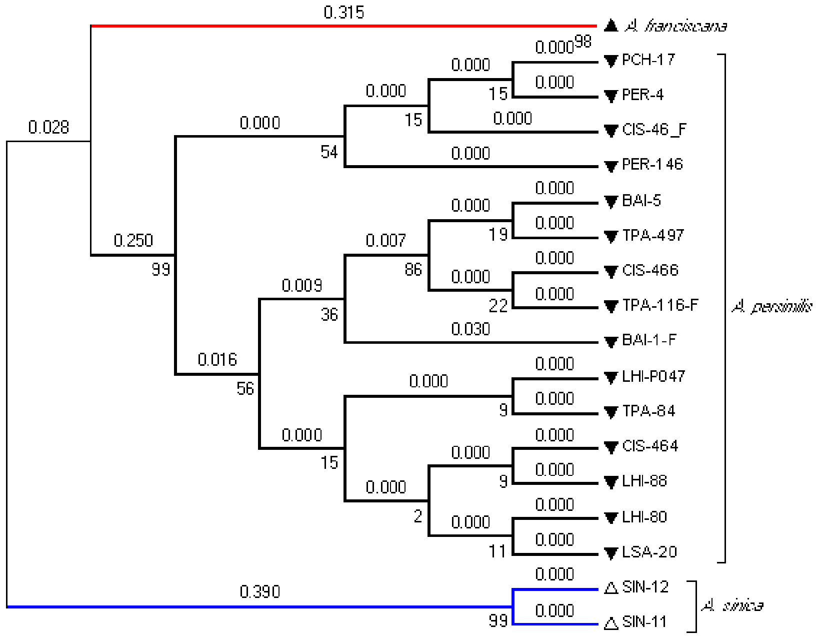


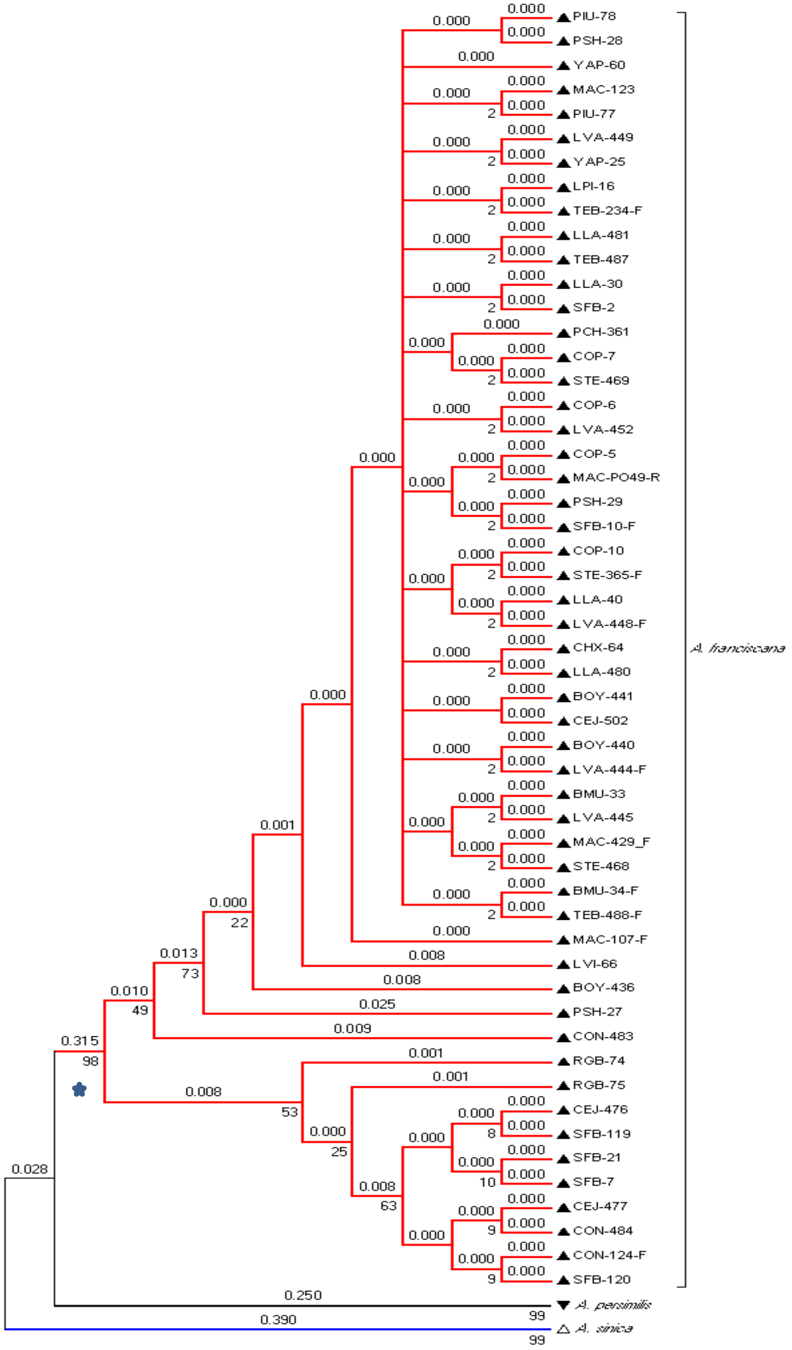
Feature				
	A. persimilis (n= 7 pops.)	*A. franciscana* (n= 19 pops.)	Consensus sequence for all individuals (*A. persimilis*+ *A. franciscana* + *A. sinic*a) (n= 27 pops.)	One consensus sequence per population (n= 27 pops.)
Nº of sequences analysed	**15**	**53**	**70**	**27**
Size of consensus sequence (pb)	**330**	**296**	**508**	**501**
Identity (%)	**96.8**	**98.9**	**64.4**	**64.0**
T+A (%)	**66.5**	**67.9**	**67.2**	**67.2**
Nº of conserved sites (%)	**294 (87.8)**	**170 (57.4)**	**64.4 (4.9)**	**44 (11.8)**
AluI-restriction sites	**1**	**2**	-	-
Nº of repeated blocks $(T)_n$	$(T)_6=1$ $(T)_5=1$ $(T)_4=2$ $(T)_3=10$	$(T)_5=2$ $(T)_4=2$ $(T)_3=13$	-	-
Nº of repeated block $(A)_n$	$(A)_5=1$ $(A)_4=4$ $(A)_3=3$	$(A)_7=1$ $(A)_5=1$ $(A)_4=2$ $(A)_3=3$	-	-

