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Genetic Nomenclature

Zhiliang Hu
Iowa State University, zhu@iastate.edu

James M. Reecy
Iowa State University, jreecy@iastate.edu

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Abstract
Genetics includes the study of genotypes, phenotypes and the mechanisms of genetic control between them. Genetic terms describe the processes, genes, alleles and traits with which genetic phenomena are described and examined. In this chapter we will concentrate on the discussions of genetic term standardizations and, at the end of the chapter, we will list some terms relevant to genetic processes and concepts in a Genetic Glossary.

Disciplines
Agriculture | Animal Sciences | Genetics

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Introduction

Genetics includes the study of genotypes, phenotypes and the mechanisms of genetic control between them. Genetic terms describe the processes, genes, alleles and traits with which genetic phenomena are described and examined. In this chapter we will concentrate on the discussions of genetic term standardizations and, at the end of the chapter, we will list some terms relevant to genetic processes and concepts in a Genetic Glossary.

A standardized genetic nomenclature is vital for unambiguous concept description, efficient genetic data management and effective communications among not only scientists, but also among canine veterinarians, breeding societies and those individuals who are interested in the subject. This issue becomes even more evident in the post-genomics era, owing to the rapid accumulation of large quantities of genetic data, and the use of computer software to manage such data, which imposes a challenge for the precise definition and interpretation of genetic terms.

For example, the Myostatin gene (MSTN) is also known as Growth and Differentiation Factor 8 gene (GDF8) (one can also find inappropriate abbreviations such as GDF-8 in the literature) and is referred to as the 'bully whippet' locus in dogs. While all these names are interchangeably used in the literature, it gets more complicated when one considers paralogous gene duplications across species, which led Rodgers et al. (2007) to propose MSTN-1 and MSTN-2 as paralogue names. Unfortunately, this naming scheme does not follow Human Gene Nomenclature Committee (HGNC) guidelines, which would indicate that the relevant genes should be named MSTN1 and MSTN2. (Note that work on the standardization of human gene nomenclature is far more advanced than that in other species.)

From the previous example, we see that there is evidently a need for all researchers to follow a standardized genetic nomenclature in order for them to communicate to each other correctly on the terms they use. When a term is used by someone to describe a genetic phenomenon, the correct use of the term will help to quickly and precisely place the subject under the unambiguously defined scope. More importantly, a standard nomenclature will help to minimize the time one has to spend in differentiating the instances where two terms may
actually mean the same or different things, which is often a costly process. The need for a standardized genetic nomenclature becomes more pressing when ontologies are employed in biological research for computers to manage the genetic terms. Ontology provides a new way to effectively use, standardize and manage genetics terms. The Gene Ontology (GO) Consortium has provided a good example (The Gene Ontology Consortium, 2000). When genomics information must be transferred across species to perpetuate genetic discoveries, the role of a standardized genetic nomenclature becomes even more important (Bruford, 2010).

The goal of this chapter is to help establish guidelines for nomenclature, with the hope that it will facilitate comparison of results between experiments and, most importantly, prevent confusion.

**Locus and Gene Names and Symbols**

**Locus name and symbol**

These guidelines for gene nomenclature are adapted and abbreviated from the Human Gene Nomenclature Committee Guidelines (http://www.genenames.org/guidelines.html).

A gene is defined as: ‘A functional hereditary unit that occupies a fixed location on a chromosome, has a specific influence on phenotype, and is capable of mutation to various allelic forms. In the absence of demonstrated function a gene may be characterized by sequence, transcription or homology’. A ‘locus’, which is not synonymous with a gene, refers to a position in the genome that can be identified by a marker. A ‘chromosome region’ is defined as a genomic region that has been associated with a particular syndrome or phenotype.

Gene names and symbols will follow the human gene when 1:1 orthology is known. Gene names should be short and specific and convey the character or function of the gene. They will be written using American spelling and contain only Latin letters or a combination of Latin letters and Arabic numerals. The first letter of a gene symbol should be the same as for the gene name. The symbol will consist of upper-case Latin letters and possibly Arabic numerals. Gene symbols must be unique.

