In search of lost hourglass
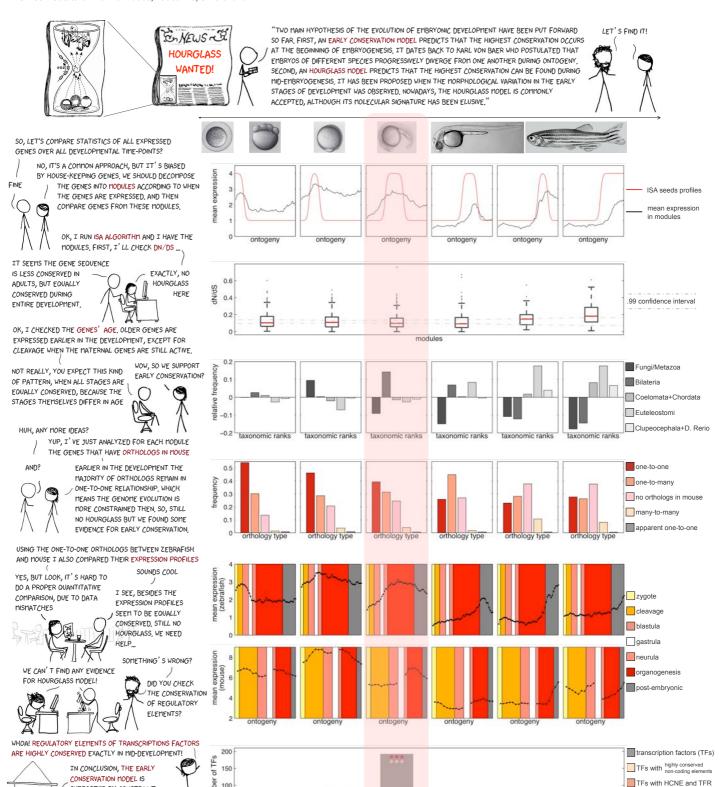
Developmental constraints on transcriptome evolution vary for different molecular features

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HOURGLASS WANTED!

"TWO MAIN HYPOTHESIS OF THE EVOLUTION OF EMBRYONIC DEVELOPMENT HAVE BEEN PUT FORWARD SO FAR. FIRST, AN EARLY CONSERVATION MODEL PREDICTS THAT THE HIGHEST CONSERVATION OCCURS AT THE BEGINNING OF EMBRYOGENESIS. IT DATES BACK TO KARL VON BAER WHO POSTULATED THAT EMBRYOS OF DIFFERENT SPECIES PROGRESSIVELY DIVERGE FROM ONE ANOTHER DURING ONTOGENY. SECOND, AN HOURGLASS MODEL PREDICTS THAT THE HIGHEST CONSERVATION CAN BE FOUND DURING MID-EMBRYOGENESIS. IT HAS BEEN PROPOSED WHEN THE MORPHOLOGICAL VARIATION IN THE EARLY STAGES OF DEVELOPMENT WAS OBSERVED. NOWADAYS, THE HOURGLASS MODEL IS COMMONLY ACCEPTED, ALTHOUGH ITS MOLECULAR SIGNATURE HAS BEEN ELUSIVE."

LET'S FIND IT!

SO, LET'S COMPARE STATISTICS OF ALL EXPRESSED GENES OVER ALL DEVELOPMENTAL TIME-POINTS?

NO, IT'S A COMMON APPROACH, BUT IT'S BIASED BY HOUSE-KEEPING GENES. WE SHOULD DECOMPOSE THE GENES INTO MODULES ACCORDING TO WHEN THE GENES ARE EXPRESSED, AND THEN COMPARE GENES FROM THESE MODULES.

FINE

OK, I RUN ISA ALGORITHM AND I HAVE THE MODULES. FIRST, I'LL CHECK DN/DS ...

IT SEEMS THE GENE SEQUENCE IS LESS CONSERVED IN ADULTS, BUT EQUALLY CONSERVED DURING ENTIRE DEVELOPMENT.

EXACTLY, NO HOURGLASS HERE

OK, I CHECKED THE GENES' AGE. OLDER GENES ARE EXPRESSED EARLIER IN THE DEVELOPMENT, EXCEPT FOR CLEAVAGE WHEN THE MATERNAL GENES ARE STILL ACTIVE.

WOW, SO WE SUPPORT EARLY CONSERVATION?

NOT REALLY, YOU EXPECT THIS KIND OF PATTERN, WHEN ALL STAGES ARE EQUALLY CONSERVED, BECAUSE THE STAGES THEMSELVES DIFFER IN AGE

HUH, ANY MORE IDEAS?

YUP, I'VE JUST ANALYZED FOR EACH MODULE THE GENES THAT HAVE ORTHOLOGS IN MOUSE

AND?

EARLIER IN THE DEVELOPMENT THE MAJORITY OF ORTHOLOGS REMAIN IN ONE-TO-ONE RELATIONSHIP, WHICH MEANS THE GENOME EVOLUTION IS MORE CONSTRAINED THEN. SO, STILL NO HOURGLASS BUT WE FOUND SOME EVIDENCE FOR EARLY CONSERVATION.

USING THE ONE-TO-ONE ORTHOLOGS BETWEEN ZEBRAFISH AND MOUSE I ALSO COMPARED THEIR EXPRESSION PROFILES

YES, BUT LOOK, IT'S HARD TO DO A PROPER QUANTITATIVE COMPARISON, DUE TO DATA MISMATCHES

SOUNDS COOL

I SEE, BESIDES THE EXPRESSION PROFILES SEEM TO BE EQUALLY CONSERVED, STILL NO HOURGLASS, WE NEED HELP...

SOMETHING'S WRONG?

WE CAN'T FIND ANY EVIDENCE FOR HOURGLASS MODEL!

DID YOU CHECK THE CONSERVATION OF REGULATORY ELEMENTS?

WHOA! REGULATORY ELEMENTS OF TRANSCRIPTIONS FACTORS ARE HIGHLY CONSERVED EXACTLY IN MID-DEVELOPMENT!

IN CONCLUSION, THE EARLY CONSERVATION MODEL IS SUPPORTED BY CONSTRAINT ON GENE DUPLICATION WHICH DECREASES DURING ONTOGENY. WHEREAS THE HOURGLASS MODEL IS SUPPORTED BY THE CONSERVATION OF REGULATORY ELEMENTS, WHICH IS THE HIGHEST DURING MID-DEVELOPMENT.

Chart legends

- ISA seeds profiles
- mean expression in modules
- mean expression (y-axis, top row), ontogeny (x-axis)
- dN/dS (y-axis), modules (x-axis), .99 confidence interval

relative frequency (y-axis), taxonomic ranks (x-axis):
- Fungi/Metazoa
- Bilateria
- Coelomata+Chordata
- Euteleostomi
- Clupeocephala+D. Rerio

frequency (y-axis), orthology type (x-axis):
- one-to-one
- one-to-many
- no orthologs in mouse
- many-to-many
- apparent one-to-one

mean expression (zebrafish), mean expression (mouse), ontogeny:
- zygote
- cleavage
- blastula
- gastrula
- neurula
- organogenesis
- post-embryonic

number of TFs (y-axis), modules (x-axis):
- transcription factors (TFs)
- TFs with highly conserved non-coding elements
- TFs with HCNE and TFR
- TFs with transposons free region
- .99 confidence interval

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