Online Mendelian Inheritance in Animals (OMIA)

enhancement and curation
by and for the animal* genomics community

* SWINE and cattle

Frank W. Nicholas & Matthew Hobbs
Genetics Laboratory
WHAT IS OMIA?

• An annotated catalogue/compendium of
  • inherited disorders
  • other (single-locus) familial traits in animals*
  • animal genes
• Modelled on, and complementary to, the human catalogue/compendium OMIM
• Available freely on the Internet

* except mice and rats (and humans)
**WELCOME TO OMIA**

Online Mendelian Inheritance in Animals (OMIA) is a catalogue/compendium of inherited disorders, other (single-locus) traits, and genes in 186 animal species, other than human and mouse and rats, which have their own resources) authored by Professor Frank Nicholas of the University of Sydney, Australia, with help from many people over the years. OMIA information is stored in a database that contains textual information and references, as well as links to relevant PubMed and Gene records at the NCBI and to OMIM and Ensembl.

OMIA is manually curated by a team of specialists. If you see an error or wish to submit an entry, please contact us.

From 1st September 2011, the OMIA number is binomial, with the format OMIAxxxx-yyy, where xxxx is the 6-digit number for a trait/disorder, and yyy is the NCBI species taxonomy id.

**Summary**

<table>
<thead>
<tr>
<th>Trait/Disorder Type</th>
<th>dog</th>
<th>cattle</th>
<th>cat</th>
<th>pig</th>
<th>sheep</th>
<th>horse</th>
<th>chicken</th>
<th>goat</th>
<th>rabbit</th>
<th>Japanese quail</th>
<th>golden hamster</th>
<th>Other</th>
<th>TOTAL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total traits/disorders</td>
<td>586</td>
<td>399</td>
<td>304</td>
<td>221</td>
<td>216</td>
<td>208</td>
<td>206</td>
<td>73</td>
<td>58</td>
<td>42</td>
<td>40</td>
<td>467</td>
<td>2820</td>
</tr>
<tr>
<td>Mendelian trait/disorder</td>
<td>221</td>
<td>146</td>
<td>77</td>
<td>49</td>
<td>88</td>
<td>40</td>
<td>125</td>
<td>13</td>
<td>28</td>
<td>32</td>
<td>28</td>
<td>151</td>
<td>998</td>
</tr>
<tr>
<td>Mendelian trait/disorder; key mutation</td>
<td>155</td>
<td>80</td>
<td>42</td>
<td>22</td>
<td>34</td>
<td>29</td>
<td>36</td>
<td>9</td>
<td>7</td>
<td>9</td>
<td>3</td>
<td>60</td>
<td>486</td>
</tr>
<tr>
<td>Potential models for human disease</td>
<td>299</td>
<td>143</td>
<td>165</td>
<td>78</td>
<td>82</td>
<td>110</td>
<td>42</td>
<td>29</td>
<td>36</td>
<td>11</td>
<td>14</td>
<td>226</td>
<td>1235</td>
</tr>
</tbody>
</table>

Key locomotion mutation identified:
On 29 August, in a paper in Nature, Andersson et al. (2012) reported a nonsense mutation in Dmrt3, which encodes a transcription factor, that plays a major role in determining mode of locomotion. For more information, and access to a copy of the paper, see [Gaitedness](http://example.com).

Two iconic Mendelian traits resolved in a week!:
One hundred and ten years after they were first described as Mendelian (single-locus) traits, the last two of the six originally-described Mendelian traits have been resolved (or partly so) at the molecular level within a week of each other!
SEARCHING OMIA

Simple Search
Simple searching is available here and also near the top right of every OMIA page. Fields included in the simple search are trait name, species common name, species scientific name and gene symbol. Multiple search terms can be combined with "OR" or "AND". A search with no search term will return all records in the database.

Enter search terms:  

combine search terms with OR  

Return a list of  

Exhaustive Search
Fields included in the exhaustive search are trait name, trait species-specific name, trait summary, trait symbol, species common name, species scientific name, gene symbol, gene description, marker, clinical features, genetic testing, inheritance details, molecular genetics, genetic mapping, history, control, pathology, prevalence, article title, article publisher, article author, breed name. Multiple search terms can be combined with "OR" or "AND".

Enter search terms:  

combine search terms with OR  

Return a list of  

Advanced Search
The advanced search function can be used to refine your search, or to search with keywords, author names, disease categories, or data within other fields. The advanced search also allows multiple search terms to be combined with AND logic. You may search specific text fields with key words or phrases. You may also enter just a portion of the key word, for a broader search. Wild-card symbols are not required.

