Climbing the gaps in the male sexual-development pathway of the Eastern spiny lobster, *Sagamiaurus verreauxi*

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**Introduction**

The Eastern spiny lobster, *S. verreauxi*, is a species with promising potential in aquaculture. As a member of the commercially valued decapods, there is a solid understanding of male sexual-differentiation, regulated by the male-specific androgenic gland (AG), which secretes the insulin-like AG hormone (IAG). Although the masculinising effect of IAG is well characterised, there are significant gaps in our knowledge of the entire male sexual-development pathway (SDP). Hence, our research focuses on the endocrinology of IAG that governs sex-differentiation and the upstream genetic pathways that initiate sex-determination.

**Methods**

Transcriptome assembly and gene identification were conducted as in ref. 2. Modelling, optimisation and electrostatics were undertaken using Discovery Studio 4.0 and the Delphi Platform. Binding interactions were assigned using PDBeSum and validated through structural alignment in Chimera 1.9 and using Haddock3 docking simulations. Differential expression analyses (DEA) were run on the cleaned transcriptome (TTPT) highlighting transcripts that were >10-fold upregulated (UR) in one of the comparative tissues; specific transcripts were also recorded. Transcripts were annotated using NCBI.

**Endocrinology of IAG**

**Evidence of an insulin-signalling system**

Transcriptome screening identified two novel insulin-like peptides, Sv-ILP1 and Sv-ILP2, and a binding-protein, Sv-IGFBP.

Sv-IGFBP consists of a structurally defined N’ insulin-binding domain and a C’ immunoglobulin domain, linked by a Kazal-type serine protease inhibitor. The protein is predicted to bind via the N’ with the C’ enclosing the ligand; the predicted binding pocket is highlighted.

The discovery of these novel ILPs and binding protein highlights the complexity of IAG endocrinology and warrants further investigation...

**Ref**


**Sex-determinants upstream of IAG**

**AG transcripts with a function in sex-determination?**

Our research shows that a relatively low number of transcripts are UR or specific to the mature AG (B and C).

**Key transcripts identified**

1. Sv-IAAG
2. Sv-MAG
3. Alpha-2 macroglobulins
4. Dynemin chain 1 (WD40)
5. Chitinase 4

No transcripts with a putative sex-determining role were identified. The predominant function of the AG-UR and specific genes relates to IAG production and bioavailability.

**Looking past the AG**

**By running DEA on α and β tissues (B) we aimed to highlight the tissues with putative function in the SDP**.

**C)** The gonads were highlighted as the pivotal tissue showing genetic sex-determination.

**D)** The testis and antennal gland showed significant male-bias in transcript expression.

Thus, we suggest these tissues are fundamental within the male SDP.

**References**