a) **3 Artemia species**

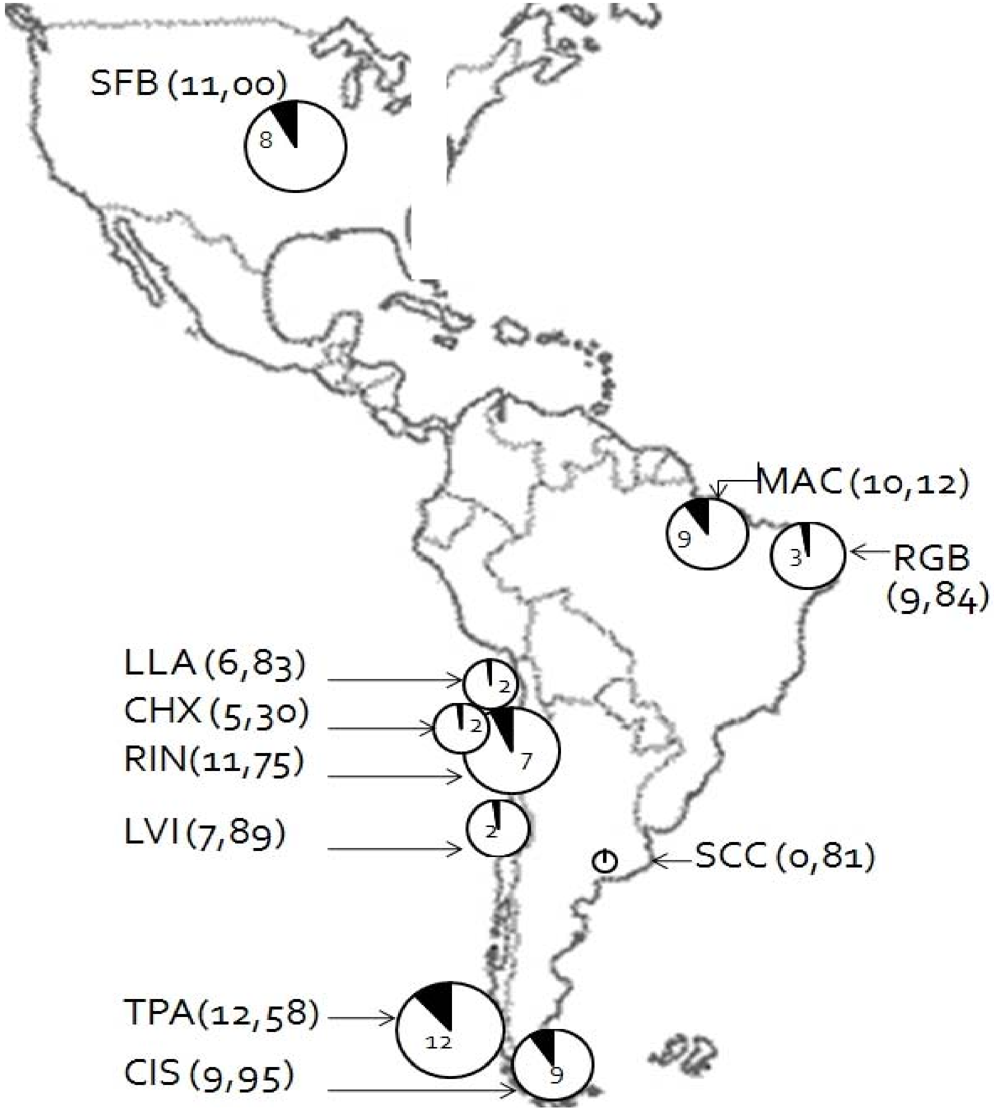


b) A. persimilis





Geographic variation in *A. franciscana and A. persimilis)*



CONCLUSIONS

- AluI sequences are a novel marker in *A. franciscana* (as compared to *A. persimilis* who resembles Old World species).
- This marker varies geographically, and perhaps it's related to *A. f ‘s* ability to establish locally adapted pops.?
- Where are these sequences located in the genome/chromosomes?
- Normally the edge of distribution of species is a source of novelty