Searching for an author name will retrieve all of the traits or diseases that have been linked to papers by that author.

The OMIA database has also classified some diseases or traits into categories. These categories can be searched for using the "category" option below.

<table>
<thead>
<tr>
<th>Trait name:</th>
<th>Type in a term that is part of a trait name; e.g. &quot;myopathy&quot;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trait id (OMIA id):</td>
<td>Type in one or more comma-separated numbers each of which is a trait record identifier (OMIA id); e.g. &quot;001081&quot; or &quot;001081,001199&quot;</td>
</tr>
<tr>
<td>Species-specific trait name:</td>
<td>Type in a term that is part of a species-specific trait name; e.g. &quot;Alport syndrome&quot;</td>
</tr>
<tr>
<td>Species-specific trait summary:</td>
<td>Type in a term that is part of a species-specific trait summary; e.g. &quot;causative mutation&quot;</td>
</tr>
<tr>
<td>Species-specific trait symbol:</td>
<td>Type in a term that is part of a species-specific trait symbol; e.g. &quot;HFMD&quot;</td>
</tr>
<tr>
<td>Species NCBI taxonomy id:</td>
<td>Type in one or more comma-separated numbers each of which is a record identifier in the NCBI taxonomy database; e.g. &quot;9913&quot; or &quot;9913,9615&quot;</td>
</tr>
</tbody>
</table>
Phene is to gene as phenotype is to genotype

22 phene records found

- **OMIA 001089-9825** Blood group system ABO in *Sus scrofa domesticus* (domestic pig) Gene: GGTA1
- **OMIA 001249-9825** Coat colour, brown in *Sus scrofa domesticus* (domestic pig) Gene: TYRP1
- **OMIA 000209-9825** Coat colour, dominant white in *Sus scrofa domesticus* (domestic pig) Gene: KIT
- **OMIA 001199-9825** Coat colour, extension in *Sus scrofa domesticus* (domestic pig) Gene: MC1R
- **OMIA 001743-9825** Coat colour, patch in *Sus scrofa domesticus* (domestic pig) Gene: KIT
- **OMIA 001216-9825** Coat colour, roan in *Sus scrofa domesticus* (domestic pig) Gene: KIT
- **OMIA 001745-9825** Coat colour, white belt, due to KIT in *Sus scrofa domesticus* (domestic pig) Gene: KIT
- **OMIA 000259-9825** Deafness in *Sus scrofa domesticus* (domestic pig) Gene: MITF
- **OMIA 001718-9825** Dwarfism, Schmid metaphyseal chondrodysplasia in *Sus scrofa domesticus* (domestic pig) Gene: COL10A1
- **OMIA 001579-9825** Ear size in *Sus scrofa domesticus* (domestic pig) Gene: PPARD
- **OMIA 000499-9825** Hypercholesterolaemia in *Sus scrofa domesticus* (domestic pig) Gene: LDLR
- **OMIA 000621-9825** Malignant hyperthermia in *Sus scrofa domesticus* (domestic pig) Gene: RYR1
- **OMIA 001085-9825** Meat quality (Rendement Napole) in *Sus scrofa domesticus* (domestic pig) Gene: PRKAG3
OMIA 000621-9825: Malignant hyperthermia in *Sus scrofa domesticus*

In other species: turkey, dog, domestic cat, horse, deer, cattle, rabbit

Possible human homologue (MIM number): 145600

Mendelian trait/disorder: yes

Mode of inheritance: Autosomal Recessive

Considered a defect: yes

Key mutation known: yes

Year key mutation first reported: 1991

Cross-species summary: A progressive increase in body temperature, muscle rigidity and metabolic acidosis, leading to rapid death.

Species-specific name: Porcine Stress Syndrome

Species-specific symbol: PSS

Species-specific description: In pigs, malignant hyperthermia (MH) leads to rapid post-mortem changes in muscle, resulting in pale soft exudative (PSE) meat. MH can be triggered by a minor stress, such as loading, transport, sexual intercourse, high ambient temperature, or exposure to the anaesthetic halothane. Susceptibility to halothane-induced MH is an autosomal recessive trait in pigs. Together, sudden death syndrome and PSE constitute porcine stress syndrome (PSS), which became a major economic problem in many countries in the 1970s, as indicated by the number of references in the list below. In part, the increasing problem of PSS was due to strong selection for increased leanness, which is associated with susceptibility to PSS.