The locus name should be in capitalized Latin letters or a combination of Latin letters and Arabic numerals. If the locus name is two or more words, each word should be in capital Latin characters. The locus symbol should consist of as few Latin letters as possible or a combination of Latin letters and Arabic numerals. The characters of a symbol should always be capital Latin characters, and should begin with the initial letter of the name of the locus. If the locus name is two or more words, then the initial letters should be used in the locus symbol. The locus name and symbol should be printed in italics wherever possible; otherwise they should be underlined.

When assigning gene nomenclature, the gene name and symbol should be assigned based on existing HGNC nomenclature where possible (i.e. 1:1 for canine:human orthologues). Ensembl has used the new EPO (Enredo, Pecan, Ortheus) pipeline (Paten et al., 2008) for whole-genome alignment of the dog genome. Initial efforts to provide information about genes predicted during the canine genome sequencing effort assigned standardized nomenclature based on human gene nomenclature for 3613 canine genes (http://uswest.ensembl.org/Canis_familiaris/Info/StatsTable).

There are two categories of novel canine genes: (i) novel genes predicted by bioinformatic gene prediction programs; and (ii) novel canine genes that were studied before the completion of the canine genome. In cases where no known strict 1:1 human orthologue exists, the LOC # or Ensembl ID should be used as a temporary gene symbol. In order to assign a name to a novel gene, it will need to be manually curated and assigned a unique name following HGNC guidelines.

**Allele name and symbol**

These guidelines for allele nomenclature are adapted from Young (1998) and mouse genome nomenclature guidelines (http://www.informatics.jax.org/mgihome/nomen/gene.shtml), in accordance with HGNC guidelines.
The allele names should be as brief as possible, yet still convey the variation associated with the allele. Alleles do not have to be named, but should be given symbols. If a new allele is similar to one that is already named, it should be named according to the breed, geographical location or population of origin. New alleles are to be named for a recognized locus, they should conform to nomenclature established for that locus. The first letter of the allele name should be lower case. However, this does not apply when the allele is only a symbol.

An allele symbol should be as brief as possible and consist of Latin letters or a combination of Latin letters and Arabic numerals. Like a gene symbol, an allele symbol should be an abbreviation of the allele name, and should start with the same letter. The allele name and symbol may be identical for a locus detected by biochemical, serological or nucleotide methods. The wild-type allele can be denoted as a + (e.g. MSTN+). Neither + nor - symbols should be used in alleles detected by biochemical, serological or nucleotide methods. Null alleles should be designated by the number zero. The initial letter of the symbol of the top dominant allele should be capitalized (e.g. AY/a' for sabled red coat colour at the Agouti locus). All alleles that are codominant should have an initial capital letter (e.g. DEA4/DEA6 of the canine blood group; DEA is short for Dog Erythrocyte Antigen). The initial letter of all other alleles should be lower case. A single nucleotide polymorphism (SNP) allele should be designated based on its dbSNP_id, followed by a hyphen and the specific nucleotide (e.g. MSTN_1234567). If the SNP occurs outside an identified gene, the SNP locus can be designated using the dbSNP_id as the locus symbol, and the nucleotide allelic variants are then superscripted as alleles (e.g. rs1234567).

The allele symbol should always be written with the locus symbol. Specifically, the allele symbol is written as a superscript following the locus symbol. For example, a SNP allele can be designated based on its dbSNP_id, followed by a hyphen and the specific nucleotide, as in MSTN_1234567. The allele symbol should be printed immediately adjacent to the locus symbol, with no gaps. The allele name and symbol should be printed in italics whenever possible, or otherwise be underlined.

Genotype terminology

The genotype of an individual should be shown by printing the relevant locus, gene or allele symbols for the two homologous chromosomes concerned, separated by a slash, e.g. MSTN=1234567-1234567.C. Unlinked loci should be separated by semicolons, e.g. CD11a Real-24002200; ESP_032 S7004200. Linked or syntenic loci should be separated by a space or dash and listed in linkage order (e.g. POUIF1AG-STCHFC-PR8S7), or in alphabetical order if the linkage order is not known. For X-linked loci, the hemizygous case should have a /Y following the locus and allele symbol, e.g. AR=571-1094 /Y. Likewise, Y-linked loci should be designated by /Y following the locus and allele symbol.

