Introduction
There is scope for improving the design of animal experiments. This would save scientific resources and reduce the numbers of animals used in biomedical research, for a given level of scientific output.

Laboratory animals are usually used as models of humans or other animals. Fundamental research usually involves exploratory models which are often used to develop scientific hypotheses and discover fundamental laws, whereas applied research involves predictive models which aim to assess a possible effect on humans. The latter may differ in their fidelity (i.e., similarity to the object being modelled) and in their ability to discriminate between treatments. Most in vitro tests are low fidelity models which have good ability to discriminate, but need formal validation.

Research scientists using mice or rats are often faced with the choice of either inbred or outbred strains or stocks. Inbred strains represent the nearest approach to pure reagents, and should be used wherever possible. Outbred stocks have a number of serious disadvantages, including increased phenotypic variability which means that larger numbers are needed to achieve a given level of precision.

Experiments using these animals need to be well designed so as to avoid bias and have a high degree of precision. An appropriate sample size should be estimated using power analysis or the resource equation method, plus some common sense. The range of applicability might be extended using factorial designs which could, for example, include both sexes or several strains without increasing total numbers. Finally, experiments should be simple so that no mistakes are made, and they should be amenable to statistical analysis.

Exactly how scientists can be encouraged to carry out such improvements is not entirely clear. Better training in experimental design and statistics would be helpful, as would better support from biologically trained statisticians. However, in the short-term they should be encouraged to think of animal research as a collaborative effort involving themselves, the animal professionals, and the statistician.

Need to improve animal experiments
Surveys of published papers and the experience of consultant statisticians, animal technicians and other animal professionals suggest that there is scope for improving the design of animal experiments. For example, in a survey of 133 papers published in the Australian Veterinary Journal, commissioned by the journal, it was estimated that 61% would have required statistical revision had they been sent to a statistical referee before publication. There were deficiencies in the design in 30%, with failure to randomise, the use of heterogeneous material, inappropriate numbers and bias being common. In 45% there were deficiencies in the statistical analysis, with use of sub-optimal methods and errors in calculation being common. Finally, there were errors in presentation in 33% of the papers with unexplained omission of data and inappropriate statistical methods being common (McCance, 1995).

A few experiments are actually so poorly designed and analysed that the results do not support the conclusions of the authors. Others, while giving the correct results are inefficient and waste scientific resources, including animals (Festing, 1994). This verges on being unethical. If all experiments could be brought up to the level of the best, then scientific output could be increased and the numbers of animals used decreased, at no extra cost.

Strategy and scientific philosophy
The first step in designing a project is to have a clear idea of the objectives of the study, a good knowledge of the literature, and a suitable research strategy. Mostly, these points will have been covered in detail in research proposals made to funding organisations, so will not be discussed here.

Choice of a suitable animal model then needs to be considered, if it was not an integral part of the research strategy. There seems to be considerable confusion about models, the way that they are used and how the results are "extrapolated" to humans. In fact, anything can be a model of anything. All that is needed is that it is taken to be one (Wartofsky, 1979). There seem to be three main types of models in biomedical research (Festing, 2000).
Exploratory models are used when the aim is to try to understand some biological process, without necessarily seeing its immediate importance to human health. Much fundamental biology falls into this category. The models, which are animals or other living matter, do not need to be validated at the time that they are used. The genetic code is universal, and at a cellular level there are substantial similarities, so many findings will be applicable to all living organisms. A good example of an exploratory model would be Mendel’s use of peas to study inheritance. He could not have foreseen that the laws of inheritance he worked out with plants would also be applicable to humans.

Explanatory models are used to gain an understanding of a situation, or to describe it. These are often physical models, graphs, diagrams, or mathematical equations.

Predictive models are used to try to discover the likely impact of some treatment on humans or other animals or on environments. Bacteria used in the Ames test, or rats used in long-term carcinogenesis assays are used as predictive models. Two properties of these models are their fidelity, i.e., the extent to which they resemble the object being modelled, and discriminating ability (Russell and Burch, 1959) to distinguish between, in this case, carcinogens and non-carcinogens. Rats have higher fidelity than bacteria, when compared with humans, but if a low fidelity model has relatively good discriminating ability (as in the case of the Ames test and other cell mutation assays as predictors of carcinogenesis) it may be useful. Low fidelity models usually have to be validated before much reliance can be placed in them. This is usually done by choosing a set of known positive and negative test chemicals, and using these to see how well the test performs (Fentem and Balls, 1997). Most animal models used in toxicity testing have never been formally validated. High reliance is placed on their high fidelity when compared with humans.

