

The first insight into the genetic structure of the Monogenean *Sparicotyle chrysophrii* from Gilthead Sea Bream (*Sparus aurata*) Along Tunisian Coasts

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Introduction

- Sparicotyle chrysophrii* (Van Beneden & Hesse, 1863) Mamaev, 1984 is a monogenean ectoparasite that specifically infects *Sparus aurata* Linnaeus, 1758. This parasite can cause severe parasitic diseases, leading to significant mortality, particularly in aquaculture. The morpho-anatomical examination of ectoparasites infesting *S. aurata* across seven Tunisian sites confirmed the presence of *S. chrysophrii*. However, few molecular studies have been conducted on this monogenean, and its genetic variability remains poorly understood. This study provides the first molecular characterization and phylogenetic analysis of *S. chrysophrii* from the Tunisian coasts, examining both wild and cage-reared hosts.

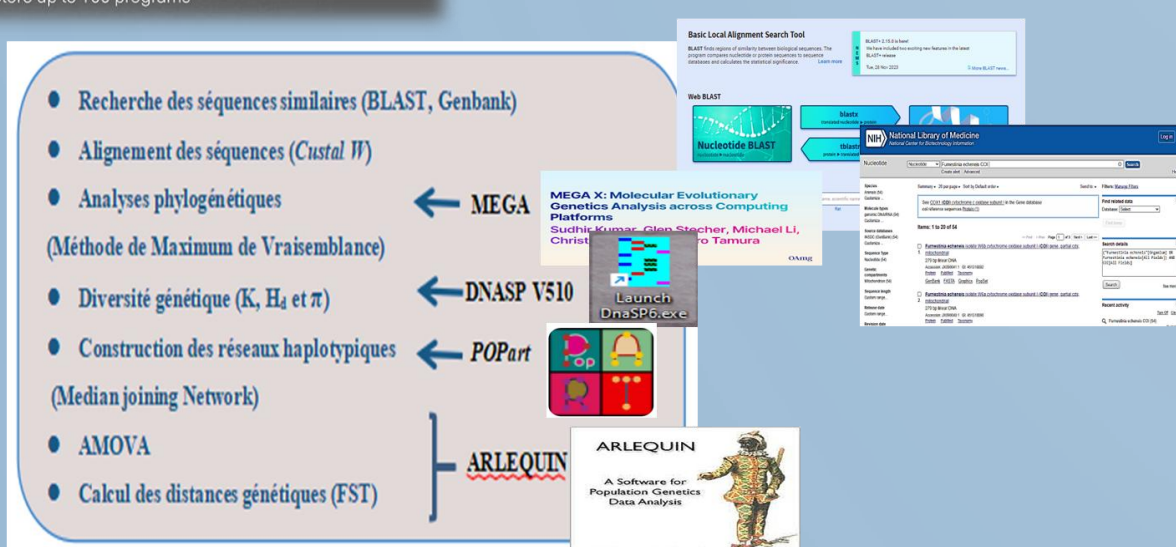
Aims

- This study presents the first investigation into the genetic structure of *S. chrysophrii*, a monogenean parasite infecting gilthead sea bream (*S. aurata*) along the Tunisian coast.
- Molecular characterization was conducted using the large subunit ribosomal RNA (28S) and mitochondrial COI genes.

