Molecular Pathogens 2024, Vol.15, No.2, 72-82
http://microbescipublisher.com/index.php/mp

Research Insight Open Access

Isolation, Identification, and Genomic Analysis of Kelp Pathogens

Fan Wang
Aquatic Biology Research Center, Cuixi Academy of Biotechnology, Zhuji, 311800, Zhejiang, China
Corresponding email: fan.wang@cuixi.org

Molecular Pathogens, 2024, Vol.15, No.2 doi: 10.5376/mp.2024.15.0008
Received: 04 Feb., 2024
Accepted: 10 Mar., 2024
Published: 05 Apr., 2024

Preferred citation for this article:
Wang F., 2024, Isolation, identification, and genomic analysis of kelp pathogens, Molecular Pathogens, 15(2): 72-82 (doi: 10.5376/mp.2024.15.0008)

Abstract Kelp, as an important marine biological resource, plays a crucial role in the ecosystem and has extensive applications in food, medicine, and other fields. However, kelp pathogens pose a serious threat to kelp health and growth, leading to decreased yield and economic losses. Research on the isolation, identification, and genomic analysis of kelp pathogens is significant as it helps understand the characteristics and virulence factors of pathogens, reveals the mechanisms of host-pathogen interactions, and provides scientific basis for disease management and breeding disease-resistant kelp. This study covers sampling methods and laboratory isolation techniques, morphological, biochemical, and molecular identification methods, DNA extraction and sequencing, genomic annotation, and bioinformatics analysis tools. Through comparative genomic analysis, the study identifies the virulence genes of kelp pathogens, explores their infection mechanisms and host defense responses, and assesses their impact on kelp health and growth. The research aims to provide references for kelp aquaculture disease management strategies, disease-resistant breeding, and sustainable farming practices, as well as to offer a scientific basis for future genomic research and disease prevention.

Keywords Kelp pathogens; Isolation; Identification; Genomic analysis; Host-pathogen interactions

1 Introduction

Kelp, large brown algae belonging to the order *Laminariales*, are foundational species in marine ecosystems, particularly in temperate and arctic coastal regions. These photosynthetic giants create essential habitats, forming underwater forests that are among the most productive marine ecosystems on Earth (Weigel and Pfister, 2019; Weigel et al., 2022). Kelp forests play a crucial role in nutrient cycling, energy capture, and transfer, and provide biogenic coastal defense (Teagle et al., 2017). They offer extensive substrata for colonizing organisms, ameliorate conditions for understory assemblages, and provide three-dimensional habitat structures for a vast array of marine plants and animals, including commercially important species (Teagle et al., 2017). The ecological significance of kelp extends to their role in supporting diverse microbial communities that facilitate the transfer of carbon from algal primary production to higher trophic levels (Lemay et al., 2018).

Despite the ecological importance of kelp, our understanding of the microorganisms associated with them, particularly pathogens, remains limited. Kelp-associated bacteria are known to play significant roles in nutrient cycling and host-microbe interactions, potentially influencing the health and productivity of kelp forests (Vollmers et al., 2017; Weigel et al., 2022). Pathogens can have profound impacts on kelp populations, leading to declines in kelp forest coverage and associated biodiversity (Vollmers et al., 2017). Understanding the dynamics of kelp pathogens is essential for managing and conserving these critical ecosystems. The study of kelp pathogens can reveal insights into disease mechanisms, host-pathogen interactions, and the potential for microbial symbionts to influence kelp health and resilience (Vollmers et al., 2017; Weigel et al., 2022).

This study synthesizes current knowledge on the isolation, identification, and genomic analysis of kelp pathogens. It aims to collect and analyze existing research on kelp-associated microbial communities, identify key pathogens affecting kelp species, explore genomic insights into kelp-pathogen interactions, and highlight gaps in current research and propose future directions. This study will contribute to a comprehensive understanding of kelp pathogens and their implications for the health and sustainability of kelp forest ecosystems.

2 Isolation of Kelp Pathogens

2.1 Sampling methods

Sampling methods for isolating kelp pathogens involve collecting samples from various parts of the kelp and its surrounding environment. For instance, bacterial strains have been isolated from coastal sediment samples and fresh kelp samples collected from kelp culture areas (Ye et al., 2022). Additionally, biofilm samples from brown macro-algae, such as *Macrocystis pyrifera*, have been collected for metagenomic analysis (Vollmers et al., 2017). Sampling also includes collecting kelp from specific locations, such as Li Island in Rongcheng, China, to isolate difficult-to-cultivate bacterial strains. These methods ensure a diverse collection of potential pathogens and associated microorganisms for further analysis.

2.2 Laboratory isolation techniques

Laboratory isolation techniques for kelp pathogens include a variety of methods to culture and identify bacterial strains. For example, strains can be isolated using standard microbiological techniques, such as growing them on specific media under controlled conditions (Ye et al., 2022). Metagenomic approaches, including shotgun and amplicon sequencing, are also employed to analyze biofilm samples and identify novel microbial species (Vollmers et al., 2017). Additionally, innovative binning approaches are used to untangle genomes of novel species from metagenomic data (Vollmers et al., 2017). Techniques such as the use of Taxoblast for detecting bacterial contaminants in kelp genomes are also crucial for ensuring the accuracy of genomicdata (Dittami and Corre, 2017).

2.3 Challenges in isolation

Isolating kelp pathogens presents several challenges. One significant challenge is the presence of bacterial contaminants and hybrid sequences in kelp genomes, which can complicate the identification of true pathogens (Dittami and Corre, 2017). Another challenge is the difficulty in cultivating certain bacterial strains, such as those from the phylum Verrucomicrobiota, which require specific conditions for growth (Ye et al., 2022). Additionally, the complex interactions between kelp and its associated microbiome can make it difficult to isolate and identify specific pathogenic organisms (Weigel et al., 2022). The need for advanced genomic and bioinformatics tools to accurately identify and characterize these pathogens further adds to the complexity of the isolation process (Dittami and Corre, 2017; Vollmers et al., 2017; Weigel et al., 2022).

