Nome News Issue 33

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Meetings Attended

Sue, Elspeth and Tam attended the 55th ASHG Annual Meeting in Salt Lake City, Utah, where they shared a booth in the exhibit hall with HUGO. Tam presented a poster on the nomenclature issues faced when dealing with variable copy number genes entitled "Now you see it, now you don't" (program number 1252). They also attended the Human Genome Variation Society (HGVS) Meeting where Tam gave an oral presentation of the same title.

Matt attended the International Committee on Standardised Genetic Nomenclature for Mice at the 19th IMGC Annual Meeting in Strasbourg, France (5th-8th November).

Matt gave a presentation on "HUMOT: Human and Mouse Orthologous Gene Nomenclature" at the 16th Mammalian Genetics and Development Workshop in London (21st-22nd November).

HCOP Search Tool Now Available

The HGNC Comparison of Orthology Predictions search tool, HCOP, is now available from our homepage. HCOP enables users to compare predicted human and mouse orthologs according to the ortholog assertions from the Ensembl, HGNC, Homologene, Inparanoid, MGI and PhIGs databases. HCOP provides a useful one-stop resource to summarise, compare and access various sources of human and mouse orthology data.

Publications

HCOP: The HGNC comparison of orthology predictions search tool.
Wright, M.W., Eyre, T.A., Lush, M.J., Povey, S., Bruford, E.A., 2005. *Mamm Genome.* Vol 16, issue 11, pages 827-828. PMID: 16284797

The HSP90 family of genes in the human genome: Insights into their divergence and evolution.
Chen B, Piel WH, Gui L, Bruford E and Monteiro A. *Genomics.* 2005 Oct 31 [Epub ahead of print]. PMID: 16269234

Hot Topic Update

Due the number of responses to our Hot Topic about variable copy number gene nomenclature, the HGNC organised a side meeting at ASHG. This meeting brought together some eminent scientists from the field of segmental duplication/copy number variation and representatives from NCBI, VEGA, UCSC and OMIM as well as members of the HGVS and HGNC. As a result of this meeting the main issues of variable copy number gene nomenclature have been clarified and the key questions summarised below.

1. It was proposed that a static ,standard reference genome', onto which the nomenclature/annotation can be applied, would be useful. If this is agreed which Build should we use?
Please choose:
A. The current Build35
B. Wait for the new Build36

2. The general consensus was that genes proven to be VCN should be tagged. However, should VCN be limited to an attribute of a gene described in the database entry or should it be made implicit in the gene symbol/name?
Please choose:
A. Limit to database attribute
B. Make implicit in the gene symbol/name

3. We need to agree upon a definition of VCN genes in order to distinguish them from segmental duplications present in virtually all humans and from spontaneous or de novo indels/rearrangements e.g. experimental evidence, number of individuals etc. One option would be to use a polymorphism definition: for example the occurrence of two or more alleles for a given locus in a population where the commonest allele has a frequency of less than 99% although the percentage would be open to discussion. Please comment.

Please email hgnc@genenames.org with your answers to the questions posed about variable copy number gene nomenclature.

If you would like to be added to our Nome News mailing list or if you have questions or comments on any human gene nomenclature issue, please email us at: hgnc@genenames.org

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