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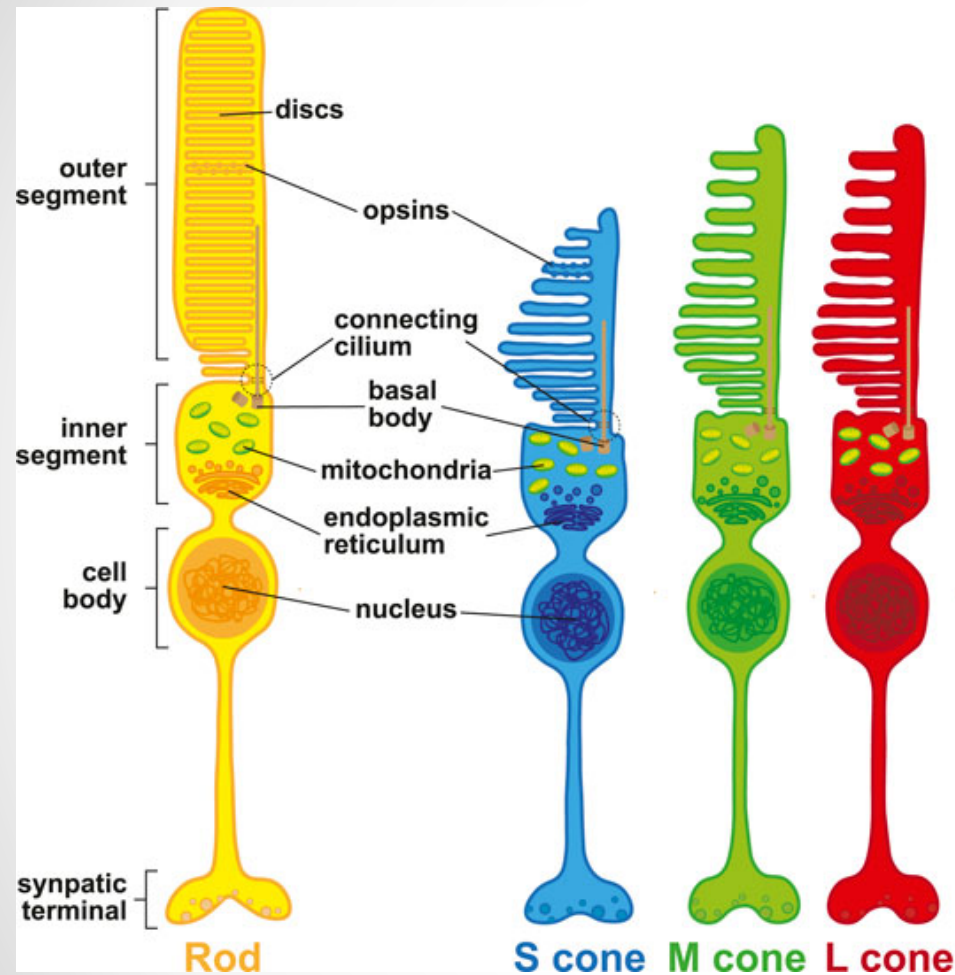
The First Opsins Prediction In *Achatina fulica* Genome

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Introduction



Light sensitivity is a fundamental property of multicellular animals, possible with the use of special cells - light-sensitive and photoreceptor cells. Photoreception is mostly based in the rods of the retina, the molecular mechanism of which is inseparably connected with the visual pigments located in the outer segment of the rods. The molecules of these visual pigments (also light-sensitive) consist of two structures: a vitamin A derivative and visual opsin. The main function of visual opsin is the triggering of the phototransduction cascade, followed by cell hyperpolarization and generation of the nerve impulse.