**Extrapolation from animals to humans**

When animal experiments are done, there seems to be an assumption that the results are "extrapolated" to humans. However, the concept of "extrapolation from animals to humans" presents a number of philosophical and practical problems. Which experiments need to be extrapolated? All animal experiments, or just some of them? If only some of them, which ones? Is it only predictive animal tests that need to be extrapolated? And what about in-vitro tests? Do we extrapolate from bacterial tests (as in the Ames test) to humans? Is that even done? The whole process is much more akin to hypothesis testing than to mathematical extrapolation. Once this process is understood, then it becomes clear that there is no "extrapolation" from animals to man. Models are chosen according to their presumed value at the time and decisions are taken on a course of action (designate the compound a carcinogen or a non-carcinogen) before the experiments are even done. The whole process is much more akin to hypothesis testing than to mathematical extrapolation. Once this process is understood, then it becomes clear that the tests must be well designed and executed and correctly analysed so that they are capable of detecting whether or not the compound is carcinogenic. A badly designed experiment will often give false negative or even false positive results.

**Genotype and choice of animal model**

Rats and mice represent over 85% of animals used in biomedical research. They are commonly used both as exploratory and predictive models. If the genotype of the animals is not intrinsic to the research project (and therefore already specified), the research worker using rats or mice is faced with the choice of using isogenic inbred strains or non-isogenic outbred stocks.

**Outbred stocks**

Outbred stocks are still widely used, particularly in toxicology. Over 70% of papers using the rat, published in one toxicology journal in 1999, used outbred rats, and they are also widely used in regulatory toxicology (McAulane et al., 1991). However, they suffer from a number of serious disadvantages. The colony is subject to genetic drift and sampling variation, leading to changes in phenotype over time. The animals also tend to be phenotypically variable so that larger sample sizes are required, and nothing is usually known about the genotype of any individual, apart from the fact that they are often albino. Colonies with the same name such as "Wistar" rats or "Swiss" mice will often be genetically quite different, causing confusion when comparing results from different laboratories. Genetic quality control is difficult, and there is even no way that "Wistar" and "Sprague-Dawley" rats can be distinguished genetically.
The use of these animals is sometimes justified on the grounds that “the aim is to model humans, humans are genetically heterogeneous, therefore genetically heterogeneous animals should be used”. This is scientific nonsense. A model does not need to resemble the object being modelled in every respect. It would be stupid to argue, for example, that because humans have no tail, and we wish to model humans, we should amputate all the tails of mice to make a better model. Only in rare instances does it appear to be scientifically justified to use outbred stocks (Festing, 1999).

Inbred strains
Inbred strains have made an enormous contribution to biomedical research, with at least 17 Nobel Prizes being at least partly dependent on the availability of these animals. Their use has resulted in the development of monoclonal antibodies and gene targeting. Studies of cancer and the oncogenic viruses found in mice have led to the discovery of proto-oncogenes which turn out to be signalling molecules which control the cell cycle and apoptosis, which are of fundamental importance in cancer and development. Studies of tissue transplantation using inbred strains have helped clarify the nature of the immune system and have led to advances such as organ transplantation (Festing and Fisher, 2000). Inbred strains stay genetically constant for long periods, they are phenotypically uniform, and they often have characteristics which are models of human diseases or physiological conditions. Nearly everyone who is using outbred stocks should now switch to the use of inbred strains (Beck et al., 2000).

Designing better experiments
Having chosen a suitable model, the next step is to design a good experiment. The first step is to define the "experimental unit", i.e. that entity which can be assigned at random and independently of all other units, to a treatment group. The experimental unit could be a cage or pen of animals, an animal, or part of an animal. For example, if the back was shaved and four compounds were painted on to different areas, then the area on the back of the animal is the experimental unit. In a crossover design, the animal for a period of time is the experimental unit. Inbred strains have made an enormous contribution to biomedical research, with at least 17 Nobel Prizes being at least partly dependent on the availability of these animals. Their use has resulted in the development of monoclonal antibodies and gene targeting. Studies of cancer and the oncogenic viruses found in mice have led to the discovery of proto-oncogenes which turn out to be signalling molecules which control the cell cycle and apoptosis, which are of fundamental importance in cancer and development. Studies of tissue transplantation using inbred strains have helped clarify the nature of the immune system and have led to advances such as organ transplantation (Festing and Fisher, 2000). Inbred strains stay genetically constant for long periods, they are phenotypically uniform, and they often have characteristics which are models of human diseases or physiological conditions. Nearly everyone who is using outbred stocks should now switch to the use of inbred strains (Beck et al., 2000).

Requirements for a good experimental design
- It should be unbiased, with the treated and control groups having the same environment.

This is achieved by independent replication of the observations, by randomisation and by blinding. Potential bias seems to be common where the experiment has to be broken down into smaller parts (e.g., because it is impossible to handle all the animals at once). All too often it is divided by treatment group, with, for example, the controls being done first, then each treatment group in turn. However, if conditions do not stay constant, this will cause problems because treatment differences will be confounded with the environmental effect (Cox, 1958).