Molecular basis: The molecular basis of MH in pigs was discovered via identification of a strong candidate gene, namely RYR1, that encodes a calcium release channel of skeletal muscle sarcoplasmic reticulum. When it was shown that this candidate gene mapped very closely to MH in pigs and in humans, the race was on to clone and sequence the RYR1 gene. The race was won by a Canadian research team led by David MacLennan (Fujii et al., 1991) who showed that MH is due to a base substitution (C-T) in the 1843rd nucleotide of the RYR1 gene. The base substitution causes an amino-acid substitution (arginine - cysteine) in the 615th position of the calcium release channel, resulting in altered calcium flow. It is remarkable that the smallest possible change (a single base-substitution) leading to a single amino-acid-substitution in a very large molecule (comprising 5,035 amino acids) can have caused a disorder that was a major financial burden for the global pig industry for several decades.

Interestingly, Bates et al. (2012) reported that "A proportion of pigs normal for RYR1 did exhibit limb rigidity during halothane gas challenge, and subsequently tended to have lower 45 min pH and greater longissimus muscle fluid loss post harvest." This suggests that the RYR1 locus is not the only factor determining reaction to halothane.

Genetic testing: Various PCR genotyping tests have been devised, all based on detection of an RFLP resulting from the causative base substitution. Over a roughly ten-year period, these tests enabled the harmful allele to be removed from most pig populations throughout the world.

Associated gene:

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
<th>Species</th>
<th>Chr acc</th>
<th>Chr name</th>
<th>Start</th>
<th>Stop</th>
<th>OMIA gene details page</th>
<th>Other Links</th>
</tr>
</thead>
<tbody>
<tr>
<td>RYR1</td>
<td>ryanodine receptor 1 (skeletal)</td>
<td><em>Sus scrofa</em></td>
<td>NC_010448.3</td>
<td>6</td>
<td>42840239</td>
<td>42960105</td>
<td><a href="#">RYR1</a></td>
<td>Homologene, Ensemble, NCBI gene</td>
</tr>
</tbody>
</table>
Gene RYR1: ryanodine receptor 1 (skeletal) in *Sus scrofa*

In other species: dog, horse

Symbol: RYR1

Synonyms: CRC, RYR

Description: ryanodine receptor 1 (skeletal)

Type of gene: protein-coding

NCBI gene id: 396718

Other designations: RYR-1; calcium release channel; halothane; porcine stress syndrome; ryanodine receptor 1; skeletal muscle calcium release channel; skeletal muscle ryanodine receptor; skeletal muscle-type ryanodine receptor; type 1 ryanodine receptor

Links: Homologue, Ensembl

Genomic location: 6:42840239..42960105 [Chromosome accession NC_010448.3]

Related phenes:

OMIA 000621-9825: Malignant hyperthermia in *Sus scrofa domesticus*

References

Note: the references are listed in reverse chronological order (from the most recent year to the earliest year), and alphabetically by first author within a year.


OMIA 000621-9825: Malignant hyperthermia in *Sus scrofa domesticus*

Overall total number of references in OMIA: 20,660
most hyperlinked to PubMed
many have a link to actual paper via doi
OMIA 001718-9825 : Dwarfism, Schmid metaphyseal chondrodysplasia in Sus scrofa domesticus

Possible human homologue (MIM number): 156500

Mendelian trait/disorder: yes

Mode of inheritance: Autosomal Dominant

Considered a defect: yes

Key mutation known: yes

Year key mutation first reported: 2000

Species-specific description: In a single paper, Nielsen et al. (2000) reported a new form of dwarfism in pigs, and its causative mutation.

Inheritance: Nielsen et al. (2000) reported autosomal dominant inheritance.

Mapping: An initial genome scan with 70 microsatellite markers implicated chromosome SSC1. Mapping with additional SSC1 markers mapped the disorder to 8.3cM from marker Sw781. The authors noted that this region is homologous to human chromosome HSA6q21-22.3, which harbours the gene COL10A1, mutations in which cause Schmid metaphyseal chondrodysplasia, a disorder very similar to the pig disorder. Thus the authors had identified a comparative positional candidate gene.

Molecular basis: Following a comparative positional candidate gene approach (described above in the Mapping section), Nielsen et al. (2000) cloned and sequenced the porcine COL10A1 gene and identified a causative missense mutation, namely "a single G to A transition in exon 3 that results in a Gly-to-Arg substitution, G590R, in the carboxyl terminus of the protein".