<https://doi.org/10.3389/fcell.2022.878350>

Introduction



However, such data on these proteins of gastropod molluscs are very scarce, and for terrestrial species are absent at all. Meanwhile, the first sequenced genome of the terrestrial gastropod, ***Achatina fulica***, was published (<https://doi.org/10.1093/gigascience/giz124>). So, the aim of this study is the prediction of the amino acid sequences of opsins in the *A. fulica* genome.

Supporting data for "A chromosomal-level genome assembly for the giant African snail *Achatina fulica*"

Dataset type: Genomic

Data released on September 25, 2019

[Guo Y](#); [Zhang Y](#); [Liu Q](#); [Huang Y](#); [Mao G](#); [Yue Z](#); [Abe EM](#); [Li J](#); [Wu Z](#); [Li S](#); [Zhou X](#); [Hu W](#); [Xiao N](#) (2019): Supporting data for "A chromosomal-level genome assembly for the giant African snail *Achatina fulica*" GigaScience Database.

<http://dx.doi.org/10.5524/100647>

DOI 10.5524/100647

Aim & Objectives

The **aim** of this study is the prediction of the amino acid sequences of rhodopsins in the *A. fulica* genome.

Objectives:

1. To form a base of amino acid sequences of rhodopsins of molluscs;
2. To perform comparative analysis of the collected sequences;
3. Predict homologous sequences in *Achatina fulica* genome;
4. Search for conserved domains in the predicted sequences of rhodopsins of *Achatina fulica*;
5. Construct phylogenetic tree for evolutionary relationship analysis.

Materials & Methods



Collect amino acid sequences at NCBI



Multiple Sequence Alignment
(Clustal Omega+MUSCLE)



*Achatina
fulica* genome

Predict sequences in *Achatina fulica* genome



(GIGA)ⁿ_{DB}



Repeated MSA (Clustal Omega+MUSCLE)

Conserve
Domains
Search



NCBI



Phylogenetic tree (Nieghbor-Joining)



Amino acid sequence collection

Organism	Number of rhodopsin sequences
<i>Aplysia californica</i>	13
<i>Biomphalaria glabrata</i>	12
<i>Pomacea canaliculata</i>	10
<i>Octopus bimaculoides</i>	5
<i>Octopus sinensis</i>	10
<i>Pecten maximus</i>	10

Results of Multiple Sequence Alignment

Type of rhodopsin	Number of identical amino acid	Number of conserved substitutions	Number of semi-conserved substitutions	Average sequence lengths
Rhodopsin	1	3	3	379
Rhodopsin-Go	2	5	5	309
Rhodopsin-Gq	1	7	2	368
Rhodopsin-like pigment	38	74	70	492

Predicted rhodopsin sequences in the *A.fulica* genome by HHMER

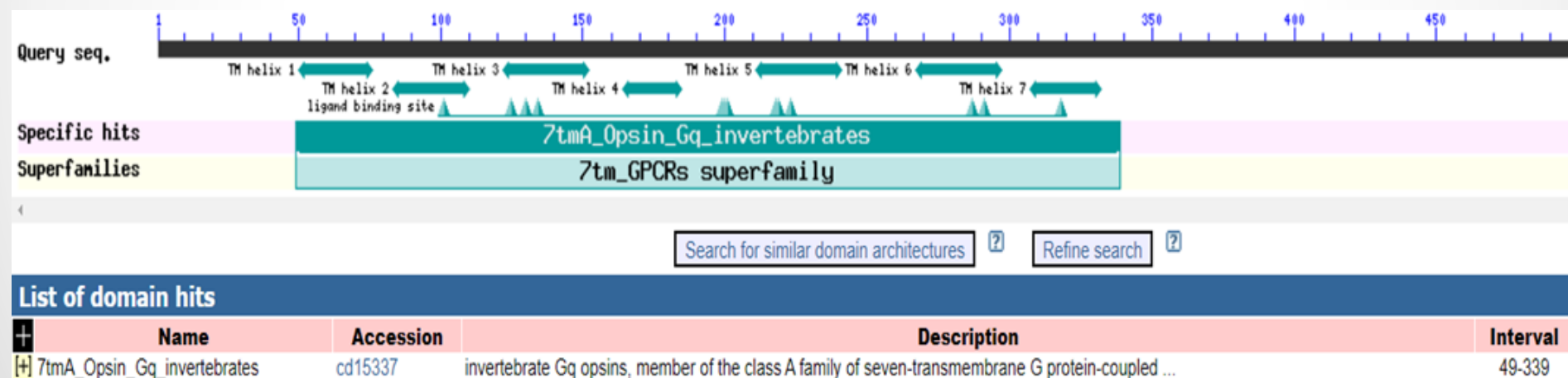
Accession # at GigaScience Database	E-value
Afu011750	2.5e-120
Afu004575	2.5e-130
Afu016848	2.7e-23
Afu005002	2.6e-106
Afu015337	1.7e-269
Afu003765	4.4e-144
Afu022267	7.1e-133