Future Prospects

The Gene Ontology project is already playing a role in robust annotation of mammalian genes in the context of mutations, quantitative trait loci, etc. (Smith et al., 2005). Undoubtedly, a standardized dog genetic nomenclature will more effectively facilitate efficient dog genome annotation and transfer of knowledge from information-rich species such as humans and the mouse, and make it possible for new bioinformatics tools to easily streamline data management and genetic analysis.

Several genome databases, GeneCards, Ensembl and NCBI GeneDB, have played a role in the usage of commonly accepted gene/trait notations. Undoubtedly, existing and new genome databases and tools will further develop and evolve. As such, a standardized genetic nomenclature in dogs will definitely become crucial for information sharing and comparisons between different research groups, across experiments and even across species.

In October 2009, the 'Gene Nomenclature Across Species' Meeting was held in Hinxton, England. The following recommendations from the meeting will be useful to guide the standardization of dog genetic terms: (i) gene nomenclature should reflect homologous relationships across vertebrate species; (ii) consensus naming has already
been implemented in the human, mouse, rat, chicken, zebra fish and *Xenopus*. Effort should be expanded to other vertebrate genomes; (iii) guidelines for the naming of genes across vertebrates should follow rules for the naming of paralogues and be published for sharing; (iv) the formation of novel species-specific gene nomenclature committees should be encouraged; (v) automated naming efforts should initially concentrate on consensus 1:1 orthologues as identified by at least two independent and comprehensive orthology resources; and (vi) there is a need to increase community awareness of standardized gene nomenclature, especially in journals (Bruford, 2010).

In summary, a standardized genetic nomenclature will benefit canine genetics by facilitating communication. Furthermore, it will facilitate information transfer between species.

**References**


**Genetic Glossary**

Bold words are glossary entries. *Italicized* words are concepts that may be independent glossary entries as well.

**Adaptation traits** – Adaptation traits contribute to individual fitness and to the evolution of animal genetic resources. By definition, these traits are also important to the ability of the animal genetic resource to be sustained in the production environment.

**Additive genetic effect** – The effect of an allele on animal performance, independent of the effect of the other allele at a locus; these effects of the two alleles at a locus add up (thus are 'additive'). Alleles at a locus may have other effects (dominance, epistasis), so that there are not genes that have just 'additive' effects and other genes with only 'dominance' effects. Additive genetic effects can be inherited; other genetic effects such as dominance and epistasis are the result of allele combinations that are lost between generations. The additive genetic effect that an animal has for a trait is equal to its breeding value.

**Allele** – One of a pair, or series, of alternative forms of a gene that can occur at a given locus on homologous chromosomes.

**Amino acid** – Any one of a class of organic compounds containing the amino (NH$_2$) group and the carboxyl (COOH) group. Amino acids are combined to form proteins.

**Ancestor** – Any individual from which an animal is descended.

**Animal model** – A system for genetic evaluation that estimates breeding values of individual animals (males, females) at the same time. The system uses production data on all known relatives in calculating a genetic evaluation.

**Assortative mating** – Assigning animals as mates based on phenotypic or genetic likeness. *Positive assortative mating* is mating animals that are more similar than average. *Negative assortative mating* is mating animals that are less similar than average.
Autosome – Any chromosome that is not a sex chromosome.

Backcross – The cross produced by mating a first-cross animal back to one of its parent lines or breeds.

Breed – Either a subspecific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species, or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity.

Breeding value – The mean genetic value of an individual as a parent. This can be estimated as the average superiority of an individual's progeny relative to all other progeny under conditions of random mating.

Categorical trait – Scores are given usually in a few categories up to several categories (e.g. scores of 1–5 for leg movement).

Centromere – Spindle-fibre attachment region of a chromosome.

Chromosome – Microscopically observable linear arrangement of DNA in the nucleus of a cell. Chromosomes carry the genes responsible for the determination and transmission of hereditary characteristics.

Codominant alleles – Alleles, each of which produces an independent effect in heterozygotes.

Combining ability – The mean performance of a line when involved in a crossbreeding system. General combining ability is the average performance when a breed or line is crossed with two or more other breeds or lines. Specific combining ability is the degree to which the performance of a specific cross deviates from the average general combining ability of two lines.

