**Comparative Analysis of the Transcriptome across Distant Species**

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RNA transcripts are the readout of a genome. Identifying common features of transcription from diverse species can reveal fundamental principles. To this end, the ENCODE and modENCODE consortia have generated large amounts of matched RNA-sequencing data for human, worm, and fly. Uniform processing and comprehensive annotation of these data allow comparison across these highly divergent animals, revealing highly conserved features of transcription.

[[MG: want to use the word transcriptome in the abs]]

[[MG: add something here like prev work has on intra phyla and here we focus on inter phyla comparisons ]]

[[JR:

Extending beyond earlier studies which have focused on transcriptome comparisons within a single phyla\cite{22012392,23258891,23258890,22560298,21150996,20969771}, we compare the transcriptome between metazoa phyla.

or

the transcriptome within the metazoan kingdom.

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Extending [[MG: moving beyond... building on...]] previous transcriptome comparisons focusing on individual or more closely related organisms\cite{22012392,23258891,23258890,22560298,21150996,20969771},

[[MG:....we integrated the data from 3 species....]]

we discovered conserved co-expression modules shared across phyla, many of which are enriched in developmental genes. We used the expression patterns to align the stages in worm and fly development, finding a novel pairing between worm embryo and fly pupae in addition to the expected embryo-to-embryo and larvae-to-larvae pairings. Furthermore, we found that the extent of non-canonical non-coding transcription is similar between the organisms, per base-pair. Finally, we found the gene expression levels in all three organisms, both coding and non-coding, can be consistently predicted by their upstream histone marks using a common “universal model”.

Our comparison used the ENCODE-modENCODE RNA resource, available online. This resource comprises: (1) deeply sequenced RNA-Seq data from many distinct samples from all three organisms; (2) comprehensive annotation of transcribed elements and (3) uniformly processed, standardized analysis files, focusing on non-coding transcription and expression patterns. Where practical, these datasets match comparable samples across organisms and to other types of functional genomics data (Fig. ED1). The resource encompasses different RNA types, including poly(A)+, poly(A)- and ribosomal-RNA-depleted RNA and short and long RNA. It represents 575 different experiments containing >67B reads. The resource represents a capstone for the decade-long annotation efforts in human, worm, and fly.

The new annotation sets have numbers, sizes and families of protein-coding genes similar to previous compilations, but the number of pseudogenes and annotated ncRNAs differ (Fig. ED2, ED3). Also, the number of splicing events is greatly increased. We find the proportion of the different types of alternative splicing (e.g., exon skipping or intron retention) is approximately similar across the three organisms; however, skipped exons predominate in human while retained introns are most common in fly\cite{Talerico, M. & Berget} (Fig. ED2, ED4, S1 and Table S1). Moreover, a considerable fraction of the transcription comes from genomic regions not associated with standard annotations, representing "non-canonical transcription” (Table S2) \cite{22955620}. Uniform processing of reads mapping outside of protein-coding transcripts, pseudogenes and annotated ncRNAs identified read-clusters (transcriptionally active regions, TARs) using a minimum-run/maximum-gap algorithm. We found across all three genomes roughly one third of the bases gives rise to "non-canonical" transcription. To address the extent that this transcription represents an expansion of the current established classes of ncRNAs, we identified the TARs most similar to known annotated ncRNAs using a supervised classifier \cite{21177971} (Fig. S2, Table S2). We validated these predictions using RT-PCR, demonstrating high accuracy. Overall, the predictions are only a small fraction of all TARs, suggesting that most TARs have features distinct from annotated ncRNAs and that the majority of ncRNAs of established classes have already been identified. To shed further light on the possible roles of TARs we intersected them with enhancers and HOT regions \cite{mod3,21177976,21177974,mod2,22955620}, finding statistically significant overlaps (Fig. ED7, Table S2).

Given the uniformly processed nature of the dataset and annotation, we were able to make comparisons across organisms and to integrate across data types. First, we built co-expression modules (Fig. 1), extending earlier analysis\cite{12934013}. To detect modules consistently across the three species, we combined across-species orthology and within-species coexpression relationships. We then searched for dense subgraphs (modules) in the resulting multilayer network, using simulated annealing\cite{17813860,15601068}. Some modules are dominated by one species, whereas others contain genes from two or three. As expected, the modules with genes from multiple species are enriched in orthologs. A phylogenetic analysis shows that the genes in the modules are more preserved across 56 animal species (Fig. 1, S3). To focus on the cross-species conserved functions, we restricted the clustering to orthologs, arriving at 16 conserved modules, which are enriched in a variety of functions, ranging from morphogenesis to chromatin remodeling (Fig. 1, Table S3). Finally, we annotated many TARs based on correlating their expression profiles with the modules (Fig. ED7).