By addressing these challenges through meticulous sampling, advanced laboratory techniques, and robust bioinformatics tools, researchers can improve the isolation and identification of kelp pathogens, contributing to a better understanding of their impact on kelp health and ecosystem dynamics.

3 Identification of Kelp Pathogens

3.1 Morphological identification

Morphological identification of kelp pathogens involves the examination of physical characteristics of the pathogens under a microscope. This method is often the first step in identifying pathogens and can provide immediate information about the presence and type of infection. For instance, fluorescence in situ hybridization (FISH) can be used to identify microbial pathogens by binding fluorescence-labeled probes to ribosomes of infectious agents, allowing for the visualization and differentiation of pathogens based on their morphology (Frickmann et al., 2017). This technique is particularly useful for identifying key pathogens in mixed species samples and provides spatial resolution that is crucial for understanding the distribution and interaction of pathogens within the kelp tissue.

3.2 Biochemical tests

Biochemical tests are essential for the further characterization and identification of kelp pathogens. These tests involve assessing the metabolic and enzymatic activities of the pathogens. For example, the API20E biochemical identification system can be used to enhance the discrimination of environmental bacteria isolated from kelp. This system evaluates various biochemical reactions, such as the production of specific enzymes or the utilization of

certain substrates, to identify bacterial species (Popović et al., 2022). In a study comparing the identification results of MALDI-TOF MS and API20E, it was found that certain biochemical reactions, such as ONPG, GLU, and OX, were consistently positive for reliable identification of specific bacterial strains, highlighting the importance of biochemical tests in confirming pathogen identity before proceeding to molecular methods (Popović et al., 2022).

3.3 Molecular identification methods

Molecular identification methods provide precise and reliable identification of kelp pathogens at the genetic level. Techniques such as sequencing and metagenomic analysis are commonly used. For instance, the use of Taxoblast, a pipeline for detecting contaminating sequences in the kelp genome, has revealed the presence of bacterial contaminants and hybrid sequences, indicating the importance of molecular tools in identifying and characterizing pathogens (Dittami and Corre, 2017). Additionally, metagenome-assembled genomes (MAGs) from kelp microbiomes have been reconstructed to determine the functional roles of microbial symbionts, which include potential pathogens. These MAGs provide insights into the metabolic potential and functional roles of bacteria associated with kelp, such as nutrient cycling and biofilm formation, which are crucial for understanding pathogen-host interactions (Weigel et al., 2022). Furthermore, sequencing of molecular markers like 5'COI and ITS1 has been used to investigate the diversity and host specificity of kelp endophytes, identifying various species of the genera *Laminarionema* and *Laminariocolax* that invade kelp tissues (Bernard et al., 2018). These molecular methods are indispensable for the accurate identification and understanding of kelp pathogens.

4 Genomic Analysis Techniques

4.1 DNA extraction and sequencing

DNA extraction and sequencing are fundamental steps in the genomic analysis of kelp pathogens. High-throughput sequencing technologies, such as Random Subcloning Sequencing (SMS), have revolutionized the ability to analyze genomic DNA from environmental samples without prior cultivation (Jo et al., 2020). For instance, whole-genome sequencing datasets have been used to study ecto- and endosymbiotic relationships on kelp, revealing various species colonizing the kelp sporophyte (Bringloe et al., 2021). Bringloe et al. (2021) isolated and performed sequencing analysis using two molecular markers (5' COI and ITS1) on 56 endophytic strains from seven different kelp species collected from Europe, Chile, Korea, and New Zealand, uncovering the molecular diversity of these endophytes (Figure 1). Additionally, Restriction Site-Associated DNA (RAD) sequencing has been used to construct a high-density SNP linkage map for kelp, facilitating genetic research and the development of molecular tools (Zhang et al., 2015).

The study from Bringloe et al., 2021 shows the scanning electron micrograph of the *Nereida* sp. MMG025 strain and the phylogenetic tree based on 100 single-copy genes. The electron micrograph details the cell morphology and surface structure of this strain, aiding in understanding its environmental adaptation mechanisms. The phylogenetic tree illustrates the evolutionary relationships of this strain with other related strains, revealing its precise classification within the Rhodobacteraceae family. These data provide important references for studying the genomic characteristics and ecological functions of this strain.

4.2 Genomic annotation

Genome annotation involves identifying and labeling genes and other functional elements within a genome. This process is crucial for understanding the genetic composition and potential functions of kelp pathogens. For example, the annotation of the mitochondrial genome of a suspected brown algal parasite revealed many atypical features, including gene duplications and rearrangements, indicative of its parasitic lifestyle (Bringloe et al., 2021). Similarly, the annotation of the draft genome sequence of the Nereida sp. MMG025 strain isolated from giant kelp suggests that it may represent a new species, providing a resource for future microbiological and biotechnological research (Alker et al., 2022). Microscopic images show the cellular morphology and surface structures of the MMG025 strain, aiding in understanding its ecological adaptation mechanisms (Figure 2). The phylogenetic tree

reveals the phylogenetic position of this strain within the Rhodobacteraceae family and its genetic relationships with other related strains. This information lays the foundation for further studies on the metabolic capabilities and ecological functions of MMG025.