Clinical features: The disorder is characterised by "Metaphyseal chondrodysplasia in the long bones" (Nielsen et al., 2000).

Breed: Yorkshire.

Associated gene:

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
<th>Species</th>
<th>Chr acc</th>
<th>Chr name</th>
<th>Start</th>
<th>Stop</th>
<th>OMIA gene details page</th>
<th>Other Links</th>
</tr>
</thead>
<tbody>
<tr>
<td>COL10A1</td>
<td>collagen, type X, alpha 1</td>
<td>Sus scrofa</td>
<td>NC_010443.4</td>
<td>1</td>
<td>91889387</td>
<td>91882389</td>
<td>COL10A1</td>
<td>Homologene, Ensembl, NCBI gene</td>
</tr>
</tbody>
</table>

Reference

OMIA 000483-9913 : Horns/Polled in *Bos taurus*

In other species: goat, sheep, water buffalo, bighorn sheep, kouprey

Possible human homologue (MIM number): **110100**

Mendelian trait/disorder: yes

Mode of inheritance: Autosomal

Considered a defect: no

Key mutation known: yes

Year key mutation first reported: 2012

Cross-species summary: There is substantial variation in the extent of horn growth, making classification difficult. However, in general, the presence or absence of horns can be attributed to the action of two alleles at an autosomal locus, with the polled condition being dominant to horned.

Species-specific description: The absence of horns (polledness) is of substantial benefit in cattle, from an economic and welfare point of view: bruising due to horns is eliminated, and the stress associated with de-horning is avoided. (Information compiled by Ulrika Tjälldé and Vanja Kinch, Uppsala, March 1998)

History: In cattle, one of the first Mendelian traits to attract attention was the presence/absence of horns. The inherited nature of this trait was well recognised (but not understood) long before the rediscovery of Mendelism (see, e.g. Darwin 1859, p. 14; Darwin 1868 [vol ii, p. 316]). In 1902, polledness was one of the first six animal traits to be shown to have Mendelian inheritance (Bateson and Saunders, 1902). In 1906, the American agricultural polymath W.J. Spillman (who is not only regarded as a founding father of agricultural economics, but also independently rediscovered Mendelism while crossing strains of wheat!) published a paper in Science (Spillman 1906a) and another in the newly-founded Journal of Heredity (Spillman 1906b), providing convincing evidence that the presence/absence of horns is a Mendelian trait, with polled being dominant to horned. This trait soon became a classic Mendelian trait, cited in many textbooks. Indeed, as delightfully recorded by Crow (1992), Erwin Schrödinger, who wrote two letters to J.B.S Haldane in 1945, in relation to the “hornless cattle problem”. In these letters, Schrödinger derived an equation that predicts the frequency of horned offspring in a closed herd after any number of generations of complete selection against horned bulls, but with no selection on cows.

Nothing much was added to our knowledge of this trait until the first wave of genomics tools provided sufficient microsatellite markers to enable us to map the presence/absence of horns to within a recombination fraction of 13% with two markers on chromosome BTA1 (Georges et al. 1993; see Mapping section). To present readers, such “loose” linkage might seem to be not worthy of much celebration. At the time, however, this result was sufficiently important and novel to warrant publication in *Nature Genetics*. Subsequent progress in mapping is summarised in the Mapping section. (Most of the wording under this heading is from Nicholas, F.W. (2012; Mendelian inheritance in Cattle, chap 2 [pp. 11-19] in Bovine Genomics [ed. J. Womack], Wiley-Blackwell, Ames, Iowa.)


Associated gene:

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
<th>Species</th>
<th>Chr acc</th>
<th>Chr name</th>
<th>Start</th>
<th>Stop</th>
<th>OMA gene details page</th>
<th>Other Links</th>
</tr>
</thead>
<tbody>
<tr>
<td>POLLED</td>
<td><em>Bos taurus</em></td>
<td>no genomic information</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>POLLED</td>
<td>Ensembl</td>
</tr>
</tbody>
</table>
OMIA 000151-9913 : Brachyspina in *Bos taurus*

Mendelian trait/disorder: yes
Mode of inheritance: Autosomal Recessive
Considered a defect: yes
Key mutation known: yes
Year key mutation first reported: 2012
Molecular basis: Charlier et al. (2012) reported the causal mutation for brachyspina in Holstein cattle as a deletion in the FANCI gene. Noting that the carrier frequency is far too high (up to 7.4%) to be consistent with a relatively rare autosomal recessive disorder, Charlier et al. (2012) also showed that a large proportion of affected calves die in utero. Thus this causal mutation also contributes to natural abortions and hence to reduced fertility.