In addition, we used the expression profiles of orthologous genes to align the developmental stages in worm and fly (Fig. 1b, ED6). Specifically, for every developmental stage, we identified stage-associated genes, i.e. genes highly expressed at a particular stage but not across all stages. We then counted the number of orthologous pairs among these stage-associated genes for each possible worm-and-fly stage correspondence, aligning stages by the significance of the overlap. Strikingly, worm stages map to two sets of fly stages (Fig. 1b). First, they match in the expected one-to-one fashion to the fly (i.e. embryos-to-embryos, larvae-to-larvae). However, worm late embryonic stages also match to fly pupal stages, suggesting a shared expression program between embryogenesis and metamorphosis. The ~50 genes involved in this dual-stage mapping are enriched in functions such as ion transport and cation-channel activity (Table S3).

To gain further insight into the stage alignment, we examined our 16 conserved modules in terms of the "hourglass hypothesis", which posits that all animals ?? [[MG: we need to chk]] go through a particular stage in embryonic development (the tight point of the hourglass or "phylotypic" stage) during which the expression divergence across species for orthologous genes is smallest\cite{21150996,22560298,21150997}. For genes in 12 of the modules, we observed canonical hourglass behavior, i.e. "inter-organism" expression divergence across closely related fly species during development is minimal\cite{21150996}(Fig. S3). Moreover, we find subset of TARs exhibit also exhibiting "hourglass" behavior (Fig. S2). Beyond looking at *inter*-species divergence, we also investigated the *intra*-species divergence within just *D. melanogaster* and *C. elegans* seaparately. Strikingly, we observed that divergence of gene expression across modules is minimized during the worm and fly phylotypic stages (Fig. 1c, Suppl. D). This suggests, for an individual species, the expression patterns of different modules are most tightly coordinated (low divergence) during the phylotypic stage, but each module has its own signature before and after this. One can, in fact, directly see this coordination as a local maximum in the between-module correlation for the worm (Fig. ED5). Finally, using genes from just the 12 "hourglass modules," we found that the alignment between worm and fly stages becomes stronger (Fig. 1b, S3). The alignment shows a gap where no changes are observed, perfectly matching the phylotypic stage.

Next, we investigated the degree to which gene expression can be predicted from upstream factor-binding and chromatin-modification data and how consistent this prediction is across organisms (Fig. 2). As previously reported\cite{20133639}, [[MG: add ENCODE paper + other refs]] we found consistent correlations in each of the three species between the expression level of the downstream gene and the signal of histone modifications. Around the TSS, H3K4me1, H3K4me2, H3K4me3 and H3K27ac are positively correlated, whereas H3K27me3 is negatively correlated (Fig. 2, ED8, S4). We then integrated the signal from these histone modifications into a statistical model, obtaining high accuracy in predicting expression for both protein-coding genes and ncRNAs. The promoter-associated marks, H3K4me2 and H3K4me3, consistently have the highest contribution to the model.

A similar statistical analysis using TFs showed the correlation between gene expression and TF binding to be the greatest in magnitude right at the TSS, positively for activators and negatively for repressors (Fig. ED8). Integrated models using the TFs in each organism also achieved high accuracy for protein coding genes and and ncRNAs, with only a few TFs necessary in each of the models (Fig. ED8). In particular, models with as few as five TFs give accurate predictions (Fig. ED9). This [[MG: say perhaps]] reflects an intricate, correlated structure to regulation. \*\*\*Or is it just that open chromatin is characteristic of gene expression and TFs bind surprisingly indiscriminately??? [[MG: put this commet in the ED caption]]\*\*\* The relative importance of the upstream regions is more peaked for the TF models than for the histone models, likely reflecting the fact that histone modifications are spread over broader regions, including the gene body, whereas most TFs bind near the promoter.

