**Targeting the xenobiotic-responsive transcriptome: in silico identification and analysis of PCB-interacting genes conserved across taxa**

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Biomarker genes conventionally investigated in ecotoxicogenomic studies are often vertebrate specific and, consequently, cannot be used to assess the functional genomic response of many invertebrate bioindicator species or standard toxicological organisms. Whole transcriptome analysis is also not a feasible option due to the associated computational challenges of large data sets. As such, a targeted approach, one that identifies a suite of xenobiotic-interacting genes conserved across taxa would benefit environmental biomonitoring efforts. PCBs are ubiquitous legacy contaminants toxic among metazoans. Using publically available online databases, a local library of PCB-interacting genes with known homologues across multiple taxa was generated. Using the sequence information available on GenBank for each PCB-interacting gene, seven complementary DNA (cDNA) sequences from six different taxonomic groups were downloaded and aligned. A conserved domain was identified for each PCB-interacting gene. With this method, a key set of evolutionarily conserved PCB-interacting genes (N=64) was determined. Of these genes, 20% involve cellular processes, 16% involve genetic information and processing, 28% involve environmental information processing, and 36% involve metabolism. For each conserved domain per gene, overall nucleotide conservation ranged from 49.50 to 72.76%, (average = 56.02 ± 5.21%) with similar nucleotide conservation profiles across each KEGG pathway.