



## July 2012 Newsletter

<http://Spbase.org>

**Newsletter.** It's been 11 months since the last newsletter announcing changes at SpBase. During that time, the SpBase team has been making incremental changes including the reagent information gleaned from published papers and links to publications on gene information pages. Hopefully, these changes have been made in an invisible manner. Now we want to apprise you of some major improvements to the web system of genomic information on echinoderms included in Build 7.

***S. purpuratus* transcriptome.** A nearly complete and much more accurate transcriptome has been assembled by Qiang Tu from RNA-seq for the purple sea urchin using 22 individual cDNA samples including 10 embryonic stages, 4 larval stages and 8 adult tissues. A total of 22,365 transcripts passed a rigorous filtering process and are mapped to the SPur3.1 assembly. These data greatly enhance the quality of the gene models for the purple sea urchin. They include improvements in 3- and 5-prime UTRs, improved exon structures and more alternate transcripts or isomers. The sequences including isomers are available on Gbrowse and on the gene information pages. An additional 900 transcripts that do not match existing SPU genes are also added as SPU numbers above SPU\_030000. All of the transcripts sequences can be searched by BLAST. An accepted preprint of the paper describing the project is available at: <http://genome.cshlp.org/content/early/2012/06/18/gr.139170.112.abstract>.

***Lytechinus variegatus* genome assembly.** A draft version of the *Lytechinus variegatus* genome assembly has been completed (Lvar0.4, GenBank: AGCV00000000.1). It is available as a BLAST database at Genbank, BCM-HGSC and SpBase. We have linked it through a new branch called Comparative Genomics under Static Links. Since there is as yet no gene model set for *L. variegatus* we have not mounted a genome browser for this species.

**Other Transcriptomes** We have moved the transcriptome pages to a new link in the Static Links sidebar of the home page entitled "Comparative Genomics". This is in anticipation of additional genomic information for other species (see below). There are now three separate transcriptome databases for other species from Baylor College of Medicine, Human Genome Sequencing Center and posted at SpBase. They are derived from BCM-HGSC submissions in support of additional genome sequencing projects: 1) *L. variegatus* (BioProject ID: PRJNA62467). 2) the sea star *Patiria miniata* (BioProject ID: PRJNA52335); 3) a combined assembly of our local Illumina reads with those from BCM-HGSC (BioProject ID: PRJNA62465) for *Eucidaris tribuloides*. In addition to a BLAST database where you can input your own sequences, we also offer a search by name or number of the best SPU gene hit to each transcriptome sequence.

**Other Species.** The *Patiria miniata* draft genome assembly is anticipated any day now. The *Eucidaris tribuloides* one is being assembled at BCM-HGSC. DNA libraries for the brittle star, *Ophiothrix spiculata* and the sea cucumber *Parastichopus parvamensis* is currently being sequenced.

**Website.** We have installed an informational Wiki under the navigation button "HowTo" right beneath the page banner. This extensively re-written document provides information on naming conventions and data organization as well as a guide for using the web system.

**Citation.** Since SpBase is grant supported, we need to justify our usefulness. If you use our resources please cite us using the journal citation on the first page of the web site.

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