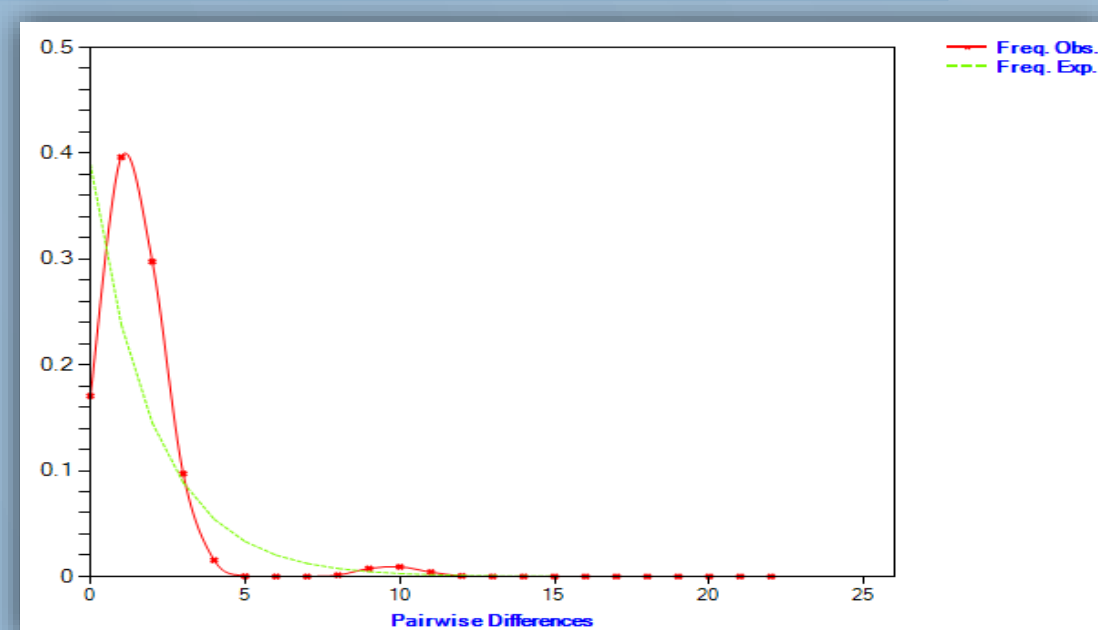
Sample collection, DNA Extraction, Amplification, Sequencing and Population Genetic Analyses



Figure 1: Map of Tunisian sampling localities of *Sparicotyle chrysophrii* specimens from the gills of wild (Blue waves) and cage-reared (Red dots) *Sparus aurata*.