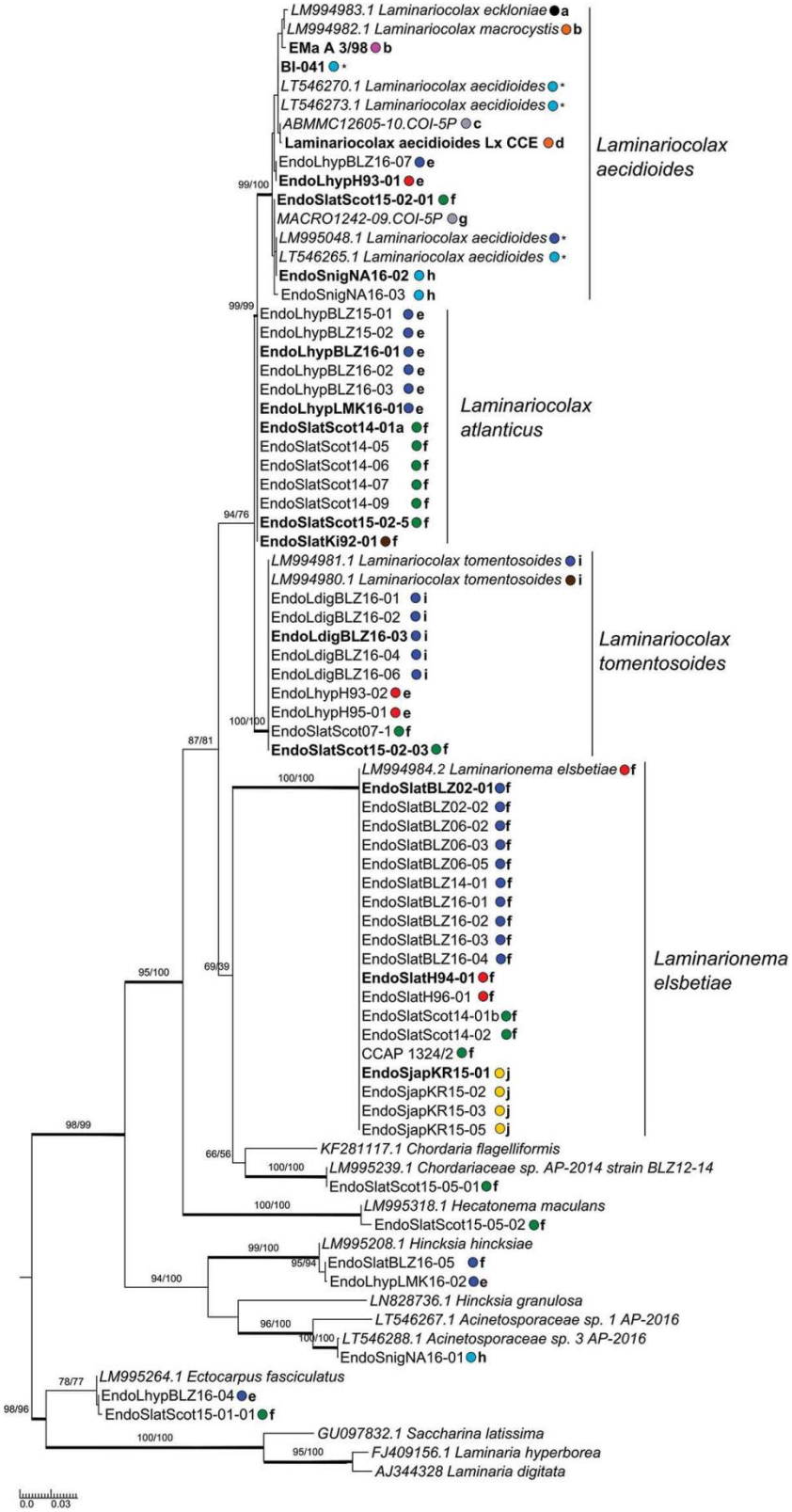

Figure 1 Phylogenetic tree of 5'COI sequences. Values at nodes indicate bootstrap support obtained by ML/BI analysis. Bootstrap

supports >95 in both analyses are indicated by a thicker line. Reference sequences from public databases are printed in italics and using the identities given in the original publications. ITS1 sequences are available for specimens shown in bold. The colours and letters behind the strain names indicate the geographic origin and host species, respectively. Origins: black = South Africa; orange = Chile; pink = New Zealand; light blue = Arctic; grey = Canadian Pacific coast; dark blue = Brittany; red = Helgoland; green = UK; brown = Kiel, western Baltic; yellow = Korea. Hosts: a = *Ecklonia maxima*; b = *Macrocystis pyrifera*; c = *Saccharina sessilis*; d = *Lessonia berteroana*; e = *Laminaria hyperborea*; f = *Saccharina latissima*; g = *Costaria costata*; h = *Saccharina nigripes*; i= *Laminaria digitata*; j = *Saccharina japonica*; * = grown from incubated substratum (Adopted from Bringloe et al., 2021)