Breed: Holstein.

Associated gene:

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
<th>Species</th>
<th>Chr acc</th>
<th>Chr name</th>
<th>Start</th>
<th>Stop</th>
<th>OMIA gene details page</th>
<th>Other Links</th>
</tr>
</thead>
<tbody>
<tr>
<td>FANCI</td>
<td>Fanconi anemia, complementation group I</td>
<td><em>Bos taurus</em></td>
<td>AC_000178.1</td>
<td>21</td>
<td>21137917</td>
<td>21198617</td>
<td>FANCI</td>
<td>Homologene, Ensembl, NCBI gene</td>
</tr>
</tbody>
</table>

References

Note: the references are listed in reverse chronological order (from the most recent year to the earliest year), and alphabetically by first author within a year.


~750,000 words = 661 A4 pages of 8-point double-column text
DOWNLOAD DATA

To download a current MySQL dump of OMIA please click on the appropriate link below.

<table>
<thead>
<tr>
<th>Format</th>
<th>Zip</th>
<th>gzip</th>
</tr>
</thead>
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</tr>
<tr>
<td>xml</td>
<td>omia.xml.zip</td>
<td>omia.xml.gz</td>
</tr>
</tbody>
</table>

A table of phenes for which there is a causal mutation in a known gene is available [here](#).

There is also a print version of the OMIA database (with all records up to 2nd July 2012) available [here](#).
<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
</tr>
</thead>
</table>
| 1974 | Lecturer in animal genetics  
→ many queries → many trips to library |
|      | Became aware of Mendelian Inheritance in Man (MIM)  
flat file on mainframe at Johns Hopkins  
print editions (printouts): 1971 3rd edn |
| 1978 | Accosted Victor McKusick at Genetics Congress in Moscow  
animal equivalent of MIM? Sure, go ahead |
|      | Key features:  
>1 species → extra dimension → strong comparative emphasis  
modelled on MIM; hence Mendelian Inheritance in Animals (MIA) |
| 1980 | Small grant → create MIA relational database on mainframe  
cf MIM flatfile |
<p>| 1980s | Gradual entry of backlog and manual servicing of queries |</p>
<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>1991</td>
<td>Birth of WorldWideWeb</td>
</tr>
</tbody>
</table>
| 1995 | both MIM and MIA launched on the web  
  → Online MIM (OMIM) and Online MIA (OMIA)  
  both using NCBI’s birx search engine |
|      | OMIA: regularly-updated flat file from database on laptop  
  published via Australian National Genomic Information Service (ANGIS)  
| 1997 | Reciprocal hyperlinks between OMIM and OMIA  
  highlight animal models of human disorders |
| 2005 | OMIA transferred to MySQL database on server  
  Interactive web page !!  
  **Instant updating by curators anywhere in the world!!** |
| 2005 | NCBI asked for an OMIA mirror integrated in their Entrez system  
  weekly dump → OMIA alongside OMIM !! |
OMIA: a brief history

Online Mendelian Inheritance in Animals (OMIA)
A database of genes, inherited disorders and traits in animal species (other than human and mouse), with textual information and links to relevant records from other NCBI databases, such as PubMed and Gene.

Online Mendelian Inheritance in Man (OMIM)
A database of human genes and genetic disorders. NCBI maintains current content and continues to support its searching and indexing in NCBI databases. However, OMIM now has a new home at omim.org, and users are directed to this site for full record displays.

Probes
A public registry of nucleic acid reagents designed for use in a wide variety of biomedical research applications, together with information on distributors, probe effectiveness, and computed sequence similarities.

Protein Clusters
A collection of related protein sequences (clusters), consisting of Reference Sequence proteins encoded by complete prokaryotic plasmids and genomes. The database provides easy access to annotation information, publications, domains, structures, external tools.

