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New Gene Family Resources

Our gene family resource continues to expand. Here is a list of the new family pages that have been added recently:

- Beta-galactoside-binding lectins
- BPI fold containing
- Heat shock proteins - includes the following subgroups: HSP70, DNAJ (HSP40), HSPB (small heat shock proteins), HSPC (HSP90) and Chaperonins
- Myosin binding proteins
- MOB kinase activators
- Rho guanine nucleotide exchange factors
- Serine peptidases
- Serine peptidase inhibitors, Kazal type
- Short chain dehydrogenase/reductase superfamily
- SKI transcriptional corepressors
- STAR-related lipid transfer (START) domain containing
- Transglutaminases
- Tropomyosins

Naming 'oncogenes'

We are aware that the term "oncogene" appears in different formats in our gene names and we would like to standardise our use of this term. Here are examples of the different formats that we have currently:

- "v-abl Abelson murine leukemia viral oncogene homolog 2" (ABL2)
- "c-ros oncogene 1, receptor tyrosine kinase" (ROS1)
- "jun proto-oncogene" (JUN)

Of the following four options, we would like to know which you would find most appropriate for use in human gene names:

1. v-[x] viral oncogene homolog
2. c-[x] oncogene
3. c-[x] proto-oncogene
4. [x] proto-oncogene

Please contact us at hgnc@genenames.org with your opinion.
Gene Symbols in the News

There have been a number of reports in the international media that include approved gene symbols over the last few months. There have been several reports of new links between certain genes and types of cancer: mutations in the STAG2 gene have been linked with three different types of cancer (melanoma, Ewing’s sarcoma and glioblastomas), while a mutation of the CASP8 gene has also been linked to melanoma. A new report showed that women carrying mutated copies of the RAD51D gene have an increased risk of ovarian cancer, while variants in the following five genes were linked to aggressive forms of prostate cancer: LEPR, RNASEL, IL4, CRY1 and ARVCF.

There have also been several reports on links between genes and particular disorders. A study on a Swiss family with a rare condition called adermatoglyphia, which results in a lack of epidermal ridges including fingerprints, has shown that these patients carry a mutation in the SMARCAD1 gene. Mutations in the AKT2 gene have been shown to cause a severe form of hypoglycaemia. The SGK1 gene has been reported as playing an important role in female reproductive success; women with unexplained fertility have high levels of endometrial SGK1, while blocking the SGK1 ortholog in mice resulted in smaller litter size, consistent with spontaneous fetal loss.

Finally, blocking the activity of the HCN2 gene product may relieve chronic pain. When researchers deleted the ortholog of the human HCN2 gene in mice, the animals were unable to feel neuropathic pain but were still sensitive to acute pain.

Meeting News

Matt and Elspeth attended the Theo Murphy International Scientific meeting on Non-protein coding RNAs, hosted by the Royal Society, from 19th-20th September in Newport Pagnell, U.K. Matt gave an invited talk on the nomenclature of long non-coding RNAs, which was followed by a fruitful discussion.

Elspeth, Matt and Ruth attended the ICHG 2011/ASHG 61st Annual Meeting in Montreal, Canada from 11th-15th October and presented a poster on our work on gene families. They were all very impressed by the high usage of approved nomenclature at this meeting, both by poster presenters and those giving talks.

Publications


The above publication describes how and why a new nomenclature was developed for the BPIF family. The new system arose from discussions that started during a session at the ‘Proteins with a BPI/LBP/PLUNC-like Domain: Revisiting the Old and Characterizing the New’ meeting held in Nottingham, U.K. back in January. Agreement was reached on the BPIF root symbol and the nomenclature has been adopted by communities working on family members from several different vertebrate organisms, in addition to those working on the human and rodent genes. We hope to continue working with researchers from across the vertebrate organism research community in any future efforts to standardise the nomenclature of gene families.


This paper describes plans for a much-needed international RNA sequence database. The HGNC looks forward to contributing data to this valuable resource.

So long, and thanks for all the fish

After 11 years working with the HGNC, Michael has recently left the HGNC and moved on to pastures new. We wish him all the best in his new job at Strangeways Research Laboratory, Cambridge.