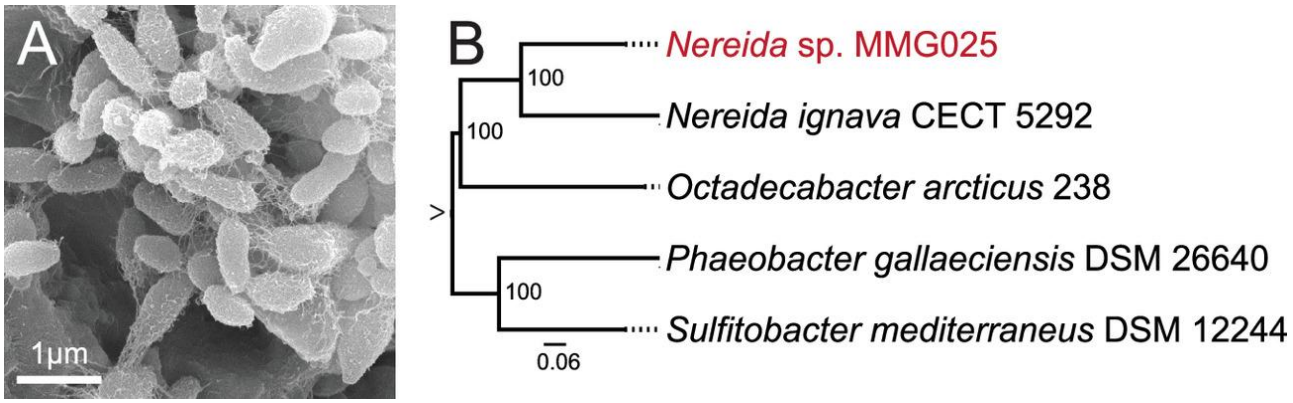

Figure 2 (A) Scanning electron micrograph of *Nereida* sp. MMG025. (B) Maximum likelihood phylogeny constructed using the codon tree method through PATRIC with 100 single-copy genes and proteins identified using cross-genus families (PGfams) (10, 21-27). The phylogeny root is indicated by an arrow for clarity. The GenBank accession numbers of the sequences used in this analysis are as follows: CVPC00000000 (*Nereida ignava* CECT 5292), CP003744 (*Octadecabacter arcticus* 238), CP006967 (*Phaeobacter gallaeciensis* DSM 26640), and QBKU00000000 (*Sulfitobacter mediterraneus* DSM 12244) (Adapted from Alker et al., 2022)

4.3 Bioinformatics tools and software

Bioinformatics tools and software are essential for analyzing and interpreting genomic data. Various tools have been developed to address specific challenges in genomic analysis. For instance, Taxoblast is a pipeline used for the post-assembly detection of contaminating sequences in kelp genomes, helping to identify bacterial contaminants and hybrid scaffolds (Dittami and Corre, 2017). Another example is the Genomic Approximation Method for Bacterial Identification and Tracking (GAMBIT), which uses k-mer based strategies for the identification of bacteria from whole genome sequence reads, ensuring high confidence in pathogen identification (Lumpe et al., 2022). Additionally, bioinformatics systems have been developed to eliminate contamination and low-complexity sequences from draft genomes, improving the accuracy of metagenomic analyses (Lu and Salzberg, 2018).

The integration of advanced DNA extraction and sequencing techniques, comprehensive genomic annotation, and sophisticated bioinformatics tools is pivotal for the isolation, identification, and genomic analysis of kelp pathogens. These methodologies enable researchers to uncover the complex interactions between kelp and their associated microbial communities, providing insights into the ecological and functional roles of these organisms.

5 Pathogen Genomics and Virulence Factors

5.1 Genomic features of pathogens

The genomic features of kelp pathogens can be elucidated through comparative genomics, which reveals significant insights into their genetic makeup and potential virulence factors. For instance, the complete genomes of *Edwardsiella piscicida* and *Edwardsiella anguillarum* were sequenced using the Oxford-Nanopore MinION platform, revealing distinct genomic features such as the number of coding genes, rRNA, and tRNA, which were 8322, 25, and 98 for *E. anguillaru*m, and 5458, 25, and 98 for *E. piscicida*, respectively. These differences suggest unique pathogenic mechanisms and the necessity for tailored preventive strategies (Byadgi et al., 2022). Similarly,

the genome of *Aeromonas hydrophila* HX-3 was sequenced, identifying 4483 genes, including those involved in quorum sensing and virulence, which are crucial for understanding its pathogenicity (Jin et al., 2020).

5.2 Identification of virulence genes

The identification of virulence genes is critical for understanding the pathogenicity of kelp pathogens. Comparative genomics has been instrumental in this regard. For example, the analysis of *Vibrio anguillarum* strains revealed that highly virulent strains possess unique accessory genomes containing pathogenic genomic islands, prophage-like elements, and virulence factors, which are absent in less virulent strains (Castillo et al., 2017). In comparative genomic analyses of multiple *Vibrio anguillarum* strains, it was found that the virulence of *V. anguillarum* is multifactorial and associated with the acquisition of mobile genetic elements (Figure 3). Additionally, the virulence factors of *Flavobacterium columnare* were identified through comparative genomics, highlighting genes involved in tissue colonization and interbacterial competition, which are unique to virulent isolates (Declercq et al., 2021). Tools like PathoFact have also been developed to predict virulence factors and antimicrobial resistance genes in metagenomic data, providing a comprehensive approach to identifying these critical genes (Nies et al., 2021).

