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A web based resource characterizing the zebrafish developmental profile of over 16,000 transcripts

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Abstract

Using a spotted 65-mer oligonucleotide microarray, we have characterized the developmental expression profile from mid-gastrulation (75% epiboly) to 5 days post-fertilization (dpf) for >16,000 unique transcripts in the zebrafish genome. Microarray profiling data sets are often immense, and one challenge is validating the results and prioritizing genes for further study. The purpose of the current study was to address such issues, as well as to generate a publicly available resource for investigators to examine the developmental expression profile of any of the over 16,000 zebrafish genes on the array. On the chips, there are 16,459 printed spots corresponding to 16,288 unique transcripts and 172 *β-actin* (AF025305) spots spatially distributed throughout the chip as a positive control. We have collected 55 microarray gene expression profiling results from various zebrafish laboratories and created a Perl/CGI-based software tool (http://serine.umdnj.edu/~ouyangmi/cgi-bin/zebrafish/profile.htm) for researchers to look for the expression patterns of their gene of interest. Users can search for their genes of interest by entering the accession numbers or the nucleotide sequences and the expression profiling will be reported in the form of expression intensities versus time-course graphical displays. In order to validate this web tool, we compared 74 genes' expression results between our web tool and the *in situ* hybridization results from Thisse et al. [Thisse, B., Heyer, V., Lux, A., Alunni, A., Degrave, A., Seiliez, I., Kirchner, J., Parkhill, J.-P., Thisse, C., 2004. Spatial and temporal expression of the zebrafish genome by large-scale in situ hybridization screening. Meth. Cell. Biol. 77, 505–519] as well as those reported by Mathavan et al. [Mathavan, S., Lee, S.G., mark, A., Miller, L.D., Murthy, K.R., Tong, Y., Wu, Y.L., Lam, S.H., Yang, H., Ruan, Y., Korzh, V., Gong, Z., Liu, E.T., Lufkin, T., 2005. Transcriptome analysis of zebrafish embryogenesis using microarrays. PLoS Genet. 1, 260–276]. The comparison indicates that our microarray-derived expression patterns are 80% and 75% in agreement with the *in situ* database (Thisse et al., 2004) and previously published microarray data (Mathavan et al., 2005), respectively. Those genes that conflict between our web tool and the *in situ* database either have high sequence similarity with other genes or the *in situ* probes are not reliable. Among those genes that disagree between our web tool and those reported by Mathavan et al. (2005), 93% of the genes are in agreement between our web tool and the *in situ* database, indicating our web tool results are quite reliable. Thus, this resource provides a user-friendly web based platform for researchers to determine the developmental profile of their gene of interest and to prioritize genes identified in microarray analyses by their developmental expression profile.

Keywords: Zebrafish developmental profile; Microarray; Gene expression; Web resource