Next, we constructed a "universal model," containing a single set of organism-independent parameters. This achieved accuracy comparable to the organism-specific models. In the universal model, the consistently important promoter-associated marks such as H3K4me2 and H3K4me3 are weighted most highly. In contrast, the enhancer mark H3K4me1 is down-weighted, perhaps reflecting the fact that signals for most human enhancers are not near the TSS. The same universal model also can predict ncRNA expression, i.e. using the same set of organism-independent parameters derived from training on protein-coding genes.

Our comparison of the transcriptomes of these three highly dissimilar metazoans, a comparison not previously reported, highlights fundamental principles conserved across [[MG: fix rep. of metazo]]metazoans. First, there are ancient co-expression modules across organisms, many of which are enriched for developmentally important “hourglass” genes. These conserved modules have highly coordinated intra-organism expression during the phylotypic stage, but display diversified expression before and after. The expression clustering also aligned developmental stages between worm and fly, revealing shared expression programs between embryogenesis and metamorphosis. We were also able to build a single model that could predict transcription in all three organisms from upstream histone marks using a single set of parameters for both protein-coding genes and ncRNAs. Overall, our results underscore the importance of comparing two divergent model organisms to human to highlight conserved biological principles (and dis-entangle them from lineage-specific adaptations).

**Fig 1 - Expression Clustering.** (A) Left: Human, worm, and fly gene-gene co-association matrix; darker blocks reflect increased likelihood pairs of genes are assigned to the same module. Blocks along the diagonal represent groups of human, worm, and fly genes. Blocks from different species with off diagonal matches form cross-species modules; whereas blocks without any off diagonal matches form species-specific modules. Right: The functional enrichment of genes within each module is shown. (B) Alignment of worm and fly developmental stages based on all worm-fly orthologs. Inset shows worm-fly stage alignment using only hourglass genes is more significant and exhibits a gap (brown) that matches the phylotypic stage. (C) Expression of 16 conserved modules shows smallest intra-organism divergence during the phylotypic stage (brown).

## Fig 2 – Histone Models for Gene Expression. Normalized correlations of two representative histone marks with expression. Relative importance of histone marks in organism-specific models and the universal model. Cross-organism prediction accuracy of the organism-specific- and universal-model.

**Figure Captions**

**[[MG: new numbering]]**

[**http://www.nature.com/nature/journal/v505/n7485/pdf/nature12946.pdf**](http://www.nature.com/nature/journal/v505/n7485/pdf/nature12946.pdf)

[**http://www.nature.com/nature/journal/v499/n7456/pdf/nature12223.pdf**](http://www.nature.com/nature/journal/v499/n7456/pdf/nature12223.pdf)

**Fig ED1**

(A) RNA-seq data generated for human (red), worm (green), and fly (blue). (B) The number and size of data sets generated (see Suppl for a detailed description of these data).

**Fig ED2**

Summary statistics for the protein coding gene annotations. (A) (top) Number of bases in 5’ UTRs (5’), 3’ UTRs (3’), coding exons (C), and introns (I), in millions of bases (black) and as percentage of the genome (grey). (bottom) Number of mapped reads in the same categories as above, in millions of reads (black) and as percentage of the total number of mapped reads (grey). For both tables, relative fractions in each category are visualised in radar plots (right). (B) Distributions of key summary statistics; note that the x axes are in log scale. Both fly and worm genes span similar genomic lengths while human genes span larger regions (mostly due to the size of human introns). (C) (left) Venn diagram of protein domains (from the Pfam database version 26.0) present in annotated protein-coding genes in each species. (right) Shared domain combinations. (For more information on domain combinations, see Fig S1h.)

**Fig ED3**

Summary of annotated ncRNAs, TARs, and ncRNA predictions in each species, showing the number of elements, the base pairs covered and the fraction of the genome for each class (see also Suppl). There are comparable numbers of tRNAs in humans and worms but about half as many in fly. While the number of lncRNAs in human is more than an order of magnitude greater than in either worms or flies, the fractional genomic coverage in all three species is, in fact, similar. Finally, humans have at least 5-fold more miRNAs, snoRNAs and snRNAs as compared to worm or fly.The fraction of the genome covered by TARs (highlighted squares) for each species is similar. A large amount of non canonical transcription occurs in the introns of annotated genes, presumably representing a mixture of unprocessed mRNAs and internally initiated transcripts. The remaining non-canonical transcription (249Mb, 16Mb, and 14Mb in human, worm, and fly) is intergenic and occurs at low levels, comparable to that observed for introns (Table S2). Overall, the fraction of the genome transcribed -- including intronic, exonic, and non-canonical transcription -- is consistent with that previously reported for human despite the methodological differences in the analysis (Fig. S2, Suppl. C).