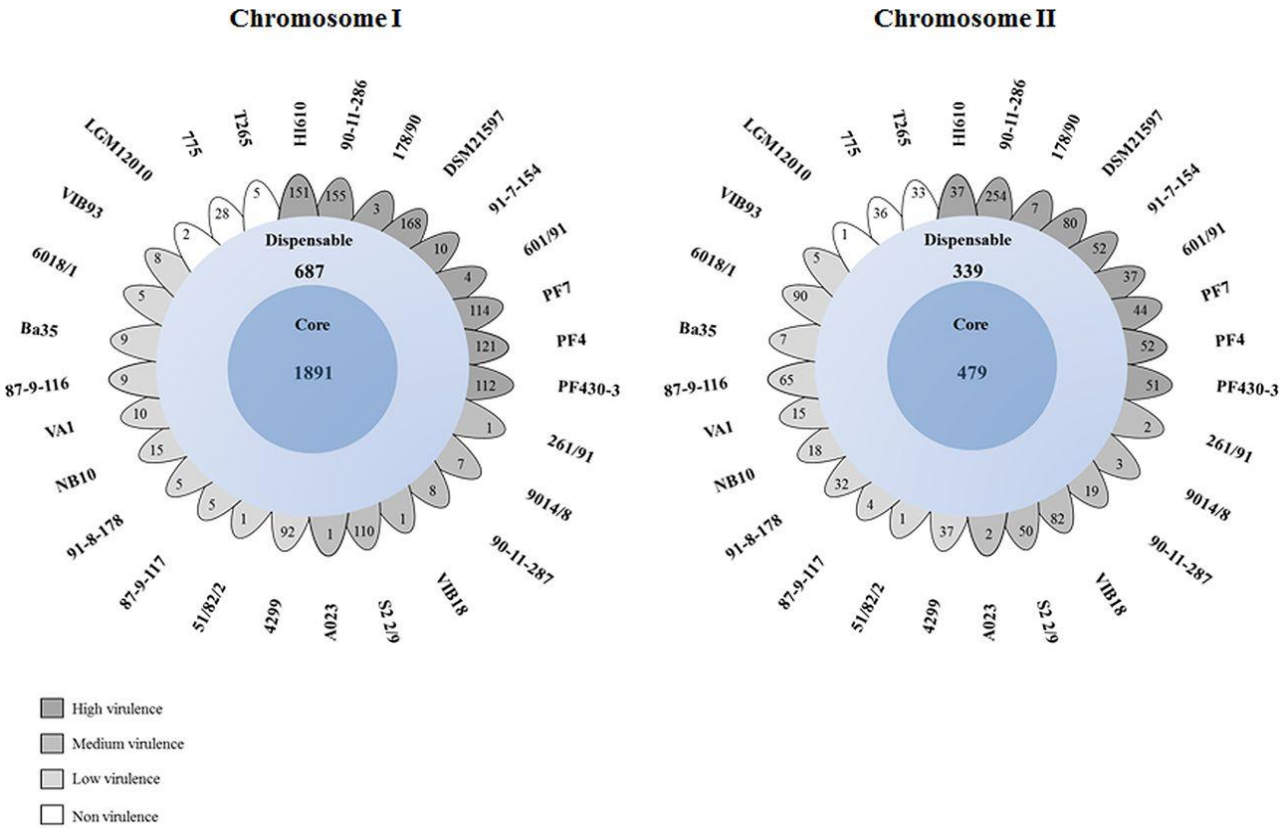

Figure 3 The pan-genome of *V. anguillarum*. The flower plots represent the number of shared (core) and specific (accessory/dispensable) genes based on cluster orthologs for each chromosome. Petals display numbers of strain-specific genes found in each genome of *V. anguillarum* strains with core gene numbers in the center. The gray colors indicate the virulence category as found in three fish larva model systems (Adopted from Castillo et al., 2017)

Figure from Castillo et al. (2017) displays the core and accessory genome composition of *Vibrio anguillarum* strains. The flower diagram shows core genes shared by all strains in the center, while the petals represent strain-specific accessory genes. This visualization illustrates the genetic diversity within *V. anguillarum*, with highly virulent strains exhibiting more unique genes. This comprehensive genomic view aids in understanding the roles of accessory genes in pathogenicity and adaptability.

5.3 Comparative genomic analysis

Comparative genomic analysis provides a deeper understanding of the genetic diversity and evolutionary relationships among pathogens. For instance, the comparative analysis of 15 *Vibrio anguillarum* isolates from different hosts and regions revealed high nucleotide identity among strains, with subtle nucleotide variations contributing to differences in virulence (Busschaert et al., 2015). Similarly, the comparative genomics of *Escherichia coli* has been used to identify polyvalent vaccine targets by analyzing the distribution of virulence factors across different pathotypes and phylogroups (Clark and Maresso, 2021). The use of platforms like VFDB and tools like VFanalyzer facilitates the systematic identification of virulence factors, enhancing our ability to conduct comparative pathogenomic studies (Liu et al., 2018).

The integration of genomic sequencing, identification of virulence genes, and comparative genomic analysis provides a comprehensive framework for understanding the pathogenicity of kelp pathogens. These approaches not only reveal the genetic features and virulence factors of these pathogens but also offer insights into their evolutionary relationships and potential strategies for disease prevention and control.

6 Host-Pathogen Interactions

6.1 Mechanisms of infection

The mechanisms of infection in kelp pathogens involve complex interactions between the host and the pathogen. For instance, the filamentous algal endophyte L*aminarionema elsbetiae* induces significant transcriptomic changes in its host, *Saccharina latissima*, and occasionally in *Laminaria digitata*. These changes include differential gene expression related to host-endophyte recognition, defense response, and cell wall modification, which are crucial for understanding the infection process and host specificity (Xing et al., 2021). Additionally, the oomycete *Anisolpidium ectocarpii* infects the giant kelp *Macrocystis pyrifera* by undergoing physiological shifts that are sensitive to autophagy inhibitors, indicating that autophagy plays a role in the pathogen's life cycle and infection process (Murúa et al., 2020).

6.2 Host defense responses

Kelp hosts exhibit various defense mechanisms in response to pathogen infection. The giant kelp *Macrocystis pyrifera* mounts local defenses through autophagy, which can directly eliminate the pathogen by xenophagy. This process involves the recycling of plastids in uninfected host cells, suggesting a systemic response mediated by autophagy (Murúa et al., 2020). Furthermore, proteomic analyses have highlighted the role of immune-related proteins in host defense responses. These proteins are upregulated during infections, helping to identify and quantify the host's immune response to pathogens (Ahmed et al., 2019). The NOD-like receptor signaling pathway has also been identified as a significant defense mechanism in tilapia, which may have parallels in kelp defense responses (Wu et al., 2019).

6.3 Impact on kelp health and growth

Pathogen infections can have profound impacts on kelp health and growth. The presence of *Laminarionema elsbetiae* in *Saccharina latissima* and *Laminaria digitata* leads to morphological changes such as twisted stipes and deformed blades, which can affect the overall growth rate of the kelp (Xing et al., 2021). In another study, the interaction between kelp and bacteria under different nitrogen concentrations showed that bacterial communities could enhance kelp growth rates under low nitrogen availability, although this effect is regulated by the genetic background of the kelp populations (Florez et al., 2021). Additionally, the spatial organization of the kelp microbiome, including the dense microbial biofilm on kelp blades, plays a crucial role in nutrient cycling and can impact kelp health and growth by modulating the chemistry of the surrounding water column (Ramírez-Puebla et al., 2020).