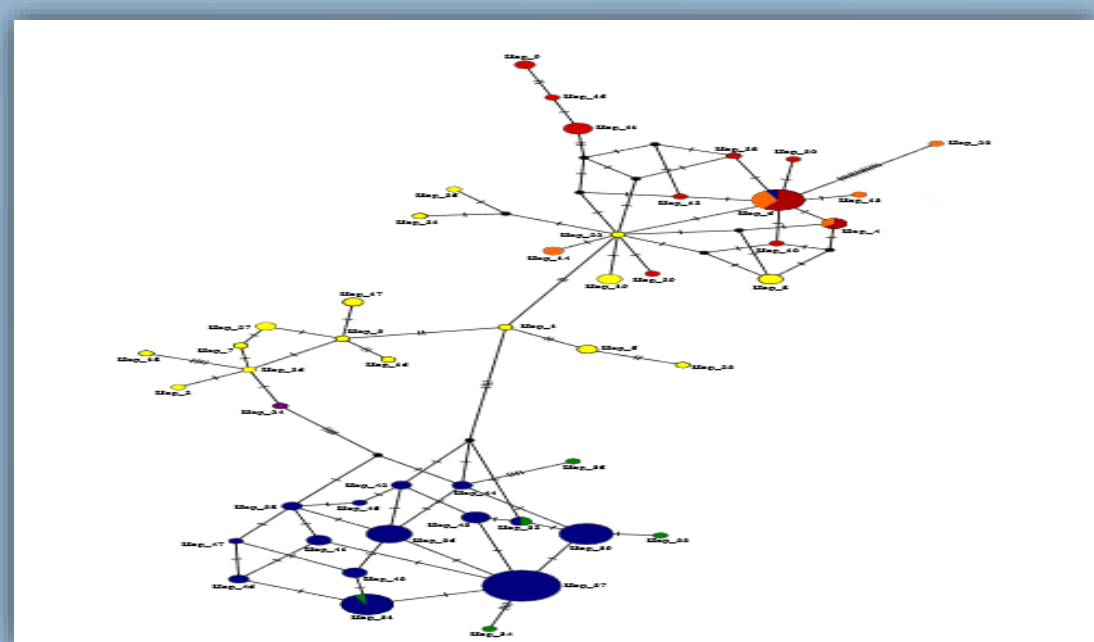
Results and Discussion



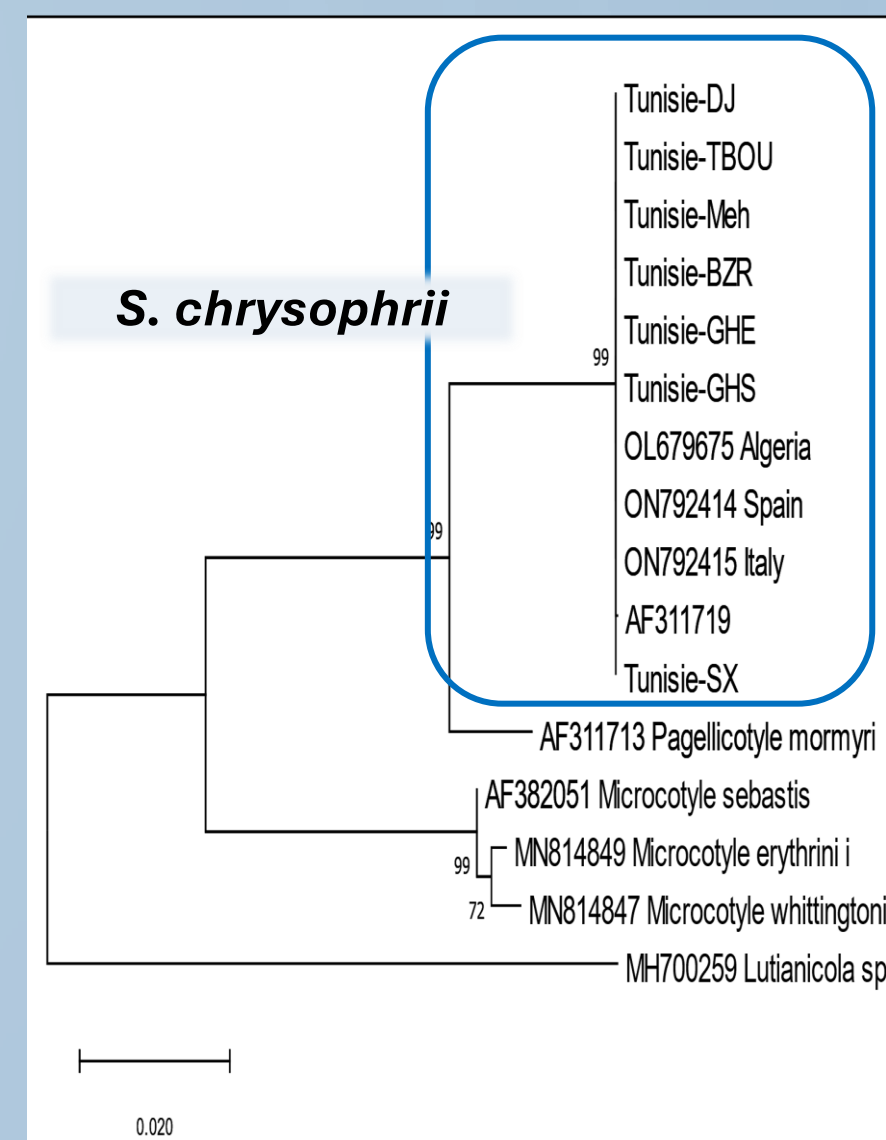
The analysis of *S. chrysophrii* discordances revealed a unimodal pattern.



