

Genome-wide identification, characterization, and expression analysis of scavenger receptor genes in orange-spotted grouper (*Epinephelus coioides*)



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Background

- Scavenger Receptors (SRs) are crucial Pattern Recognition Receptors (PRRs) in innate immunity, responsible for recognizing diverse pathogens and damage-associated molecules and modulating immune responses.
- The intensively farmed grouper, *Epinephelus coioides*, faces major threats from *Vibrio harveyi* infection and acute low-salinity stress.
- Both stressors can compromise immune competence, yet the underlying molecular mechanisms, particularly the role of SRs, remain poorly defined.
- Systematic research on the SR family in *E. coioides* is lacking, and its response patterns to bacterial challenge and osmotic stress are poorly characterized.

Methods & Results

1 Identification of SRs genes in *E. coioides*

Gene	Number of amino acids	Molecular weight (kDa)	Theoretical pI	Subcellular localization
EcSCAR3	571	62416.47	6.07	plasma membrane
EcMARCO	370	39370.19	6.95	plasma membrane
EcCOLEC12	739	79935.41	5.26	plasma membrane
EcSCAR5	367	40220.83	5.49	cytoplasm
EcCD36	488	54246.76	8.87	plasma membrane
EcSCARB1	479	54247.16	8.12	plasma membrane
EcMEGF10	1120	121192.31	6.57	plasma membrane
EcSCARF1	755	80089.22	6.54	plasma membrane
EcSCARF2	948	103119.17	8.60	cytoplasm
EcSTAB2	2460	265586.69	7.60	plasma membrane
EcSTAB1	2553	278544.88	6.16	plasma membrane
EcLRP1	4515	503563.47	5.01	plasma membrane
EcLRP2	4328	483158.38	4.92	plasma membrane

Gene Species	Homo sapiens	Mus musculus	Galus gallus	Leptotenus oculatus	Callorhynchus milii	Danio rerio	Parachanna obtusirostris	Tilapia zilli	Epinephelus luncolatus	Oryzias latipes	Epinephelus coioides
SR-A	5	4	4	4	4	4	4	4	4	4	4
SR-B	2	2	2	2	2	2	2	2	2	2	2
SR-D	1	1	1	1	1	1	1	1	1	1	1
SR-E	2	2	2	2	2	2	2	2	2	2	2
SR-F	3	3	3	3	3	3	3	3	3	3	3
SR-G	1	1	1	1	1	1	1	1	1	1	1
SR-H	2	2	2	2	2	2	2	2	2	2	2
SR-I	2	2	2	2	2	2	2	2	2	2	2
SR-J	1	1	1	1	1	1	1	1	1	1	1
SR-K	1	1	1	1	1	1	1	1	1	1	1
SR-L	2	2	2	2	2	2	2	2	2	2	2
Total	22	22	16	15	14	17	16	11	11	13	13

2 Phylogenetic analysis

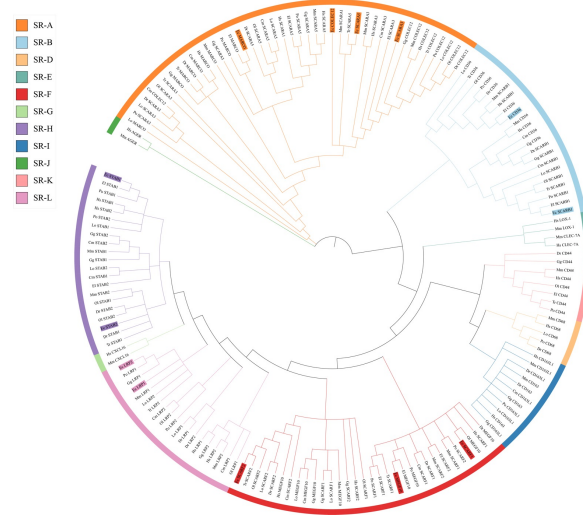


Fig. 1. Phylogenetic map of SR gene families of eleven vertebrates

3 Gene structure, conserved domains and motif analysis

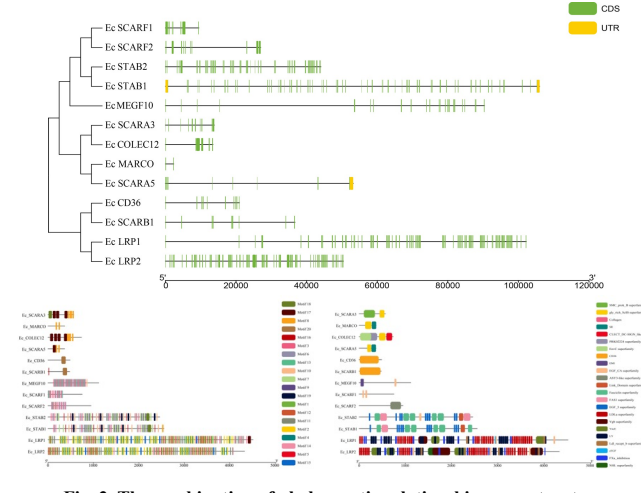


Fig. 2. The combination of phylogenetic relationship, gene structure, Conserved motif structure and conserved domain analysis of EcSRs

4 Selection pressure analysis

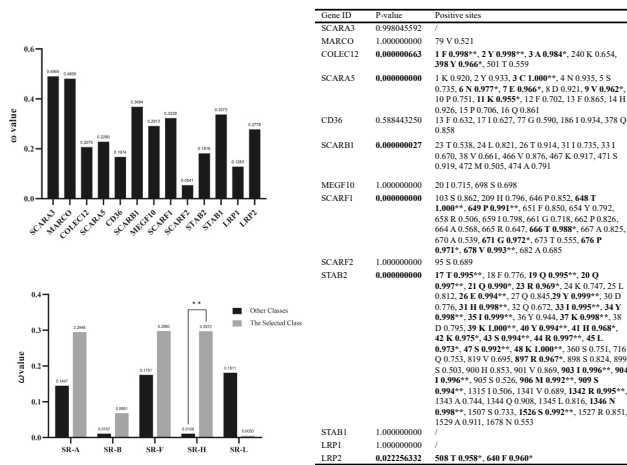


Fig. 3. Estimated ω values (dN/dS) for SR genes in *E. coioides* under the M0 model. BM tests for each EcSRs class. ** indicates $P < 0.01$ via LRTs.