**Fig ED4**

(A) Orthologous genes do not share the same exon/intron structure or alternative splicing. (B) Distribution of the number of isoforms per gene. (C) Comparison of the fraction of various alternative splicing event classes in human, worm, and fly -- skipped exons “SE”, retained introns “RI”, alternative 3' splice sites “A3SS”, alternative 5' splice sites “A5SS”, alternative first exons “AFE”, alternative last exons “ALE”, tandem 3' UTRs “TandemUTR”, coordinately skipped exons “CSE”, and mutually exclusive exons “MXE”.

**Fig ED5**

(A) Pie charts reflect gene conservation across 56 Ensembl species for the blocks in the heatmap enclosed with the same symbol; species-specific modules tend to have fewer orthologs across 56 Ensembl species. The functional enrichment of genes within each module is shown. (B) The expression levels of a conserved module (Module No. 5) in D. melanogaster and its orthologous counterparts in other 5 Drosophila species are plotted against time. The x-axis represents the middle time points of two-hour periods at fly embryo stages. The boxes represent the log10 modular expression levels from microarray data of 6 Drosophila species centred by their medians. The modular expression divergence (inter-quartile region) becomes minimal during the fly phylotypic stage (brown, 8-10 hours). (C) It shows the modular expression correlations over a sliding 2-hour window (Pearson correlation per 5 stages, middle time of two-hour period in x-axis) among 16 modules in worm. We found that the modular correlations (median shown as bar height in y-axis) are highest during the worm phylotypic stages (brown), 6-8 hours. (More details on all parts of this in Suppl. D and Figure S3.) One can, in fact, directly see this coordination as a local maximum in the between-module correlation for the worm, which has a more densely sampled developmental time course.

**Fig ED6**

(A) An alignment of worm and fly developmental stages based on all worm-fly orthologues (11,403 pairs, including one-to-one, one-to-many, many-to-many pairs). (B) Alignment of worm and fly developmental stages based on all worm-fly orthologs. This make sense: since the expression values of genes in all hourglass modules converge at the phylotypic stage, no hourglass genes can be phylotypic-stage specific, and hence, the gap. (C) Key aligned stages from Figure 1B. Worm “early embryo” and “late embryo” stages are matched with fly “early embryo” and “late embryo” respectively in the “lower diagonal” set of matches, and they are also matched with fly “L1” and “prepupa-pupa” stages respectively in the “upper diagonal” set of matches.

**Fig ED7**

(A) The left column highlights ncRNA/TARs that are highly correlated with corresponding HOX orthologues in human (HOXB4), worm (lin-39), and fly (Dfd). The expression of mir-10 correlates strongly with Dfd in fly (r=0.66, p<6e-4 in fly), as does mir-10a in human, which correlates strongly with HOXB4 (r=0.88, p<2e-9). A TAR (chrIII:8871234-2613) strongly correlates with lin-39 (r=0.91, p<4e-13) in worm. The right column shows TARs in human (chr19:7698570-7701990), worm (chrII:11469045-440), and fly (chr2L:2969620-772) that are negatively correlated with the expression of three orthologous genes: SGCB (r=-0.91, p<3e-16), sgcb-1 (r=-0.86, p<2e-7), and Scgb (r=-0.82, p<4e-8), respectively. (B) The overlap of enhancers and distal HOT regions with supervised ncRNA predictions and TARs in human, worm, and fly. The overlap of enhancers and distal HOT regions with respect to both supervised ncRNA predictions as well as TARs are significantly enriched compared to a randomised expectation (see Suppl. C).

**Fig ED8**

(A) Binding/expression correlations of various histone marks and (C) TFs. H3K36me3 shows positive correlation in worm and fly, but weak negative correlation in human at the promoter, with positive correlation over the gene body. (B) TF and histone mark model positional accuracy for mRNA and ncRNA expression about the TSS.

**Fig ED9**

Average predictive accuracy of models with different number of randomly selected TFs. We randomly selected n TFs as predictors and examined the predictive accuracy by cross-validation, with n was taken from 2 to 28. The curve shows the average predictive accuracy (Fig. S4 indicate the standard deviation of all models with the same number of predictors). The prediction accuracy of the TF model is also presented as a function as the number of independent TFs that are included.

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