Conservative Domain Search in predicted rhodopsin sequences of *A. fulica*

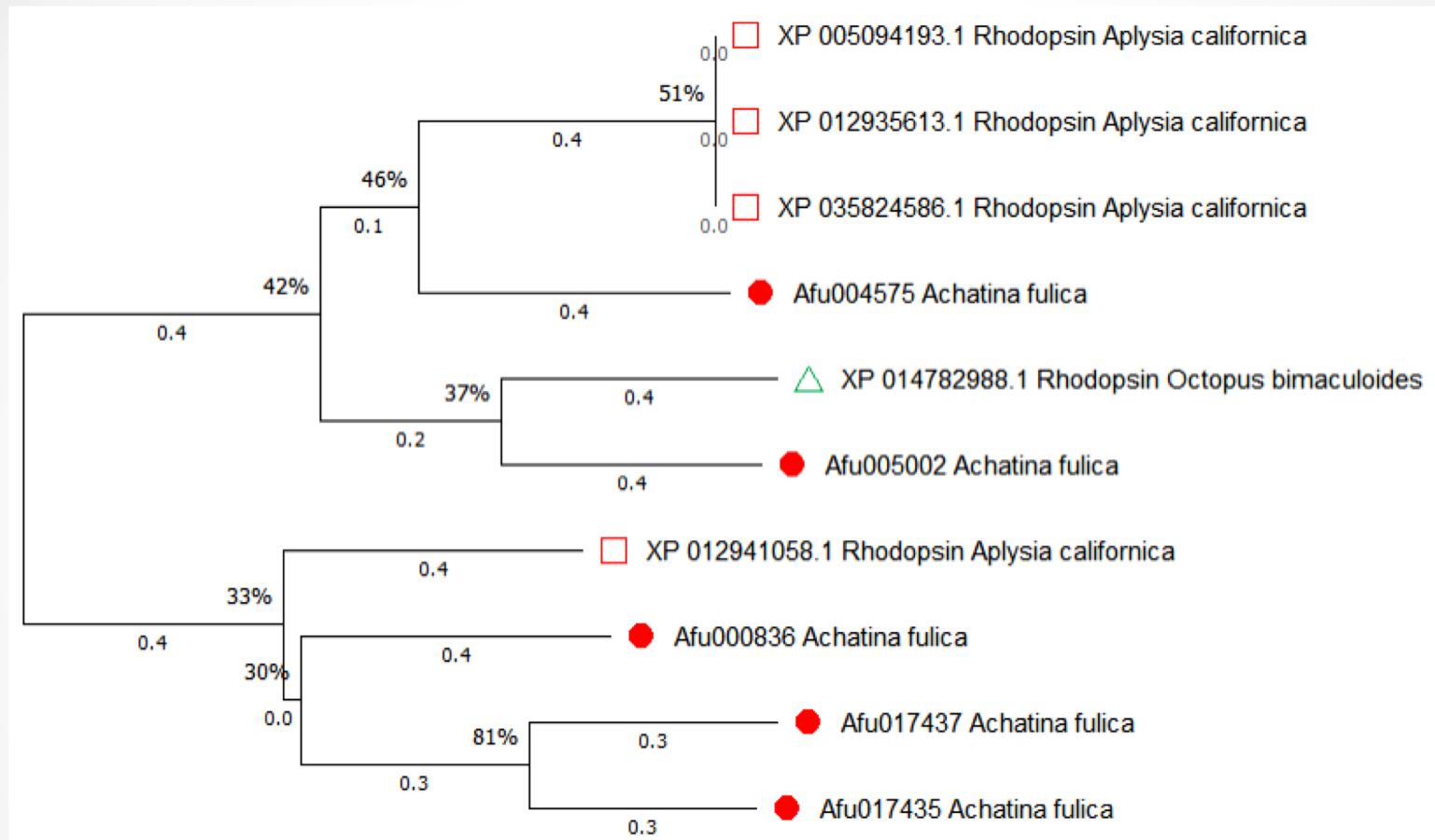
Accession # at GigaScience Database	Number of Transmembrane Domains	Detected Conservative Domains
Afu011750	4	7tm_GPCRs super family
Afu004575	7	7tm_GPCRs super family
Afu016848	7	7tm_classA_rhodopsin-like
Afu005002	7	7tmA_Opsin_Gq_invertebrates
Afu015337	>20 и 2	7tm_GPCRs super family и 7tm_classA_rhodopsin-like
Afu003765	8	7tm_GPCRs super family
Afu022267	2x6 и 4	7tm_GPCRs super family и 7tm_classA_rhodopsin-like