Blinding is another way of avoiding bias. As far as possible, experimental units should be coded so that the people working with the animals do not know to which treatment group they belong. This is particularly important when there is a subjective element in making the observations or measurements on the animals.

• The experiment needs high precision so that there will be a good chance of detecting a treatment effect

Uniformity of material and blocking
High precision requires uniform material such as isogenic strains and narrow weight/age ranges. Heterogeneous material can often be accommodated using a randomised block design. The experiment is divided into a series of mini-experiments, typically with one animal on each treatment group in each block, chosen so that there is minimal variation between experimental units within a block. For example, if the experiment involved four treatment groups and the animals were heterogeneous with respect to weight, they would all be weighed and the four heaviest would be assigned to block 1. These would then be assigned at random to the four treatment groups. Block 2 would consist of the four next heaviest animals, etc. However, at the end of the experiment the inter-block variation must be removed as part of the statistical analysis. Typically, this would be done using an analysis of variance.

Size of experiment
Experiments which are unnecessarily large will clearly be wasting resources. However, experiments which are too small to detect biologically important effects will also, in the long run, waste scientific resources because the wrong conclusions may be reached.

Determination of an appropriate sample size is not easy, and often is hardly discussed in statistical textbooks. There are two scientifically respectable methods, the power analysis and the resource equation methods, but neither is entirely satisfactory. They should be used as a guide, rather than as being definitive. Neither of them, for example, takes account of the costs of the experimental units or of reaching an incorrect conclusion.
A power analysis is suitable for expensive, but relatively simple experiments. It is based on the mathematical relationship between:

- the sidedness of the test;
- the effect size of interest,
- the standard deviation,
- the required power;
- the significance level; and
- the sample size.

The first decision to be made is the sidedness of the statistical test. A two-sided test would be used if it is not known whether the treatment will increase or decrease the means of the treated groups. However, if there is a good biological reason why the response can only go in one direction, then a one-sided test can be used.

If the aim of the experiment is to detect a large treatment effect, then the experiment can be relatively simple. Thus, the next step in doing a power analysis is to decide the effect size of interest. This might be relatively simple for a clinical trial where it is known, for example, that on the standard drug treatment the average survival is five years. A new drug would be of little interest if it only increased the survival from 50% to 52%, but it might be of very great importance if it increased survival to 60%. However, for a biological experiment with ten different treatment groups (say five drug treatments and both sexes) and several dependent variables (e.g., 10 haematological and five biochemical parameters), it is often extremely difficult to decide how large an effect is likely to be of biological interest. But this must be decided if the method is to be used.

An estimate of the standard deviation (for quantitative characters) is also needed. This poses problems because the experiment has not yet been done. Thus, an estimate of the standard deviation must be obtained from the published literature, or from previous experiments. Sometimes this can be obtained from a pilot experiment. However, pilot experiments are usually quite small so that the estimate of the standard deviation is often inaccurate. The results of the power analysis are also highly influenced by the estimate of the standard deviation.

The desired power also needs to be specified. The power of an experiment is the probability (often expressed as a percentage) that it will be able to detect the specified effect size and indicate that it is statistically significant for a given significance level. Clearly, it would be ideal always to have powerful experiments. However, power comes at a price. A high-powered experiment requires large sample sizes, which may be costly or simply impractical. Typically, a power between 80% and 90% is specified, though the choice is somewhat arbitrary.

The significance level must also be specified. This usually presents no problem as a 5% level is almost universally used, but a 1% level may be used occasionally.

Once these parameters have been specified, they can be combined to give an estimate of the required sample size. However, the formulae are complex and depend on the nature of the data, the type of statistical test to be used, and the number of treatment groups. Fortunately, computer programs such as nQuery Advisor (Elashoff, 1997), a Windows program, are available to do the calculations.

The power analysis can also be used for experiments where no significant differences are observed, and where the aim of the experiment is to show no effect (Muller and Benignus, 1992). For example, with an experiment to determine safety of a chemical, it is important to know that the treatment is safe, and that implies no significant treatment effect. However, this may be due to the fact that there really is no effect, or to the sample size being too small to detect an effect. A power analysis can be done for a specified effect size, and if the power is high it can be claimed that the experiment shows that there is no biologically important effect (at specified power and significance levels). Without a power analysis all that can be claimed is that the experiment shows no evidence of an effect. However, absence of evidence is not evidence of absence.

The resource equation is an alternative method for determining sample size which depends on the law of diminishing returns. Increasing the size of a small experiment gives good returns in terms of information, but once it has reached a certain size, diminishing returns set in, and it becomes not worthwhile to increase the size of the experiment any further. This method is suitable for complex but relatively inexpensive experiments, or for those where there is no prior information on the standard deviation, which is necessary for the power analysis method. It is only applicable to quantitative characters.

