

Unveiling AjSWD: A Key Antibacterial Defender in Sea Cucumber Immunity

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DESCRIPTION

In the aquatic world, where threats from microbial pathogens are constant and intense, marine invertebrates such as the sea cucumber *Apostichopus japonicus* rely heavily on innate immunity to survive. Among the molecular sentinels playing a vital role in this defense are the whey acidic protein domain-containing proteins. These molecules, first recognized in mammals, are now known to be widespread across the animal kingdom, particularly in invertebrates. A recent study has highlighted a novel WD protein, designated as AjSWD, in *A. japonicus*, revealing its structural characteristics, antibacterial properties, and functional significance in immune defense.

Exploring the molecular sentinel of bacteria

AjSWD is a unique WD protein containing two distinctive functional domains: a Whey Acidic Protein (WAP) domain and a KAZAL domain. These domains are known to contribute to immune responses through protease inhibition and antimicrobial activities. The structure of Whey Acidic Protein (WAP) domain, defined by eight conserved cysteine residues that form four stabilizing disulfide bonds, gives the protein a resilient framework to interact with microbial membranes and disrupt their integrity.

The expression profile of AjSWD across the tissues of *A. japonicus* revealed a broad distribution, with the highest expression in the body wall, a key interface between the organism and its environment. This suggests a front-line role for AjSWD in defense against pathogens. Notably, after a challenge with *Vibrio splendidus*, a notorious pathogen in aquaculture responsible for high mortality and economic losses in sea cucumber farming, the expression of AjSWD was significantly upregulated, both at the mRNA and protein levels. This upsurge in expression clearly indicates AjSWD's involvement in the immune response triggered by bacterial invasion.

Further *in vitro* studies showed that the recombinant AjSWD protein (rAjSWD) and its isolated WAP domain (rAjSWD-WAP) could agglutinate bacteria, bind Pathogen-Associated Molecular Patterns (PAMPs), and exhibit direct antibacterial activity.

Importantly, the antibacterial mechanism was identified as the disruption of bacterial cell membranes, leading to the death of pathogens. These findings align with the well-documented function of WAP domains in other species, reinforcing the evolutionary conservation of this immune mechanism.

AjSWD particularly interesting is the enhanced antibacterial efficacy observed in its WAP domain alone (rAjSWD-WAP), compared to the full-length protein. This discovery not only reveals the core functional component of the molecule but also opens potential avenues for its application in disease prevention strategies, especially in aquaculture where antibiotic overuse poses risks of resistance development and environmental harm.

Implications for aquaculture and innate immunity research

The discovery of AjSWD provides both practical and theoretical value. On a practical level, the demonstrated ability of rAjSWD and rAjSWD-WAP to improve survival rates in juvenile sea cucumbers following *V. splendidus* challenge suggests that these proteins or their mimetics, could be developed into biotherapeutics or immune-boosting agents in aquaculture. Given the substantial economic losses associated with bacterial diseases in *A. japonicus*, incorporating such natural immune enhancers into management practices could represent a sustainable alternative to traditional antibiotics.

On a broader scientific scale, this study enriches our understanding of WD proteins in non-mammalian species, particularly marine invertebrates. While much of the prior research has focused on WD proteins in crustaceans and vertebrates, the immunological roles of these proteins in echinoderms have remained largely unexplored. AjSWD thus represents a valuable model for studying innate immunity in this phylum and may help uncover additional immune molecules with similar or novel functions.

The characterization of AjSWD also emphasizes the modular nature of immune proteins in invertebrates, where the combination of domains like WAP, KAZAL, and others leads to multifunctionality. This modularity allows these organisms to rapidly adapt to the diverse microbial threats present in their

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Received: 26-Feb-2025, Manuscript No. IGOA-25-38441; **Editor assigned:** 28-Feb-2025, Pre QC No. IGOA-25-38441 (PQ); **Reviewed:** 14-Mar-2025, QC No. IGOA-25-38441; **Revised:** 21-Mar-2025, Manuscript No. IGOA-25-38441 (R); **Published:** 28-Mar-2025, DOI: 10.35248/IGOA.25.10.255

Citation: Chi H (2025) Unveiling AjSWD: A Key Antibacterial Defender in Sea Cucumber Immunity. Immunogenet Open Access. 10:255.

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environments, despite lacking an adaptive immune system. In this context, AjSWD stands as a prime example of structural versatility translates into biological effectiveness.

Furthermore, the study prompts deeper questions about the evolution of innate immune molecules across species. The shared functional themes between invertebrate and vertebrate WD proteins suggest that nature has repeatedly favored the WAP domain as a reliable scaffold for immune defense. From sea cucumbers to humans, the conservation of this domain points to a universal mechanism that has been refined through evolutionary time.

CONCLUSION

In conclusion, the identification and functional elucidation of AjSWD from *A. japonicus* underscore its vital role in defending against bacterial pathogens. The findings not only broaden our understanding of immune strategies in marine invertebrates but also highlight the potential of leveraging natural immune effectors in aquaculture. As continues to delve into the molecular arsenal of marine species, proteins like AjSWD may well lead the way toward innovative and eco-friendly solutions to disease management in aquaculture.