**Supplementary Material S1. Comparing the performance between Trinotate and EnTAP pipelines for the annotation of *Totoaba macdonaldi* liver’s transcriptome.**

After comparing EnTAP (Hart et al. 2020) and Trinotate (Bryant et al. 2017) results, we realize that the choice of the database is key for elucidating the biological relevance of the transcriptome. In addition, Trinotate showed a higher number of similarity alignments that were translated into GO terms. These results are shown below.

Gráfico, Gráfico de barras

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**Figure 1.** Evaluation of independent sequence similarity search results across different protein databases. Sequence similarity search with EnTAP and Trinotate pipelines. Numbers inside the stacked bars indicate the total number of sequences with at least one alignment against a specific database (green bars) and the total number of sequences without alignment against a specific database (red bars).

From the figure above, we observe that the Trinotate pipeline, using the Swiss-Prot database, produces the highest number of sequences with correct alignments (hits) in the similarity search.

Gráfico

Descripción generada automáticamente

**Figure 2.** Evaluation of GO and KEGG assignment. **A)** GO annotation rate of transcripts with at least one GO term with EnTAP (Best Overall) and Trinotate (Swiss-Prot) pipelines. **B)** Number of GO terms assigned to the totoaba transcriptome with EnTAP (Best Overall) and Trinotate (Swiss-Prot) pipelines. **C)** Number of KEGG terms assigned to the totoaba transcriptome with EnTAP (Best Overall) and Trinotate (Swiss-Prot) pipelines. **D)** Number of unique and shared sequences annotated with EnTAP (Best Overall) and Trinotate (Swiss-Prot) pipelines.

Therefore, we believe that our transcriptome annotation approach based on the Trinotate pipeline is not an artifact of a mammalian bias. Furthermore, it is worth mentioning that *de novo* assembled transcriptome sequences are uninformative on their own and must be assigned to human-readable identifiers that have their functional and evolutionary properties characterized to elucidate the functions of the sequences (Raghavan et al. 2022). Therefore, we believe that our transcriptome annotation, based on the Swiss-Prot and Trinotate pipeline, is suitable for this study.

**References:**

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