Differential Expression of Transcriptome and Proteome in Developing and Diapause Embryos of Turquoise Killifish

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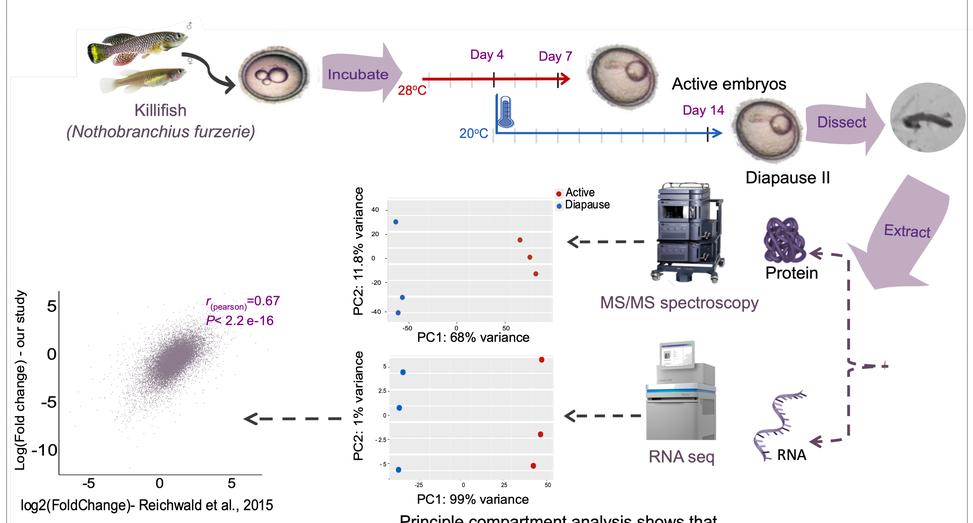
1. Abstract

Diapause is a programmed suspension of development and ageing that allows survival in sub-optimal environments. Presumably, cellular components required to resume development must be preserved throughout diapause, while metabolic activities are profoundly reduced. Our analysis of the transcriptome and proteome of diapause and actively developing embryos reveals that levels of transcripts and proteins are decoupled in numerous instances, most notably for genes involved in translation, suggesting extensive post-transcriptional regulation of gene expression.