Composite (synthetic) breed – A hybrid with at least two and typically more breeds in its background. Composites are expected to be bred to their own kind, retaining a level of hybrid vigour normally associated with traditional crossbreeding systems.

Correlation coefficient – A measure of the interdependence of two random variables that ranges in value from -1 to +1, indicating perfect negative correlation at -1, absence of correlation at zero, and perfect positive correlation at +1. It determines the degree to which the movement of two variables is associated. No cause and effect is implied.

Covariance – The degree to which two measurements vary together. A positive covariance is when two measurements tend to increase together. A negative covariance is when one measurement increases and the other tends to decrease.

Crossbreeding – Matings between animals of different breeds or lines.

Crossover – The process during meiosis when chromosomal segments from different members of a homologous pair of chromosomes break, and part of one will join a part of the other, so that two gametes that form possess new combinations of genes. The frequency of crossover between two loci is proportional to the physical distance between them.

Crossover unit – Each unit is equal to a one per cent frequency of crossover gametes.

Cytoplasm – The protoplasm outside a cell nucleus.

Descendant – An individual descended from other individuals.

DNA – Deoxyribonucleic acid, the chemical material which carries information to code for a gene.

Dominance genetic effects – The effect that an allele has on animal performance, which depends upon the genotype at the locus. For example, the 'a' allele may have a different effect on animal performance in 'aa' animals than in 'Aa' animals. See Additive genetic effect.

Dominant – Applied to one member of an allelic pair of genes, which has the ability to express itself wholly or largely at the exclusion of the expression of the other allele. Depending on the location and on the type of chromosomes, there could be autosomal dominant or X-linked dominant genes.

Environment – The aggregate of all the external conditions and influences affecting the life and development of an organism.

Environmental correlation – When two traits tend to change in association with each other as a result of environmental effects.

Environmental variance – Variation in phenotype which results from variation in environmental effects.

Epistasis – When the gene at one locus affects the expression of the gene at another locus.

Estimated breeding value – A prediction of a breeding value. See Breeding value.

Family size – The mean number of offspring per parent that successfully reproduce.

Full sibs – Individuals with the same male and female parents.

Gamete – A sperm or egg cell containing the haploid (1n) number of chromosomes.

Gene – A functional hereditary unit that occupies a fixed location on a chromosome, has a specific influence on phenotype, and is capable of mutation to various allelic forms.
Genetic abnormality – A disease or phenotypic disorder that is inherited genetically.
Genetic correlation – When two traits tend to change in the same or opposite directions as a result of genetic effects.
Genetic disorder – see Genetic abnormality.
Genetic distance – A measure of gene differences between populations (hence genetic relationships among them) described by some numerical quantity; gene differences are usually referred to as measured by a function of gene frequencies.
Genetic drift – Changes in gene frequency in small breeding populations due to chance fluctuations.
Genetic evaluation – Predictive assessment of conformational characteristics or phenotypic improvement of potential gains to be derived by the use of the individual in question in a breeding programme.
Genetic gain – The amount of increase in performance that is achieved through genetic selection after one generation of selection.
Genetic map – See Linkage map.
Genetic marker – A gene or DNA sequence having a known location on a chromosome and associated with a particular gene or trait; a gene phenotypically associated with a particular, easily identified trait and used to identify an individual or cell carrying that gene.
Genetic merit – Inherited performance qualities.
Genetic resistance – Genetically determined resistance to certain infectious agents.
Genetic variance – Variation in phenotype which results from variations in genetic composition among individuals.
Genome – The complete set of genes and non-coding sequences present in each cell of an organism, or the genes in a complete haploid set of chromosomes of a particular organism.
Genotype – The genetic constitution of one or a few gene(s) or locus (loci), or total genetic make-up (genes) of an individual organism.
Genotype-environment interaction – When the difference in performance between two genotypes differs, depending upon the environment in which performance is measured. This may be a change in the magnitude of the difference or a change in rank of the genotypes.
Half sibs – Individuals that share only one common parent.
Haplotype – A set of alleles at a closely linked group of loci, so closely linked that the allelic set behaves almost as one allele in terms of inheritance.
Hardy–Weinberg law – A population is in genotypic equilibrium if p and q are the frequencies of alleles A and a, respectively, and $p^2$, 2pq and $q^2$ are the genotypic frequencies of AA, Aa and aa under the condition of random mating.
Heritability – Degree to which a given trait is controlled by inheritance; the proportion of total phenotypic variation that is attributable to genetic variation (in contrast to environment-caused variation).
Heterosis – The degree to which the performance of a crossbred animal is better or worse than the average performance of its parents.
Heterozygote, adj. heterozygous – An organism with unlike members of any given pair or series of alleles, which consequently produces unlike gametes.
Homologous chromosomes – Chromosomes which occur in pairs and are similar in size and shape, one having come from the male and one from the female parent.
Homozygote, adj. homozygous – An organism whose chromosomes carry identical members of a given pair of genes. The gametes are therefore all alike with respect to this locus.
Inbreeding – Matings among related individuals which results in progeny that have less heterozygosity and hence more homozygous gene pairs than the average of the population.
Inbreeding coefficient – A measurement of the increase in homozygosity; each unit is equal to a 1% increase in homozygosity relative to the average homozygosity in the base population.
Inbreeding depression – The decreased performance normally associated with accumulation of inbreeding. Many recessive genes result in undesired traits or decreased performance when they are expressed. Inbred animals have more recessive genes in the homozygous condition that are expressed and result in reduced performance or undesired traits.
Introgression – A breeding strategy for transferring specific favourable alleles from a donor population to a recipient population. This would, for example, be of great interest for genes responsible for disease resistance, which could be introgressed into a susceptible but otherwise economically superior breed.
Karyotype – The appearance of the metaphase chromosomes of an individual or species which shows the comparative size, shape and morphology of the different chromosomes.
Liability – Both internal (e.g. genetic merit) and external (e.g. nutrition, disease, exposure) forces that influence the expression of a threshold character (e.g. disease, conception, abnormalities, etc.).