- Chile has two species that are important to be tested with regard to their AluI sequence differences and genome amplification

- On the genomics of adaptation and speciation: few/lots genes involved? Role of non-coding regions?
- What parts of the genome more involved?
- etc.

The brine shrimp *Artemia* as an invaluable model organism

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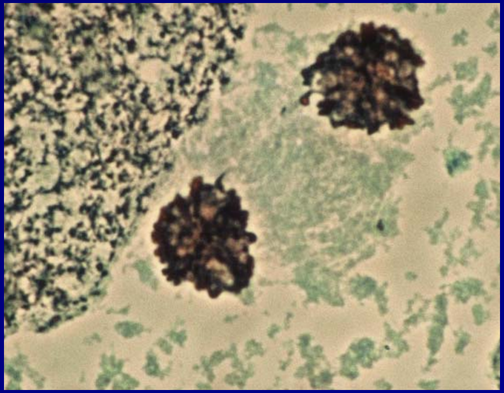
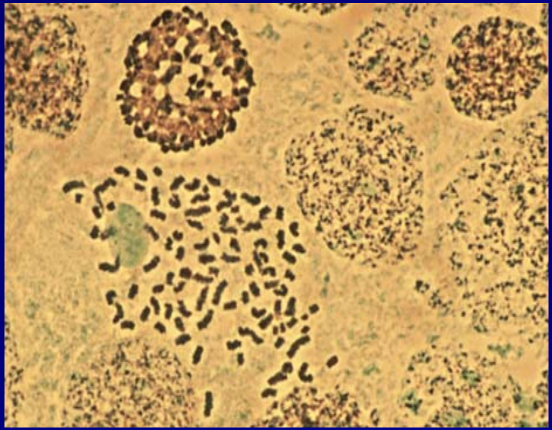
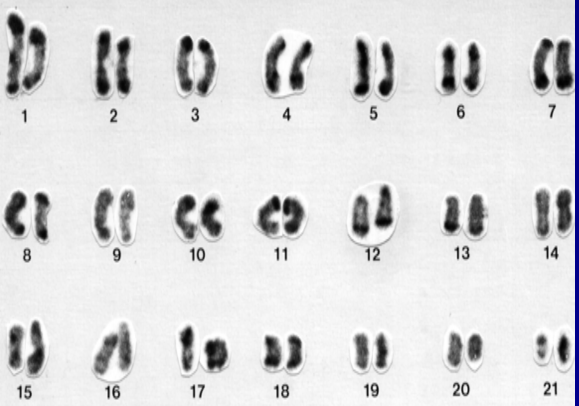
Late anaphase