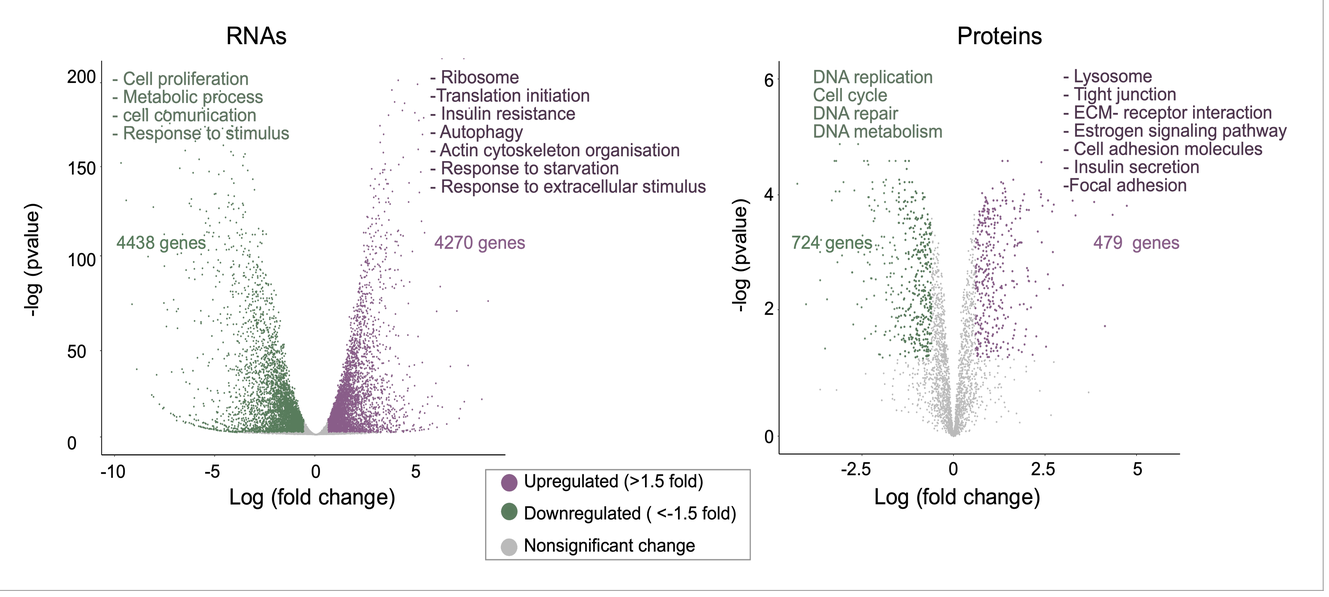
2. Workflow



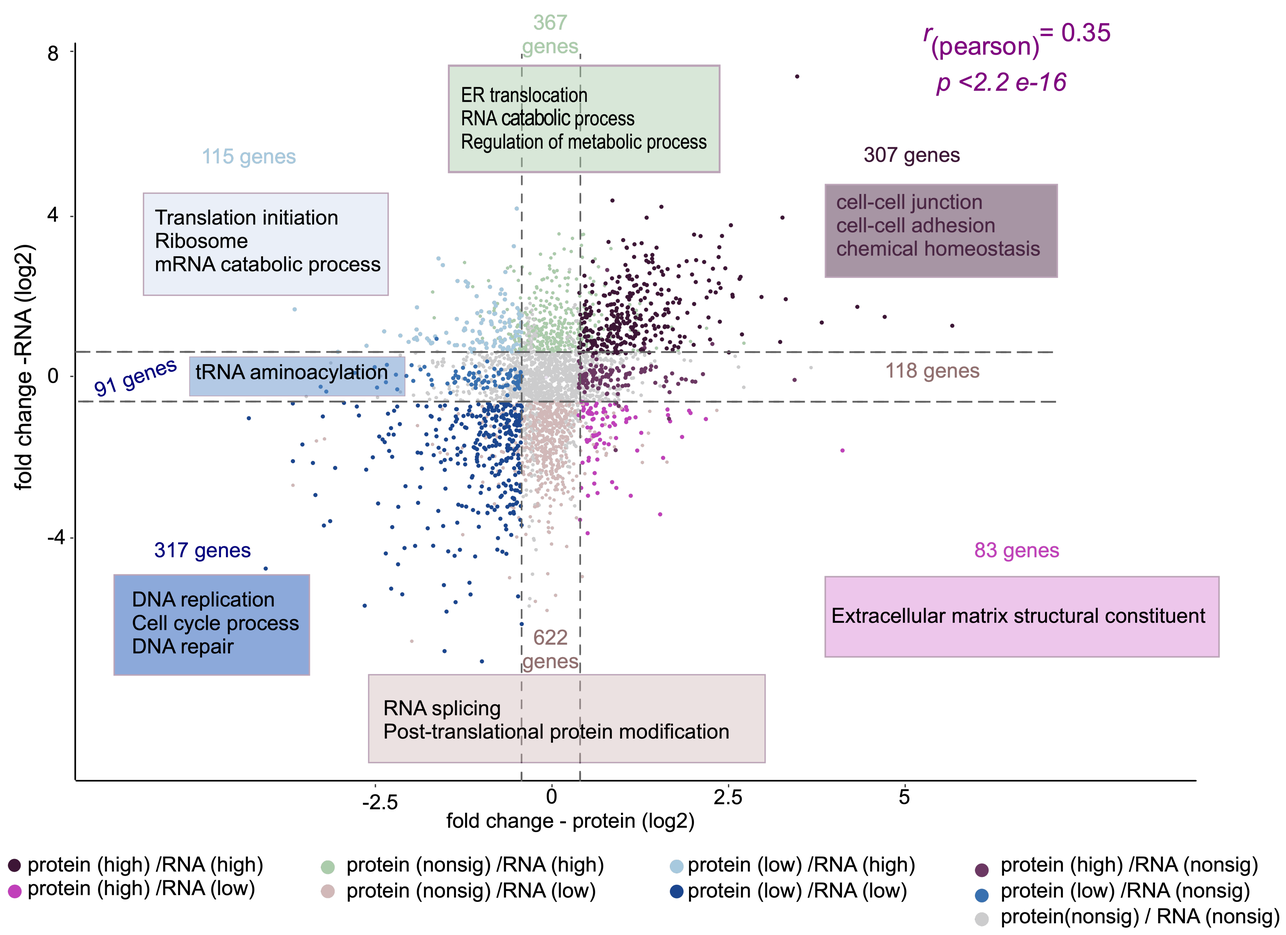
Diapuse transcriptome data is consistent with the published one[2].

Principle compartment analysis shows that the proteome and transcriptome of Diapause are quite different from actively developed ones

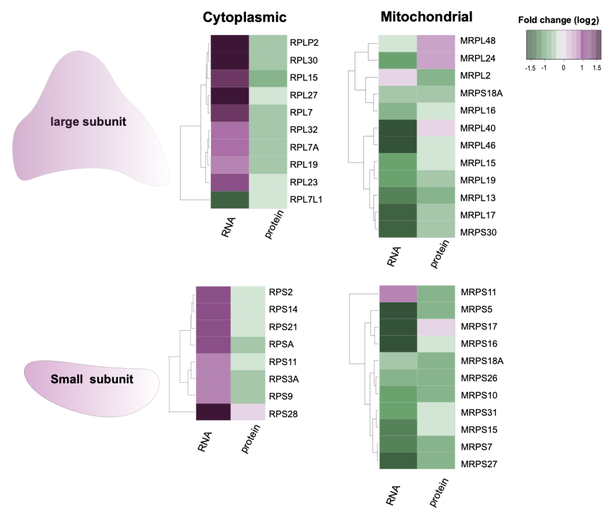
3. Differential regulation of protein and transcript levels in diapause



4. Relationship between transcripts and corresponding proteins



5. Differential regulation of ribosomal proteins



While transcripts encoding cytoplasmic ribosomal proteins are elevated in diapause as reported before[3], their protein products are relatively depleted.

6. Conclusion

- Integrated transcriptome and proteome analysis illustrates how genome regulation is re-programmed in Diapause.
- The weak positive correlation between transcripts and corresponding proteins levels (R = 0.35) suggests regulation at the level of translation/protein turnover.
- Discrepancy between the abundance of ribosomal proteins and transcripts during Diapause supports “translation-on-demand” for rapid re-entry into development when conditions allow.

7. References:

1. Hu, C.-K. *et al.* Vertebrate diapause preserves organisms long term through Polycomb complex members. *Science* **367**, 870–874 (2020).
2. Blažek, R., Polačik, M. & Reichard, M. Rapid growth, early maturation and short generation time in African annual fishes. *EvoDevo* **4**, 24 (2013).
3. Reichwald, K. *et al.* insights into sex chromosome evolution and aging from the genome of a short-lived fish. *Cell* **163**, 1527–1538 (2015).