Protein Database
A database that includes protein sequence records from a variety of sources, including GenPept, RefSeq, Swiss-Prot, PIR, PRF, and others.
### OMIA: a brief history

<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>2011</td>
<td>Revised web site with improved curation tools based on a django framework (Matthew Hobbs)</td>
</tr>
<tr>
<td></td>
<td>Vicki Meyers-Wallen (Cornell): dogs and cats</td>
</tr>
<tr>
<td>2012</td>
<td>Zhiliang Hu: reciprocal links with AnimalGenome.org</td>
</tr>
<tr>
<td></td>
<td>Fiona Cunningham: reciprocal links with Ensembl (thanks to Dave Burt)</td>
</tr>
<tr>
<td></td>
<td>Thomas Peterson &amp; Maricel Kann, University of Maryland, Baltimore County systematic catalogue of all ORF causal mutations in HGVS notation protein domain hotspots of disease mutations</td>
</tr>
</tbody>
</table>
Zhiliang’s handywork!!!
Incorporating molecular and functional context into the analysis and prioritization of human variants associated with cancer

Thomas A Peterson,1 Nathan L Nehrt,1,2 DoHwan Park,1 Maricel G Kann1

Nehrt et al. BMC Genomics 2012, 13(Suppl 4):S9
http://www.biomedcentral.com/1471-2164/13/S4/S9

Domain landscapes of somatic mutations in cancer

Nathan L Nehrt1,2†, Thomas A Peterson1†, DoHwan Park3, Maricel G Kann1*
OMIA now

- Alternatives?
  - several dog web catalogues
    (COGNOSAG: Keith Huston, Paul Millar, JJ Lauvergne and S. Dolling)
  - many reviews

**AIM: to check OMIA entries against each review (far from complete!!)
OMIA now

Obvious problem with “static” reviews:
  • rapidly out of date
  • no functional links to other information
  • but still valuable, from time to time

Given that OMIA
  1. exists (albeit in an incomplete state)
  2. is freely available
  3. is/can be kept up to date
  4. is increasingly hyperlinked to other relevant databases

There is no point in anyone starting from scratch to collect information and references for a review

OMIA: a one-stop global resource for animal genetics/genomics ??
Already have a team of volunteers and a handbook

- Frank Nicholas
- Imke Tammen
- Mohammad Shariflou
- Bethany Wilson
- Matthew Hobbs
- Vicki Meyers-Wallen
- Martha Maloney-Huss
- Paul McGreevy
- Mark Haskins
- Tosso Leeb
- Hamutal Mazrier
- Marilyn Menotti-Raymond
- Peter Windsor
- Jerry Wei
- Carole Charlier
- Michel Georges
- Blanca Hasse
- Ben Dorshorst
- Mario Van Poucke
- Emily Piper
- Zhiliang Hu
- Zena Wolf

OMIA CURATION GUIDE
by Frank Nicholas
Version 120129

and a practice site:

http://sg-web-prd-1.ucc.usyd.edu.au/

and curation tools:
CURATION TOOLS

OMIA ADMINISTRATION

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</tr>
<tr>
<td>Species</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Species-specific phenes</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Auto-fill:
- PubMed refs
- Species names
- Phene names
- Gene symbols
- Breed names
### ADD SPECIES-SPECIFIC PHENE

<table>
<thead>
<tr>
<th>Field</th>
<th>Auto-complete</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phene:</td>
<td></td>
</tr>
<tr>
<td>Species:</td>
<td></td>
</tr>
<tr>
<td>Breeds:</td>
<td></td>
</tr>
<tr>
<td>Species-specific phene name:</td>
<td></td>
</tr>
<tr>
<td>Symbol:</td>
<td></td>
</tr>
<tr>
<td>Summary:</td>
<td></td>
</tr>
<tr>
<td>History:</td>
<td></td>
</tr>
<tr>
<td>Prevalence:</td>
<td></td>
</tr>
</tbody>
</table>

Type in part of a species common name, or the beginning of a species scientific (binomial) name, or an NCBI taxonomy database species identifier, and make a selection from the suggested list.

Type in part of a breed name and make a selection from the suggested list. Multiple selections can be accrued. Clicking on the green [+] icon opens a separate window allowing the creation of a new breed record.
### Genetics (Hide)

<table>
<thead>
<tr>
<th>Single locus:</th>
<th>unknown</th>
<th>Key mutation known:</th>
<th>no</th>
<th>Year key mutation reported:</th>
<th></th>
<th>Key mutation published:</th>
<th>N/A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mode of inheritance:</td>
<td>--------</td>
<td>---------------------</td>
<td>----</td>
<td>-----------------------------</td>
<td>---</td>
<td>---------------------------</td>
<td>-----</td>
</tr>
</tbody>
</table>

**Inheritance details:**

**Genes:**

*Auto-complete*

Type in part of a gene symbol or description and make a selection from the suggested list. Multiple selections can be accrued.