Conservative Domain Search in predicted rhodopsin sequences of *A. fulica*

Conservative domain 7tmA_Opsin_Gq_invertebrates amino acid sequence of *Achatina fulica* Afu005002 detected by NCBI Conserved Domain Search algorithms



Phylogenetic Analysis

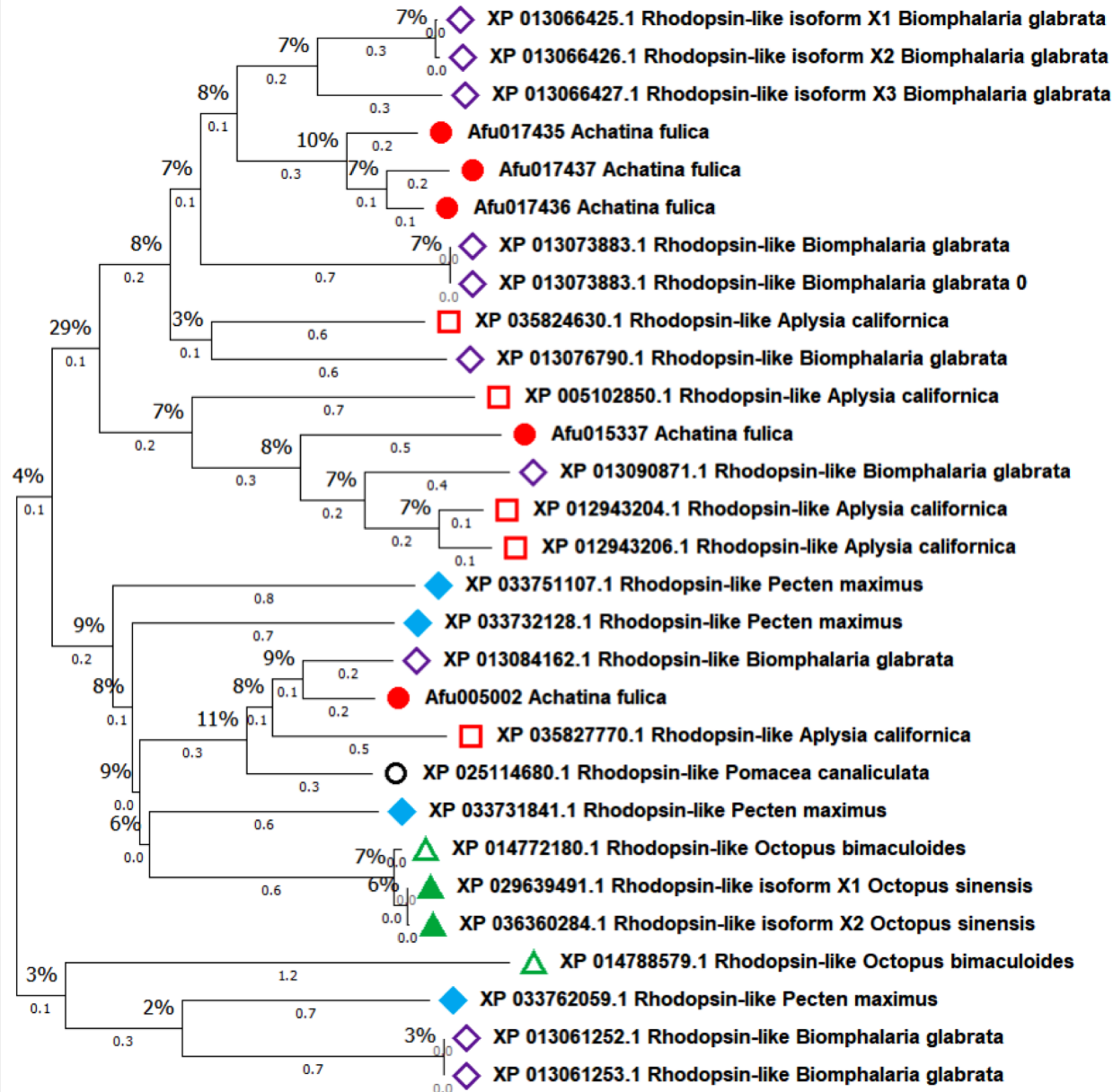


Phylogenetic tree of rhodopsins constructed by the Neighbor-Joining method