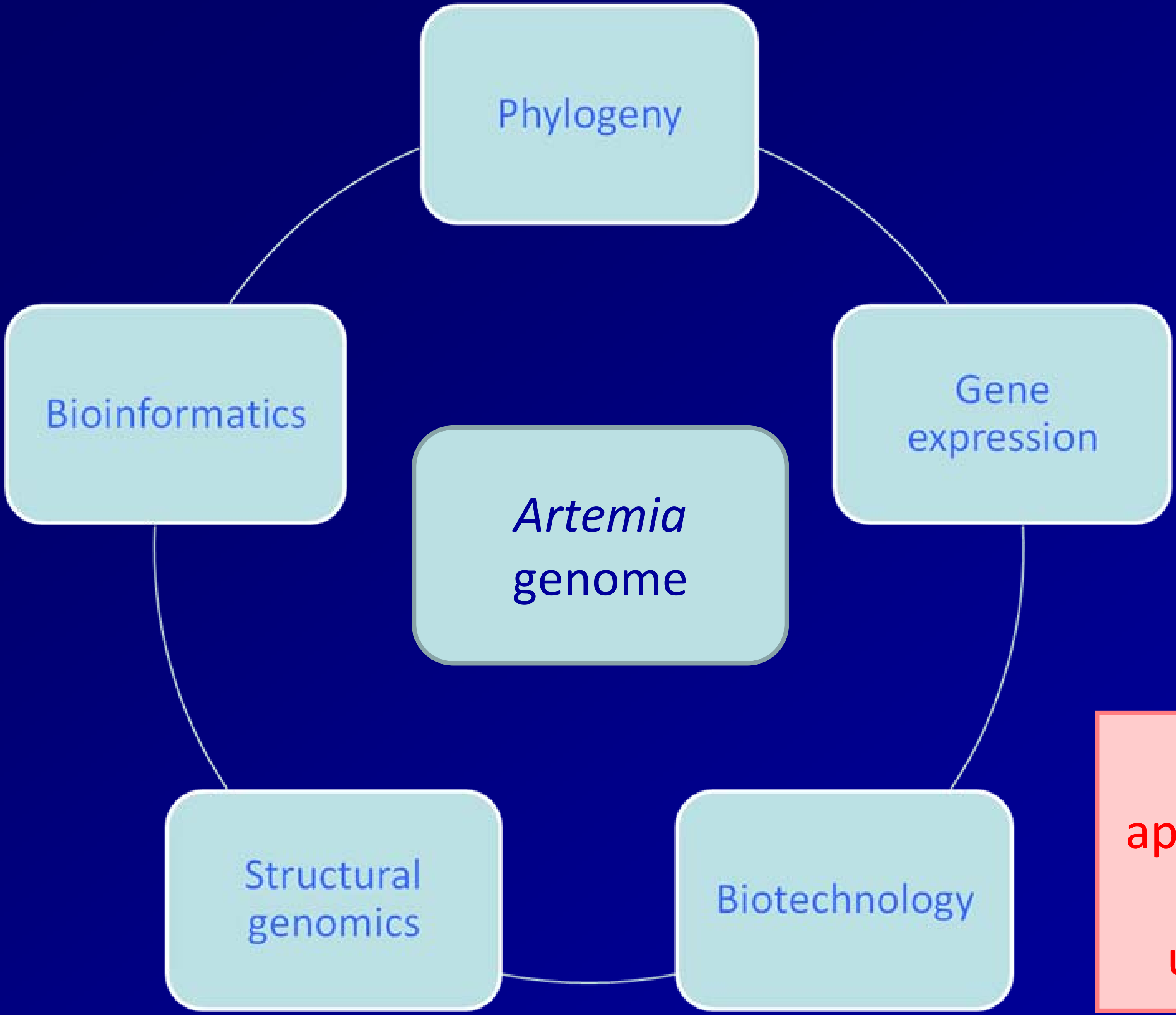
Heterochromatic associations, nucleolus organizer