5 Tissue expression profiling

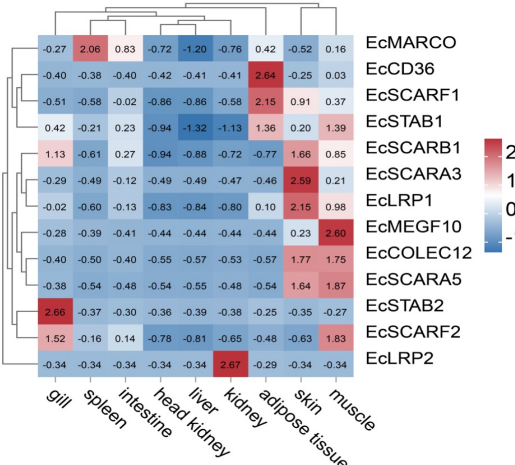


Fig. 4. Heatmap of SR gene expression profiles across nine tissues of *E. coioides* based on qPCR analysis.

6 *V. harveyi* challenge and Low-salinity exposure

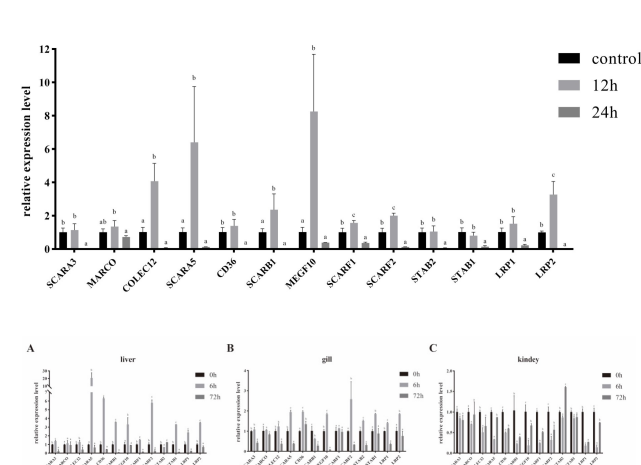
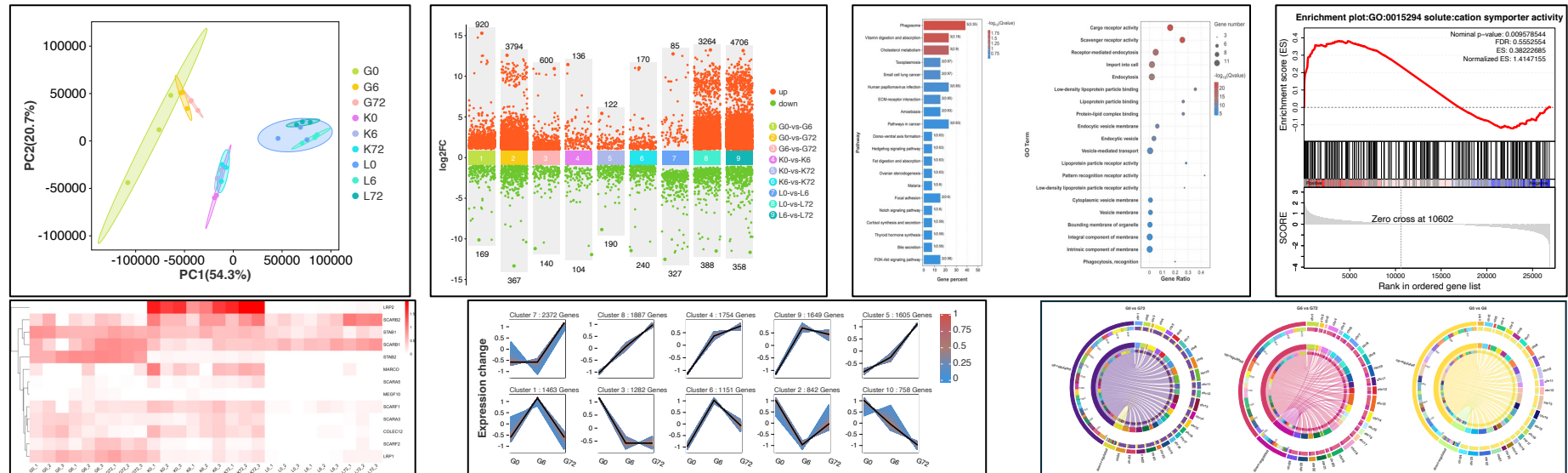


Fig. 5. The expression pattern of EcSRs genes in response to *V. harveyi* infection and low-salinity stress using qPCR.

7 RNA-Seq and enrichment analysis



Conclusion

- We identified 13 SRs in *E. coioides* and found key members respond to both infection and low-salinity stress, indicating their role in dual stress responses.
- This study provides a foundational resource for understanding fish immune adaptation and informs strategies for enhancing disease resistance in aquaculture.