**Genetic testing:**

**Genetic mapping:**

**Marker:**

**Molecular basis:**
Most fields in most entries currently empty!!
More fields can be added in any section!!
Essentially OMIA has been a one-person operation til now
Retired “early” at age 60, primarily to work on OMIA
But can’t do it complete justice
Now 65, and still fit and able, albeit with
- one pre-cancer operation in 2011
- contemporaries having strokes !!
Serious need for Plan B
- colleagues with motivation and time to become curators
  - species
  - traits (across species)
A flood of KOs in non-laboratory animals?

OMIA 000499-9825 : Hypercholesterolaemia in Sus scrofa domesticus

In other species: rabbit, dog
Possible human homologue (MIM number): 143890
Mendelian trait/disorder: yes
Mode of inheritance: Autosomal Recessive
Considered a defect: yes
Key mutation known: yes
Year key mutation first reported: 1998
Species-specific name: familial hypercholesterolemia, recessive
Species-specific symbol: FH

History: This trait was the first in non-laboratory animals to be investigated via the use of Transcription Activator-Like Effector Nucleases (TALENs) (Carlson et al., 2012) to create knockouts of the key gene (in this case, LDLR) (Carlson et al., 2012).

Molecular basis: A genome scan conducted by Hastierrapacz et al. (1998) showed that the gene for this disorder in pigs maps near to the centromere of chromosome 2, which is homologous to the region of human chromosome 19 containing the gene for low-density lipoprotein receptor (LDLR), a strong candidate for involvement in this disorder. Sequence analysis of the LDLR gene from homozygous normal and affected pigs showed that the disorder is due to a single missense mutation (resulting in the amino-acid substitution Arg84Cys). The causal mutation was thus identified via the comparative positional candidate gene approach.

In a proof-of-principle study, Carlson et al. (2012) used Transcription Activator-Like Effector Nucleases (TALENs) to create cloned pigs with a range of mutations in the porcine LDLR gene, namely 289_290insA, 285_287delATG, 211_292del128, 289_290del10 and 289_290insA. The phenotypes of these mutant pigs were not reported in this paper.

Associated gene:

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
<th>Species</th>
<th>Chr acc</th>
<th>Chr name</th>
<th>Start</th>
<th>Stop</th>
<th>OMIA gene details</th>
<th>Other Links</th>
</tr>
</thead>
<tbody>
<tr>
<td>LDLR</td>
<td>low density lipoprotein receptor</td>
<td>Sus scrofa</td>
<td>NC_010444.3</td>
<td>2</td>
<td>70205817</td>
<td>70193425</td>
<td>LDLR</td>
<td>Homologene, Ensembl, NCBI gene</td>
</tr>
</tbody>
</table>

References

Note: the references are listed in reverse chronological order (from the most recent year to the earliest year), and alphabetically by first author within a year.

Potential curators:

- authors of recent species reviews
- postgrads/postdocs, as a part of their training (Ernie Bailey):
  - to work through reviews critically is a really useful exercise
    - gives a feeling for the history of discovery
    - is there sufficient data to justify the Mendelian claim?
    - is there sufficient evidence to justify the claim of a causal mutation?
  - check OMIM links (is this a valid model of a human disorder?)
  - sort out confusing nomenclature/terminology
    - rename/merge/split entries
  - updating entries as an assessment task
- tools for curators to check and release new/revised text (Matthew)

Updating McKusick: An Educational Exercise for Medical Students

Joann N. Bodurtha, J. Ives Townsend, Virginia K. Proud, and Walter E. Nance

Department of Human Genetics, Medical College of Virginia, Richmond, Virginia


II. RECENT INNOVATIONS IN HUMAN GENETICS EDUCATION

The Curricularization of McKusick

Joann N. Bodurtha,* Sandi Verbin,* Klara K. Papp, † and Walter E. Nance*

*Department of Human Genetics and †Center for Educational Development and Faculty Resources, Medical College of Virginia, Richmond

*Why is this an OMA Landmark paper?* It is first of two adjacent papers (the other being Bateson and Saunders, 1902) that first reported Mendelian inheritance in animals. This paper reported five Mendelian poultry traits, namely Pea comb, Rose comb, polydactyly, shank colour, and white plumage (dominant white).

Bateson, W., Saunders, E.R.:  

*Why is this an OMA Landmark paper?* It is the second of two adjacent papers (the other being Bateson, 1902) containing the very first reports of Mendelian inheritance in domesticated animals. In addition to the five Mendelian poultry traits reported in the preceding paper (Bateson, 1902), this paper also reported polled in cattle as being a Mendelian trait.