7 Implications for Kelp Aquaculture

7.1 Disease management strategies

Effective disease management strategies are crucial for the sustainability of kelp aquaculture. The integration of

molecular and genomic tools has revolutionized disease surveillance and diagnostics, enabling more precise identification and control of pathogens. For instance, the use of genomic data for disease surveillance can enhance the accuracy of pathogen detection and inform better decision-making processes in aquaculture management (Stärk et al., 2019). Additionally, metagenomics and other omics approaches can provide comprehensive insights into microbial communities and antimicrobial resistance, which are essential for developing targeted disease management strategies (Nogueira and Botelho, 2021). The implementation of these advanced diagnostic tools can significantly reduce the incidence of disease outbreaks and improve the overall health of kelp farms.

7.2 Breeding for disease resistance

Breeding for disease resistance is a promising approach to mitigate the impact of infectious diseases in kelp aquaculture. Advances in genomic technologies, such as genome-wide association studies (GWAS) and genotyping by sequencing (GBS), have identified key genetic loci associated with disease resistance in various aquaculture species (Robledo et al., 2017; Zhou et al., 2019; Griot et al., 2021). These technologies can be applied to kelp to identify and select for disease-resistant traits, thereby enhancing the resilience of kelp populations to pathogens. For example, the identification of single-nucleotide polymorphisms (SNPs) associated with disease resistance can inform selective breeding programs aimed at producing kelp strains with superior resistance to bacterial and viral infections (Zhou et al., 2019; Griot et al., 2021). Moreover, machine learning models have shown potential in predicting disease resistance, offering a valuable tool for optimizing breeding strategies (Palaiokostas et al., 2021).

7.3 Sustainable aquaculture practices

Sustainable aquaculture practices are essential to ensure the long-term viability of kelp farming. The use of plant-enriched diets has been shown to improve the growth, immunity, and disease resistance of aquaculture species, presenting a sustainable alternative to traditional feed practices (Reverter, 2020). This approach can be adapted to kelp aquaculture by incorporating plant-based supplements that enhance the health and productivity of kelp. Additionally, the detection and removal of bacterial contaminants from kelp genomes using tools like Taxoblast can prevent the spread of pathogens and maintain the genetic integrity of kelp populations (Dittami and Corre, 2017). By adopting these sustainable practices, kelp aquaculture can reduce its environmental footprint and contribute to the overall health of marine ecosystems.

In conclusion, the integration of advanced genomic tools, selective breeding for disease resistance, and sustainable aquaculture practices can significantly enhance the resilience and productivity of kelp aquaculture. These strategies not only improve disease management but also promote the sustainable growth of the industry, ensuring its long-term success.

8 Concluding Remarks

The research on kelp pathogens has significantly revealed the potential impacts of microbial communities associated with kelp on kelp health. Key findings include the identification of bacterial contaminants in kelp genomes and the characterization of new bacterial species associated with kelp, such as Kordiimonas marina and Kordiimonas laminariae, which exhibit unique metabolic capabilities and adaptations to the marine environment. Metagenomic studies have uncovered diverse microbial taxa associated with kelp, which may play roles in biofilm formation and antimicrobial activity. Additionally, the discovery of potential phaeophycean parasites in kelp highlights the complexity of kelp-associated microbial communities and their potential pathogenic interactions.

Genomic studies are crucial for understanding the complex relationships between kelp and their associated microbial communities. The use of high-throughput sequencing and metagenomic approaches has enabled the reconstruction of bacterial genomes from kelp surfaces, revealing their metabolic potential and functional roles. These studies have shown that kelp-associated bacteria can contribute to nutrient cycling, biofilm formation, and the provision of essential vitamins to their host. Comparative genomic analyses have also provided insights into the evolutionary adaptations of kelp-associated bacteria, such as the ability to degrade sulfated polysaccharides

and produce secondary metabolites. Furthermore, the identification of novel microbial species and their genomic characteristics can inform the development of biotechnological applications, such as the use of kelp-associated bacteria in marine drug discovery.

Future research should focus on long-term monitoring of changes in kelp-associated microbial communities under different environmental conditions to identify potential pathogenic shifts and their triggers. Functional genomics approaches should be employed to elucidate the specific roles of microbial genes in kelp health and disease, including studying gene expression profiles and metabolic pathways in response to biotic and abiotic stressors. Investigating the molecular mechanisms underlying host-microbe interactions, including the signaling pathways involved in microbial colonization and host defense responses, should also be a priority. Exploring the potential of kelp-associated microbes for biotechnological applications, such as developing probiotics for kelp aquaculture or discovering novel antimicrobial compounds, is crucial. Additionally, developing rapid and accurate methods for identifying kelp pathogens and assessing the efficacy of various control strategies, including using natural microbial antagonists and genetic resistance in kelp, is essential. By addressing these research areas, we can enhance our understanding of kelp pathogens and develop effective strategies to mitigate their impact on kelp ecosystems and aquaculture.

Acknowledgments

The author sincerely thanks the two anonymous peer reviewers for their detailed review and valuable feedback on the manuscript of this study.

Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

Ahmed F., Kumar G., Soliman F., Adly M., Soliman H., El-Matbouli M., and Saleh M., 2019, Proteomics for understanding pathogenesis immune modulation and host pathogen interactions in aquaculture, Comparative Biochemistry and Physiology, Part D Genomics and Proteomics, 32: 100625. https://doi.org/10.1016/j.cbd.2019.100625

Alker A., Hern N., Ali M., Baez M., Baswell B., Baxter B., Blitz A., Calimlim T., Chevalier C., Eguia C., Esparza T., Fuller A., Gwynn C., Hedin A., Johnson R., Kaur M., Laxina R., Lee K., Maguire P., Martelino I., Melendez J., Navarro J., Navarro J., Osborn J., Padilla M., Peralta N., Pureza J., Rojas J., Romo T., Sakha M., Salcedo G., Sims K., Trieu T., Niesman I., and Shikuma N., 2022, Draft genome sequence of *Nereida* sp. Strain MMG025 isolated from giant kelp, Microbiology Resource Announcements, 11(6): e00122-22. https://doi.org/10.1128/mra.00122-22