● - *Achatina fulica*; □ - *Aplysia californica*; △ - *Octopus bimaculoides*

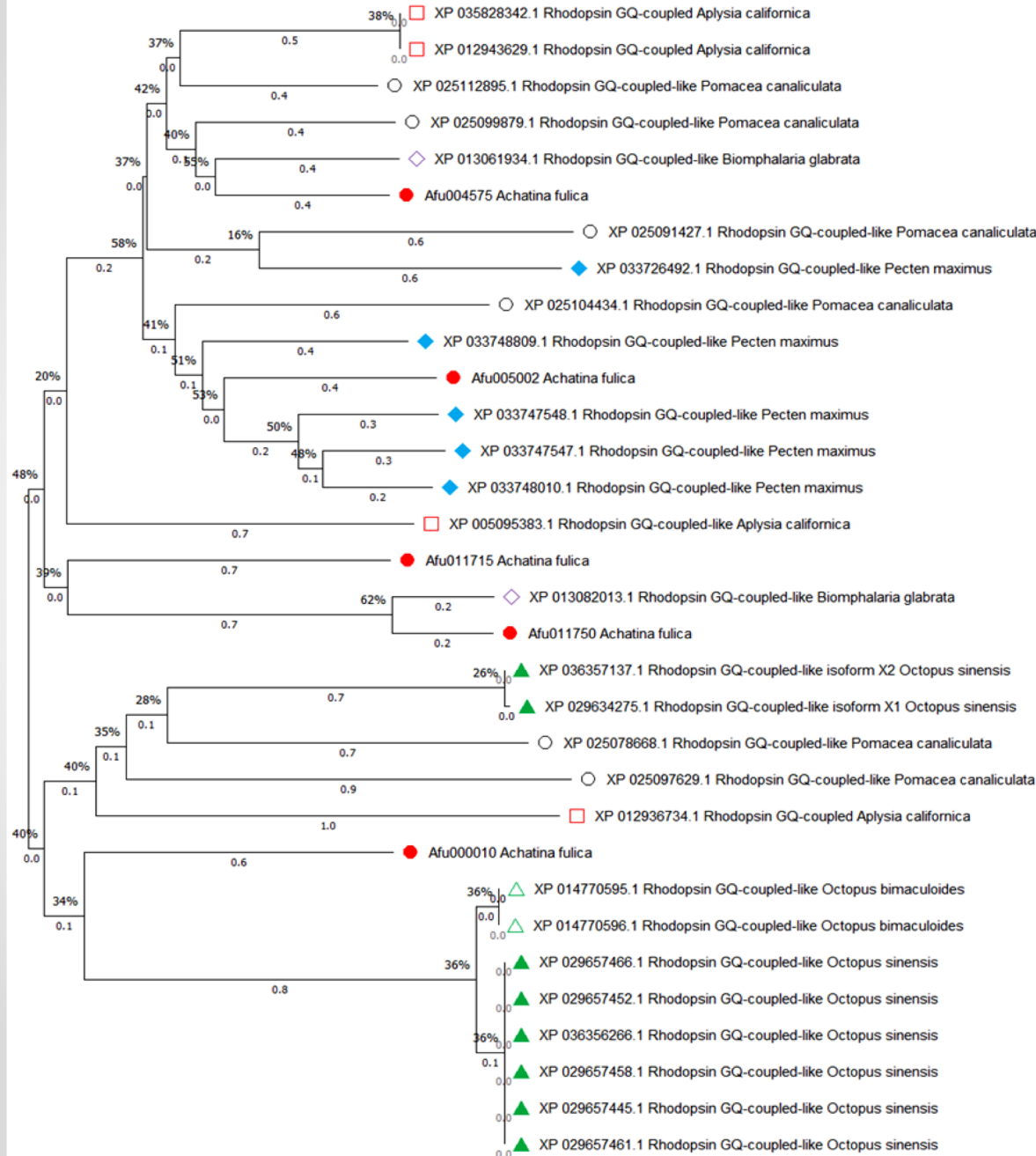
Phylogenetic Analysis

Phylogenetic tree of rhodopsin-like pigment constructed by the Neighbor-Joining method



- - Achatina fulica;
- - Aplysia californica;
- △ - Octopus bimaculoides;
- ▲ - Octopus sinensis;
- ◆ - Pecten maximus;
- ◇ - Biomphalaria glabrata;
- - Pomacea canaliculata