Line breeding – Mating of selected individuals from successive generations to produce animals with a high relationship to one or more selected ancestors. It is a mild form of inbreeding.

Linkage – Association of genes physically located on the same chromosome. A group of linked genes is called a linkage group.

Linkage map – A linear map of an experimental population that shows the position of its known genes and/or genetic markers relative to each other in terms of recombination frequency.

Locus, pl. loci – A fixed position on a chromosome occupied by a given gene or one of its alleles.

Major gene – A gene that has an easily recognizable and measurable effect on a characteristic.

Marker – Specific and identifiable sequences of the DNA molecule. These markers may or may not be functional genes.

Marker assisted selection (MAS) – Selection for specific alleles using genetic markers.

Maternal heterosis – The advantage of the crossbred mother over the average of pure-bred mothers.

Mating systems – The rules which describe how selected breeds and/or individuals will be paired at mating.

Meiosis – The process by which the chromosome number of a reproductive cell becomes reduced to half the diploid (2n) or somatic number. It results in the formation of eggs or sperm.

Migration – Movement of animals, and consequently genes, from one population to another.

Mitochondria – Small bodies in the cytoplasm of most plant and animal cells responsible for energy production.

Mitochondrial inheritance – Inheritance carried by genes in mitochondrial DNA.

Mitosis – Cell division process in which there is first a duplication of chromosomes, followed by migration of chromosomes to the ends of the spindle and a dividing of the cytoplasm, resulting in the formation of two cells with the diploid (2n) number of chromosomes.

Molecular genetics – The branch of genetic studies that deals with hereditary transmission and variation on the molecular level. It deals with the expression of genes by studying the DNA sequences of chromosomes.

Multiple alleles – Three or more alternative forms of a gene representing the same locus in a given pair of chromosomes.

Mutation – A sudden change in the genotype of an organism. The term is most often used in reference to point mutations (changes in base sequence within a gene), but can refer to chromosomal changes.

Natural selection – Natural processes favouring reproduction by individuals that are better adapted, and tending to eliminate those less adapted to their environment.

Nucleus – Part of a cell containing chromosomes and surrounded by cytoplasm.

Outcrossing – Mating of individuals that are less closely related than the average of the population.

Overdominance – A form of dominance where the performance of the heterozygote exceeds that of the best homozygote.