1908 Bateson, W., Punnett, R.C.:  

*Why is this an OMA Landmark paper?* It was the first paper to describe a phenotype resulting from the interaction of two genes, i.e. epistasis. The two genes were Rose-comb and Pea-comb in chickens. Birds with mutant alleles at both loci have a “walnut” comb, which is markedly different from either Rose-comb or Pea-comb. Another landmark paper (Linsland et al., 2012) has provided a molecular explanation for this pleiotropy.

1928 Serebrovsky, A.S., Petrov, S.G.:  

*Why is this an OMA Landmark paper?* It presents the first-ever linkage map for any domesticated animal species.


*Why is this an OMA Landmark paper?* It is the very first report of a causal mutation in domesticated non-laboratory animals. The discovery was made possible by the specific clinical signs, which suggested only one possible candidate gene, namely the TSH gene, encoding thyroglobulin.


*Why is this an OMA Landmark paper?* It was the first report of the causal mutation of one of the most investigated and economically-important disorders to have occurred in domesticated animals. Extensive comparative mapping between humans and pigs eventually suggested the RYR1 gene encoding the ryanodine receptor as a very likely candidate gene. It turned out to be a huge gene (120 kb), the sequencing of which was a mammoth task at that time (late 1980s, early 1990s). These authors were the first to show that the smallest possible mutation (a single-base missense mutation) that charged just one amino acid in a very large molecule comprising 5,035 amino acids, was the cause of a disorder that had been a major financial burden for the global pig industry for several decades.
\textbf{INCENTIVES FOR CURATORS?}

\textbf{Acknowledgement:}
- at bottom of each edited page
- at end of a section of text
- but these not much help on CV

\textbf{Publications:}
- publish static OMIA reviews from time to time (highly cited 😊)

\textbf{Create specific OMIA roles, e.g. OMIA Chief Swine editor}

\textbf{Become regarded as the “guardian/authority” of information for a species or for a set of traits}
Co-author Matthew Hobbs has done an amazing job
- 500 hours in 2012 ≈ $50,000
- the last of my leftover funds

But still a long shopping list of enhancements required for OMIA

On the web in **Roundup Issue Tracker**
Two major enhancement issues:

1. ONTOLOGIES
   - Matthew: entire MPO (Jackson lab) as auto-complete on test site, but very slow
   - Very useful collaboration with Zhiliang Hu
   - Still a long way to go

2. AUTOMATIC TEXT MINING
   - Now: use myNCBI daily searches for phenes or authors
     - Many irrelevant refs
   - Automatic addition of new refs for each entry
     - e.g. Miotto et al. (2005) Supporting the curation of biological databases with reusable text mining. Genome Inform.16(2):32-44
   - Curator check; then go live
OMIA SUMMARY

- Developed over the last 35 years
- Freely available at http://omia/angis.org.au
- Covers (incompletely) 186 non-human animal species
- 2,820 phene-species entries
  - Nearly 1,000 Mendelian phene-species entries
    - Including 486 with known key mutation
- Hyperlinks with NCBI, OMIM, Ensembl, AnimalGenome
- 20,000 references
  - Most hyperlinked to PubMed
  - Many with doi access to full paper
- = Groundwork for others to build-on/develop
- Curation tools and development/testing/learning version
OMIA SUMMARY

† OMIA has the potential to be the global one-stop shop for up-to-date information on
  † inherited disorders
  † single-locus traits

† Of course, the world does not owe a living to OMIA or to me

† Aim of this talk
  † make people aware that if I am knocked out, OMIA is dead!

† If sufficient people feel OMIA should be maintained and improved, then
  † need a Plan B for curation
  † need (modest) funding for enhancement

† Here at PAG, I am willing to
  † help anyone work through curation tools
  † correct/update/create entries
Acknowledgements

› Ernie Bailey and Max Rothschild (and Ann Shuey)
  - Support provided by USDA-NRSP8 coordinators funds from the horse and Swine genome programs
› Zhiliang Hu and Jim Reecy
› Sue Lamont, Noelle Cockett, Jim Womack
› Zhihua Jiang, Joan Lunney
› Danika Bannasch, Chipper Swiderski
› Sue Lamont, Douglas Rhoads, Carl Schmidt
› The many colleagues who have been involved in the development of OMIA: http://omia.angis.org.au/acknowledgements/
  - especially Xuan Zhang (NCBI)
› And the >30,000 scientists who have contributed to the collective knowledge that is embodied in OMIA