G-banding karyotype of *A. franciscana*

(n = 42)



Artemia genome

Phylogeny

Gene expression

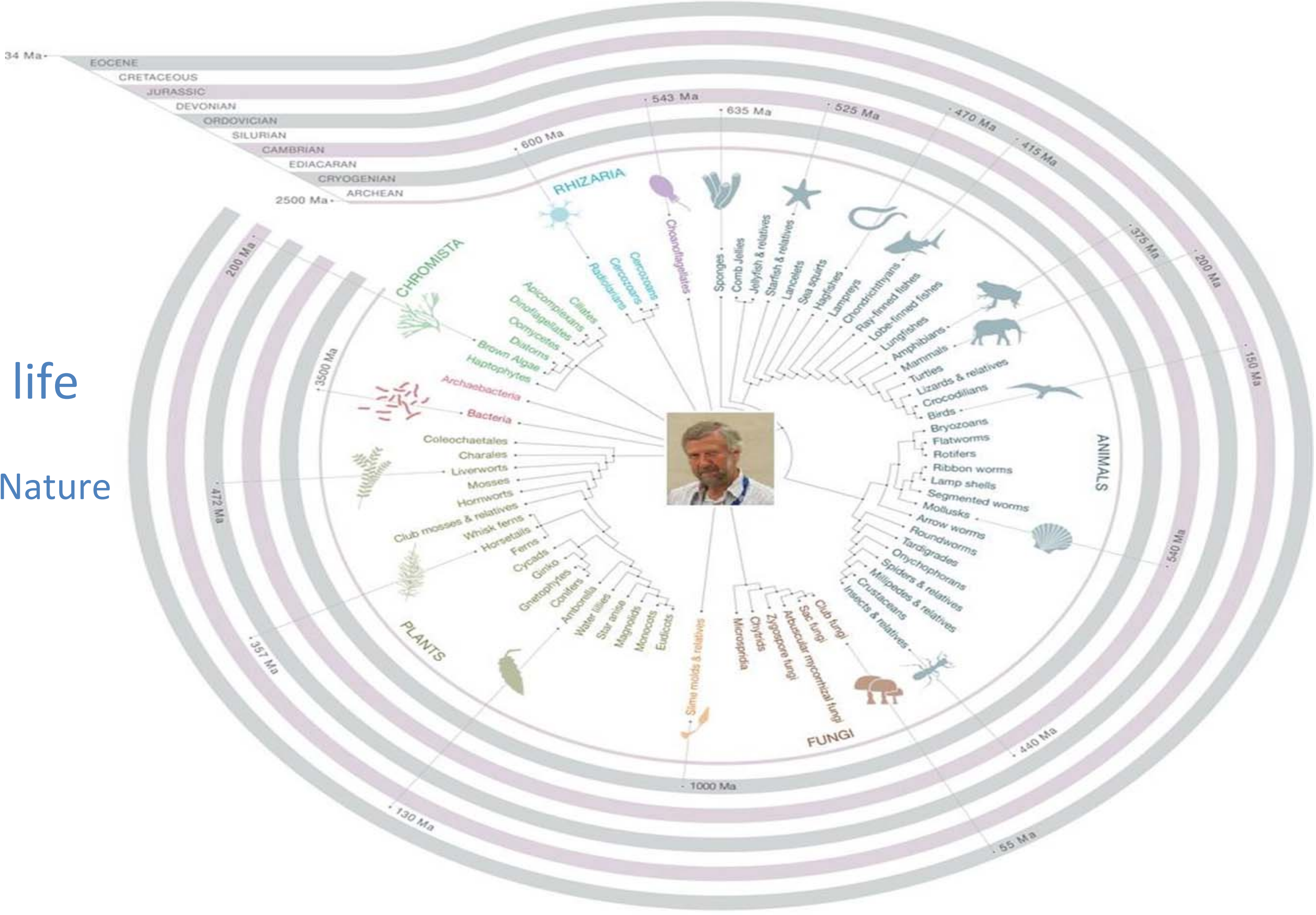
Biotechnology

Structural genomics

Bioinformatics

Potential applications are practically unlimited!!!

Thanks Patrick for all you have done for *Artemia*, Larviculture and your friends around the world during your academic lifetime.



Tree of life

Soource: Nature