A gene’s pattern of expression is generally assumed to correlate to its function, yet recent work has called this fundamental assumption into question. If a fraction of gene expression corresponds to non-functional regulation, how can it be distinguished from the functional component? From an evolutionary perspective, if a gene’s expression profile in a specific context is under selection it is expected to be conserved throughout evolution, whereas free of selection, it may change and adopt different expression profiles. Thus, comparisons of expression profiles in related species can identify which expression profiles are under selection and likely to be functional. This approach is similar to comparing homologous gene sequences, where conservation is generally interpreted as separating the functional from the non-functional domains. Nematodes constitute a fitting test-bed for this approach since the early embryonic development of C. elegans is indistinguishable from that of C. briggsae, yet their genomes are roughly as distant as the human and mouse genomes. We conducted an embryonic time-course in both organisms, using a custom whole-genome microarray for each. Comparing the temporal profiles of orthologous genes we found that only ~60% are correlated between the two organisms. Genes whose profile evolved are significantly less likely to produce lethality when disrupted than genes with conserved profiles, suggesting that their embryonic expression is not under selection. These results indicate that expression comparisons over multiple species and developmental stages will identify the functional component of expression. C. elegans and C. briggsae last shared an ancestor ~100 million years ago (MYA) yet are morphologically near-identical.

Symmetry in profile divergence frequencies

Each of the 6,174 ortholog pairs is represented by two profiles, red (C. briggsae) and black (C. elegans), the pairs are organized according to cluster pairs for the 12 most populated clusters. Note that the clustering does not reveal large-scale changes unique to one organism, but rather that the patterns of changes are symmetrical in nature.

Widespread evolution of temporal expression profiles

Pearson’s correlation coefficient can be used to quantify the degree of conservation between orthologs: the range is -1 to 1, where 1 is a perfect correlation and -1 is perfect anti-correlation.

Distribution of binned correlation coefficients for 6,174 one-to-one orthologs (blue), 25 development genes (green), and 27 olfactory receptors with expression significant profiles.