Bernard M., Strittmatter M., Murúa P., Heesch S., Cho G., Leblanc C., and Peters A., 2018, Diversity biogeography and host specificity of kelp endophytes with a focus on the genera *Laminarionema* and *Laminariocolax* (Ectocarpales Phaeophyceae), European Journal of Phycology, 54(1): 39-51. https://doi.org/10.1080/09670262.2018.1502816

Bringloe T., Sauermann R., Krause-Jensen D., Olesen B., Klimova A., Klochkova T., and Verbruggen H., 2021, High-throughput sequencing of the kelp Alaria (Phaeophyceae) reveals epi-endobiotic associations including a likely phaeophycean parasite, European Journal of Phycology, 56(4): 494-504. https://doi.org/10.1080/09670262.2021.1882704

Busschaert P., Frans I., Crauwels S., Zhu B., Willems K., Bossier P., Michiels C., Verstrepen K., Lievens B., and Rediers H., 2015, Comparative genome sequencing to assess the genetic diversity and virulence attributes of 15 *Vibrio anguillarum* isolates, Journal of fish diseases 38(9): 795-807. https://doi.org/10.1111/jfd.12290

Byadgi O., Rahmawaty A., Wang P., and Chen S., 2022, Comparative genomics of *Edwardsiella anguillarum* and *Edwardsiella piscicida* isolated in Taiwan enables the identification of distinctive features and potential virulence factors using Oxford-Nanopore MinION® sequencing., Journal of fish diseases, 46(4): 287-297. https://doi.org/10.1111/jfd.13743

Castillo D., Alvise P., Xu R., Zhang F., Middelboe M., and Gram L., 2017, Comparative Genome Analyses of Vibrio anguillarum Strains Reveal a Link with Pathogenicity Traits, mSystems, 2(1): 10-1128. https://doi.org/10.1128/mSystems.00001-17

Clark J., and Maresso A., 2021, Comparative pathogenomics of *Escherichia coli*: polyvalent vaccine target identification through virulome analysis, Infection and Immunity, 89(8): 1. https://doi.org/10.1128/IAI.00115-21

Declercq A., Tilleman L., Gansemans Y., Witte C., Haesebrouck F., Nieuwerburgh F., Smet A., and Decostere A., 2021, Comparative genomics of *Flavobacterium columnare* unveils novel insights in virulence and antimicrobial resistance mechanisms, Veterinary Research, 52: 1-13. https://doi.org/10.1186/s13567-021-00899-w

Dittami S., and Corre E., 2017, Detection of bacterial contaminants and hybrid sequences in the genome of the kelp Saccharina japonica using Taxoblast, Peer J., 5: e4073.
https://doi.org/10.7717/peerj.4073

Florez J., Camus C., Hengst M., and Buschmann A., 2021, A mesocosm study on bacteria-kelp interactions: Importance of nitrogen availability and kelp genetics, Journal of Phycology, 57(6): 1777-1791.
https://doi.org/10.1111/jpy.13213

Frickmann H., Zautner A., Moter A., Kikhney J., Hagen R., Stender H., and Poppert S., 2017, Fluorescence in situ hybridization (FISH) in the microbiological diagnostic routine laboratory: a review, Critical Reviews in Microbiology, 43(3): 263-293.
https://doi.org/10.3109/1040841X.2016.1169990

Griot R., Allal F., Phocas F., Brard-Fudulea S., Morvezen R., Bestin A., Haffray P., François Y., Morin T., Poncet C., Vergnet A., Cariou S., Brunier J., Bruant J., Peyrou B., Gagnaire P., and Vandeputte M., 2021, Genome-wide association studies for resistance to viral nervous necrosis in three populations of European sea bass (*Dicentrarchus labrax*) using a novel 57k SNP array DlabChip, Aquaculture, 530: 735930. https://doi.org/10.1016/j.aquaculture.2020.735930

Jin L., Chen Y., Yang W., Qiao Z., and Zhang X., 2020, Complete genome sequence of fish-pathogenic *Aeromonas hydrophila* HX-3 and a comparative analysis: insights into virulence factors and quorum sensing, Scientific Reports, 10(1): 15479.
https://doi.org/10.1038/s41598-020-72484-8

Jo J., Oh J., and Park C., 2020, Microbial community analysis using high-throughput sequencing technology: a beginner's guide for microbiologists, Journal of Microbiology, 58: 176-192.
https://doi.org/10.1007/s12275-020-9525-5

Lemay M., Martone P., Keeling P., Burt J., Krumhansl K., Sanders R., and Parfrey L., 2018, Sympatric kelp species share a large portion of their surface bacterial communities, Environmental Microbiology, 20: 658-670.
https://doi.org/10.1111/1462-2920.13993

Liu B., Zheng D., Jin Q., Chen L., and Yang J., 2018, VFDB 2019: a comparative pathogenomic platform with an interactive web interface, Nucleic Acids Research, 47: D687 - D692.
https://doi.org/10.1093/nar/gky1080

Lu J., and Salzberg S., 2018, Removing contaminants from databases of draft genomes, PLoS Computational Biology, 14(6): e1006277. https://doi.org/10.1371/journal.pcbi.1006277

Lumpe J., Gumbleton L., Gorzalski A., Libuit K., Varghese V., Lloyd T., Tadros F., Arsimendi T., Wagner E., Stephens C., Sevinsky J., Hess D., and Pandori M., 2022, GAMBIT (Genomic Approximation Method for Bacterial Identification and Tracking): A methodology to rapidly leverage whole genome sequencing of bacterial isolates for clinical identification, PLOS ONE, 18(2): e0277575.
https://doi.org/10.1371/journal.pone.0277575

Murúa P., Müller D., Etemadi M., West P., and Gachon C., 2020, Host and pathogen autophagy are central to the inducible local defences and systemic response of the giant kelp *Macrocystis pyrifera* against the oomycete pathogen *Anisolpidium ectocarpii*, The New Phytologist, 226(5): 1445 - 1460. https://doi.org/10.1111/nph.16438