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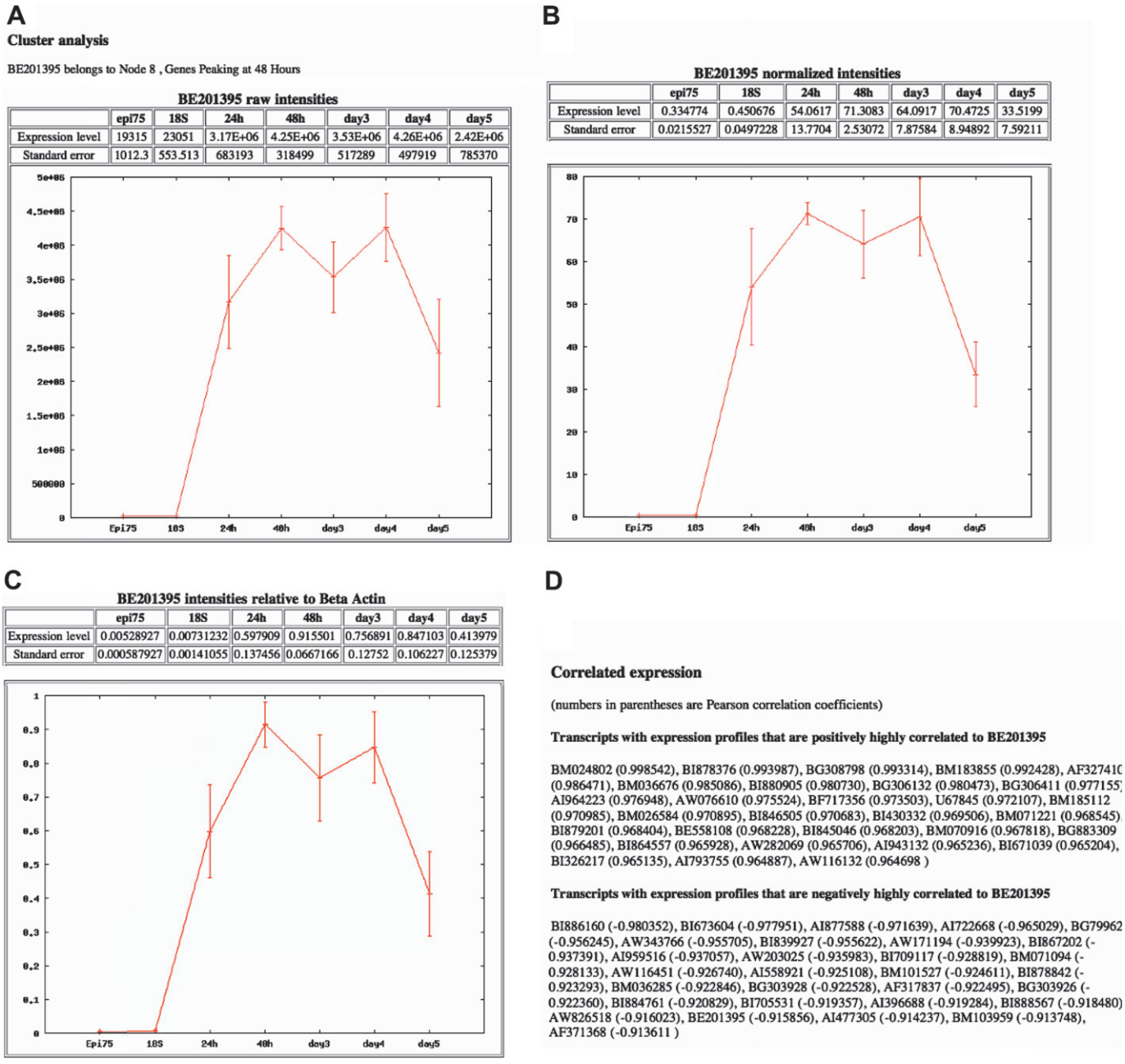

Fig. 1. Web tool "output" for zebrafish microarray analyses. To demonstrate the functions of the web resource, the expression profile of zgc:103639 (BE201395) retrieved from the web (http://serine.umdnj.edu/~ouyangmi/cgi-bin/zebrafish/profile.htm) and used as an example. (A) BE201395 raw intensities display. (B) BE201395 normalized intensities display. (C) BE201395 intensities relative to *β-actin*. (D) Transcripts with expression profiles that are highly positively or negatively correlated to BE201395.

Microarray profiling is a powerful technology that enables researchers to compare gene expression across samples (Lee and Saeed, 2007). In order to study gene expression in zebrafish embryos at various developmental stages, we have printed zebrafish DNA microarray chips at the Kimmel Cancer Center (Thomas Jefferson University) comprising more than 16,000 unique transcripts from the Zebrafish oligo library from Compugen/Sigma-Genosys. The Kimmel Cancer Center microarray profiling service has been used by many investigators in the zebrafish community to investigate a variety of interesting biological problems and proven to be a useful resource for the community (Linney et al., 2004; Sumanas et al., 2005; Covassin et al., 2006; Kassen et al., 2007; Kreiling et al., 2007; Robu et al., 2007). Using a spotted 65-mer oligonucleotide microarray, we have characterized the developmental expression profile from mid-gastrulation (75% epiboly) to 5 days post-fertilization (dpf) for 16,288 unique transcripts in the zebrafish genome, representing about a third to one half of all genes in the genome, according to current predictions (zebrafish genome project zv7, http://www.sanger.ac.uk/Projects/D_rerio/Zv7_assembly_information.shtml). We have analyzed zebrafish gene