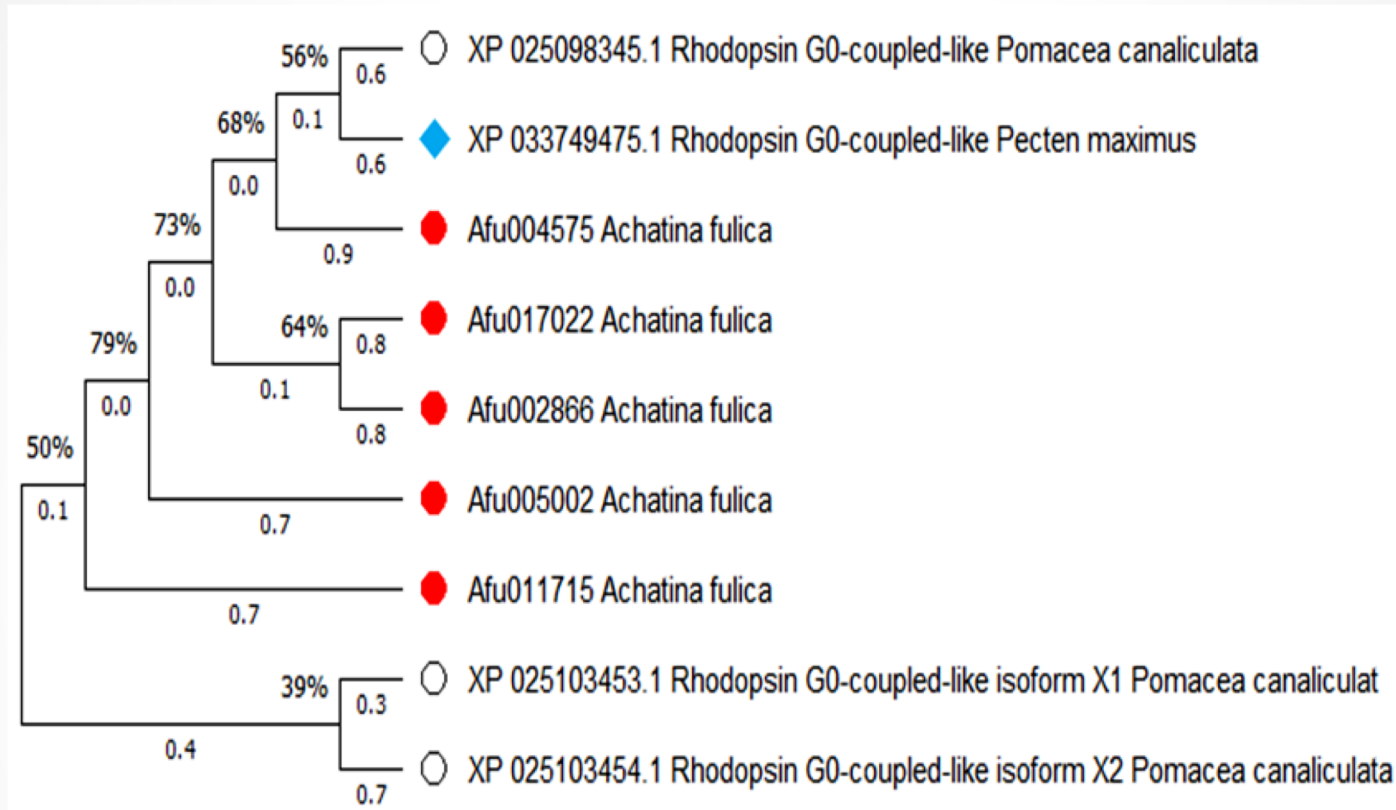
Phylogenetic Analysis



Phylogenetic tree of rhodopsin-Gq pigment constructed by the Neighbor-Joining method

- - *Achatina fulica*;
- - *Aplysia californica*;
- △ - *Octopus bimaculoides*;
- ▲ - *Octopus sinensis*;
- ◆ - *Pecten maximus*;
- ◇ - *Biomphalaria glabrata*;
- - *Pomacea canaliculata*

Phylogenetic Analysis



Phylogenetic tree of rhodopsin-Go pigment constructed by the Neighbor-Joining method

- - Achatina fulica; □ - Aplysia californica; ▲ - Octopus bimaculoides;
- ▲ - Octopus sinensis; ◆ - Pecten maximus; ◇ - Biomphalaria glabrata;
- - Pomacea canaliculata

Conclusion

So, we determined five rhodopsin G-coupled protein sequences in *A. fulica* genome among them are

- **Afu011750,**
- **Afu004575,**
- **Afu005002,**
- **Afu003765,**
- **Afu022267.**

This is the first attempt to annotate the *Achatina fulica* genome, which was started by searching for opsins. Our study opens up new opportunities for further more detailed evolutionary and genetic studies of molluscs, including the study of visual mechanisms. But it should be noted that opsins form a diverse multifunctional group of proteins, of which only some are part of visual pigments. Therefore, work towards the identification of visual opsins in *Achatina fulica* should be continued.

Thank You For Your Attention