Nies L., Lopes S., Busi S., Galata V., Heintz-Buschart A., Laczny C., May P., and Wilmes P., 2021, PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data, Microbiome, 9: 1-14.
https://doi.org/10.1186/s40168-020-00993-9

Nogueira T., and Botelho A., 2021, Metagenomics and other omics approaches to bacterial communities and antimicrobial resistance assessment in aquacultures, Antibiotics, 10(7): 787.
https://doi.org/10.3390/antibiotics10070787

Palaiokostas C., 2021, Predicting for disease resistance in aquaculture species using machine learning models, Aquaculture Reports, 20: 100660. https://doi.org/10.1016/J.AQREP.2021.100660

Popović N., Kepec S., Kazazić S., Strunjak-Perović I., Bojanić K., and Čož-Rakovac R., 2022, Identification of environmental aquatic bacteria by mass spectrometry supported by biochemical differentiation, PLoS ONE 17(6): e0269423.
https://doi.org/10.1371/journal.pone.0269423

Ramírez-Puebla S., Weigel B., Jack L., Schlundt C., Pfister C., and Welch J., 2020, Spatial organization of the kelp microbiome at micron scales, Microbiome, 10(1): 52.
https://doi.org/10.1101/2020.03.01.972083

Rana S., Valentin K., Bartsch I., and Glöckner G., 2019, Loss of a chloroplast encoded function could influence species range in kelp, Ecology and Evolution, 9: 8759 - 8770.
https://doi.org/10.1002/ece3.5428

Reverter M., Tapissier-Bontemps N., Sarter S., Sasal P., and Caruso D., 2020, Moving towards more sustainable aquaculture practices: a meta-analysis on the potential of plant-enriched diets to improve fish growth immunity and disease resistance, Reviews in Aquaculture, 13(1): 537-555. https://doi.org/10.1111/raq.12485

Robledo D., Palaiokostas C., Bargelloni L., Martínez P., and Houston R., 2017, Applications of genotyping by sequencing in aquaculture breeding and genetics, Reviews in Aquaculture, 10: 670 - 682.
https://doi.org/10.1111/raq.12193

Stärk K., Pękala A., and Muellner P., 2019, Use of molecular and genomic data for disease surveillance in aquaculture: Towards improved evidence for decision making., Preventive veterinary medicine, 167: 190-195.
https://doi.org/10.1016/j.prevetmed.2018.04.011

Teagle H., Hawkins S., Moore P., and Smale D., 2017, The role of kelp species as biogenic habitat formers in coastal marine ecosystems, Journal of Experimental Marine Biology and Ecology, 492: 81-98.
https://doi.org/10.1016/J.JEMBE.2017.01.017

Vollmers J., Frentrup M., Rast P., Jogler C., and Kaster A., 2017, Untangling genomes of novel planctomycetal and verrucomicrobial species from monterey bay kelp forest metagenomes by refined binning, Frontiers in Microbiology, 8: 472.
https://doi.org/10.3389/fmicb.2017.00472

Weigel B., and Pfister C., 2019, Successional dynamics and seascape-level patterns of microbial communities on the canopy-forming kelps *Nereocystis luetkeana* and *Macrocystis pyrifera*, Frontiers in Microbiology, 10: 346.
https://doi.org/10.3389/fmicb.2019.00346

Weigel B., Miranda K., Fogarty E., Watson A., and Pfister C., 2022, Functional insights into the kelp microbiome from metagenome-assembled genomes, mSystems, 7(3): e01422-21.
https://doi.org/10.1128/msystems.01422-21

Wu W., Li L., Liu Y., Huang T., Liang W., and Chen M., 2019, Multiomics analyses reveal that NOD-like signaling pathway plays an important role against Streptococcus agalactiae in the spleen of tilapia., Fish and shellfish immunology, 95: 336-348.
https://doi.org/10.1016/j.fsi.2019.10.007

Xing Q., Bernard M., Rousvoal S., Corre E., Markov G., Peters A., and Leblanc C., 2021, Different early responses of laminariales to an endophytic infection provide insights about kelp host specificity, Frontiers in Marine Science, 8: 742469.
https://doi.org/10.3389/fmars.2021.742469

Ye M., Jin C., Liu X., Tan X., Ye Y., and Du Z., 2022, Description and genomic characterization of *Oceaniferula flavus* sp. nov., a novel potential polysaccharide-degrading candidate of the difficult-to-cultivate phylum verrucomicrobiota isolated from seaweed, Marine Drugs, 21(1): 31. https://doi.org/10.3390/md21010031

Ye Y., Hao Z., Yue Y., Ma L., Ye M., and Du Z., 2022, Characterization of *Kordiimonas marina* sp. nov. and *Kordiimonas laminariae* sp. nov. and comparative genomic analysis of the genus Kordiimonas a marine-adapted taxon, Frontiers in Marine Science, 9: 919253. https://doi.org/10.3389/fmars.2022.919253

Zhang N., Zhang L., Tao Y., Guo L., Sun J., Li X., Zhao N., Peng J., Li X., Zeng L., Chen J., and Yang G., 2015, Construction of a high density SNP linkage map of kelp (*Saccharina japonica*) by sequencing *Taq* I site associated DNA and mapping of a sex determining locus, BMC Genomics, 16: 1-11.
https://doi.org/10.1186/s12864-015-1371-1

Zhou Q., Su Z., Li Y., Liu Y., Wang L., Lu S., Wang S., Gan T., Liu F., Zhou X., Wei M., Liu G., and Chen S., 2019, Genome-wide association mapping and gene expression analyses reveal genetic mechanisms of disease resistance variations in *Cynoglossus semilaevis*, Frontiers in Genetics ,10: 1167.
https://doi.org/10.3389/fgene.2019.01167