Partial dominance – A form of dominance where the performance of the heterozygote is intermediate between that of the two homozygotes, but more closely resembles the performance of the homozygous dominant type.

Pedigree – Usually refers to pedigree chart or what a pedigree chart represents in genetics. It is a document to record the ancestry of an individual. A pedigree can also be used to illustrate the family structure or breeding scheme.

Penetrance – The proportion of the individuals with a particular gene combination that expresses the corresponding trait.

Permanent environmental effects – Environmental effects that result in permanent effects on the phenotypic expression of a trait. For example, severe mastitis during lactation may have a permanent effect on milk production and litter weaning weight for an animal in subsequent litters.

Phenotype – Actual exhibit of observable traits. Normally, this refers to characteristics of an individual such as size, shape, colour or performance.

Phenotypic correlation – When two traits tend to change in the same or a different direction as a net result of genetic and environmental effects.

Phenotypic value – A performance record; a measure of an animal’s performance for a trait.

Phenotypic variation – Variation in phenotype which results from variation in genetic and environmental effects on the individuals.

Pleiotropy – The property of a gene whereby it affects two or more characters, so that, if the gene is segregating, it causes simultaneous variation in the characters it affects.
Polymorphism – Where DNA or genes have more than two forms or alleles in the population.
Population – Entire group of organisms of a kind that interbreed.
Population genetics – The branch of genetics which deals with frequencies of alleles in groups of individuals.
Progeny – Offspring or individuals resulting from specific matings.
Progeny test – A test used to help predict an individual’s breeding values, involving multiple matings of that individual and evaluation of its offspring.
Protein – Any of a group of complex nitrogenous organic compounds that contain amino acids as their basic structural units, occur in all living matter, and are essential for the growth and repair of animal tissue.
Qualitative trait – A trait that can generally be classified into a limited number of categories, and the animal can be said to ‘possess’ the quality or not. Examples include hair colour, skin colour and ear stature.
Quantitative trait – A trait that is represented by an almost continuous distribution of measurements. Examples include body weight and height.
Quantitative trait locus (QTL) – A locus that affects a quantitative trait.
Random mating – A mating system in which animals are assigned as breeding pairs at random, without regard to genetic relationship or performance.
Recessive – Applies to one member of an allelic pair which lacks the ability to manifest itself when the other, dominant, member is present. Depending on the location and on the type of chromosomes, there could be autosomal recessive or X-linked recessive genes.
Reciprocal cross – A breeding scheme where males of breed A are mated to females of breed B and males of breed B are mated to females of breed A.
Recombination – The observed new combinations of DNA segments, or loci, or traits, which are different from those combinations exhibited by the parents.
Recurrent selection – A method of selection for combining ability or heterosis. Selection within one line is based on performance of crossbred progeny from matings with a ‘tester’ line.
Repeatability – The proportion of total phenotypic variation that is attributable to variations caused by genetic and permanent environmental effects. It is a measure of the degree to which early measures of a trait can predict later records of the same trait.
RNA – Ribonucleic acid, involved in the transcription of genetic information from DNA.
Segregation – The separation of paired alleles at loci during germ cell formation.
Selection – Any natural or artificial process favouring the survival and propagation of certain individuals in a population.
Selection criteria – The character(s) upon which selection decisions are based, with the intent of changing the character(s) in the selection objective.
Selection differential – The difference in mean performance of the selected group of animals relative to the mean performance of all animals available for selection.
Selection index – The combining of measurements from several sources into an estimate of genetic value; when more than one measurement on a trait, and/or measurements of the trait on relatives, and/or measurements of more than one trait are combined into a single estimate of overall genetic value.
Selection intensity – The proportion of animals selected to be parents relative to the total number available for selection. The smaller the proportion selected, the higher the selection intensity.
Selection objective – The character(s) which are intended to be modified by selection.
Sex chromosomes – The X or Y chromosomes.
Sex-influenced – Traits for which the expression depends on the sex of the individual.
Sex-limited – A trait that can be expressed only in one sex, such as milk production.
Sex linked – Genes that are located on the sex (X or Y) chromosomes.
Zygote – The cell produced by the union of mature gametes (egg and sperm) in reproduction.