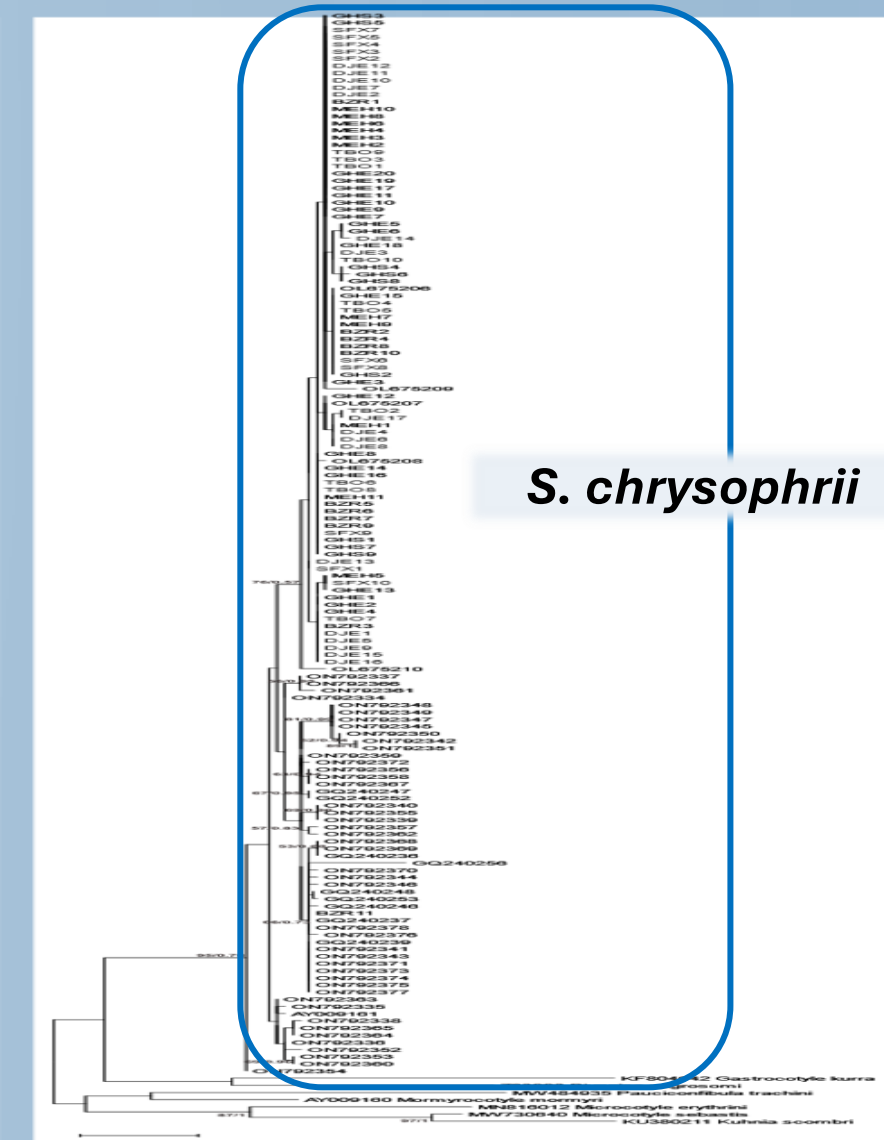
Prevalence ranged 37.5%-63.6% in wild and 29.4%-90% in cage reared fish.



The haplotype network exhibited a star-like pattern.



The sequences of 28S gene, from Tunisian and other Mediterranean populations formed a monophyletic group.



Analysis of the COI sequences revealed the absence of significant phylogenetic ramifications, with samples from different Mediterranean regions clustering into a monophyletic clade.

Genetic diversity indices, characterised by low nucleotide diversity and high haplotype diversity.

Population	n	S	h	k	Pi	Hd	Tajima's D	Fu's Fs
Ghar El Melh (C)	20	5	8	1.336	0.00440	0.815	-0.15742	-3.745
Tboulba	10	5	6	1.466	0.00482	0.888	-0.68235	-2.691
Mehdia	11	4	5	0.981	0.00323	0.709	-1.02918	-2.111
Bizerte	11	11	5	2.836	0.00933	0.781	-1.05320	0.425
Djerba	17	4	7	1.308	0.00431	0.830	0.32498	-2.954
Sfax	10	3	5	1.177	0.00387	0.755	0.39804	-1.849
Ghar El Melh (W)	9	4	5	1.777	0.00585	0.861	0.84519	-1.113

AMOVA analysis attributed 92.77% of the variance to individual differences, with a moderate F_{ST} value (0.07227).

Source of variation	df	Sum of squares	Variance components	% variation	P-value
Among groups	2	2.479	-0.00269 Va	-0.39	***
Among populations	4	5.034	0.05206 Vb	7.62	***
Within groups	81	51.327	0.63367 Vc	92.77	***
Within populations	87	58.841	0.68303		
Total					

Conclusion

- The analysis of nuclear ribosomal 28S sequences revealed no intraspecific genetic variation, confirming a strongly supported monophyletic group.
- COI sequences formed a monophyletic clade clustering specimens from both the northern Mediterranean (France, Adriatic Sea, and the Italian and Spanish coasts) and the southern Mediterranean (Algeria and Tunisia), with no significant phylogenetic divergence.
- The haplotype network showed no distinct haplogroups, suggesting strong genetic flow between farmed and wild fish populations. This is reflected by low nucleotide diversity (0.00445) alongside high haplotype diversity (0.821).
- Populations of *S. chrysophrii* from the Tunisian coast were closely related to those from Algeria, as supported by the haplotype network and genetic distances based on COI sequences.
- Shared haplotypes further indicated the potential for pathogen transmission between wild and cultured hosts along the Tunisian coast.
- These findings suggest an absence of genetic structuring within the *S. chrysophrii* population. The study demonstrates that the species disperses homogenously without significant barriers, likely due to high gene flow among parasite populations, facilitated by host dispersion.

References

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