The method is based on the suggestion that the degrees of freedom for error E, should be between 10 and 20 (Mead, 1988). E is simply estimated as:

\[ E = N - T - B \]

where N is the total degrees of freedom (number of animals minus one), T is the treatments degrees of freedom (number of treatments minus one) and B is the blocks degrees of freedom (number of blocks minus one).

This is a rule-of-thumb method which seems to work reasonably well, and was widely used before computer programs for doing power analysis were readily available. It does not specify the power or the effect size, but depends on diminishing returns. The upper cut-off point of E=20 is somewhat arbitrary. In order to balance the experiment (with equal numbers in each group) or if experimental units...
are cheap (e.g. with many in-vitro experiments), E could well be substantially greater.

Both the power analysis and the resource equation methods need to be judged in the context of available facilities and costs of experimental units and of reaching an incorrect conclusion.

The range of applicability of each experiment
All experiments are done against a background of variables which can be controlled in various ways. For example, the species, strain and sex of animals may be chosen for the work. The animals will be housed in cages or pens, they will be fed specified diets, given bedding of some sort, they will be looked after by specific people, and the physical environment will be more or less controlled. At the end of the experiment, certain conclusions will be reached. The question then arises whether, with different species, strain or sex, the same conclusions would have been reached. In most cases it can be assumed that if the animal house temperature had been, say, a few degrees colder, or the humidity a little lower, it would not have influenced the results. However, with a different sex or strain of animals the results may have been very different. Thus, part of a good experimental strategy is often to discover the range of applicability of the results. Are the results of an experiment done using males also applicable to females, or to animals of another strain or animals fed a different diet? These sorts of questions can be answered using factorial experimental designs. These are powerful designs which make much better use of the experimental material than single factor designs, though the analysis is more complex, and there may be problems if much of the data is missing, say because animals have died.

As an example, suppose an experiment is set up to detect the effect of a compound on blood pressure in rats. Sixteen males of a hypertensive rat strain are allocated at random to a control and a treated group (eight per group), and at the end of the experiment (done blind with the rats coded in a random order) the blood pressure is determined. The mean blood pressure in the two groups can be compared using a t-test or an analysis of variance. The question then arises as to whether the same effect is seen in females. However, rather than repeating the study with another sixteen female rats, it might have been better in the first experiment to use four males and four females in each group. The results would then be analysed using a two-way analysis of variance. If the sex times compound effect was not statistically significant, then it would be concluded that there is no evidence that males and females respond differently. The means for the two sexes can then be combined, and nothing has been lost, but the range of applicability of the results has been extended to both sexes. If the sex times compound interaction is statistically significant, then it does not make sense to combine the results, but again useful biological information has been gained. Factorial designs of this sort are extremely powerful and efficient ways of using scientific resources. The experiment should be reasonably simple so that no mistakes are made.

While Mead (1988) suggested that most experiments should have between 10 and 50 different treatment groups, care needs to be taken that the experiment is not so complex that mistakes are made. Written protocols should be prepared, and the details of the experiment will need to be discussed with the animal house staff.

Experiments should be amenable to a statistical analysis
All experiments should be amenable to statistical analysis. This should be checked before the experiment is started. Often, it is useful to do a pro-forma analysis of some synthetic data to get a feel for how the analysis might be done. If in any doubt, a professional statistician should be consulted. Experiments which form part of a series should also be analysed before the next experiment is started, in case the design of subsequent experiments needs to be modified.

Implementation
Although there clearly is scope for improving experimental design, it is not so easy to see how this will be achieved. What seems to be clear is that scientists need to be better educated in laboratory animal genetics, experimental design, statistics and possibly also in some experimental philosophy. In the UK applicants for a Project Licence, which defines the way that they will be using animals, must take a one and a half day course which includes ethics, the law, and about three to four hours on experimental design and statistics, with a strong emphasis on the design rather than the statistics. This is very well received, but there is no way that such a short course can make much impact on the way people actually design and analyse experiments. Even to be able to consult a statistician more effectively, they really need a 10 — 20 hour course, which seems to be impractical at present.

There is also a problem because consultant statisticians often seem unable to converse with biologists. Very often they have a mathematical background and use language which is not understood by biologists. Statisticians with a good background in biology — biometricians — are more suitable for consulting work of this sort than mathematical statisticians. Basically, what is required is the recognition that animal research must be a team effort involving the research scientist, the animal professionals, and the statistician or biometrician.
Genetic nomenclature for laboratory animals

Introduction

Nomenclature is a subject that is potentially very dull, very important, and provokes strong passions. Faced with a new situation, authors tend to develop a nomenclature system to which they become strongly attached, particularly when they have used their system in published appears, and have also persuaded colleagues to use the system. Unfortunately, if others have developed a rival system the same entity (e.g., a gene locus or an inbred strain) may have different names, or different loci or strains can have the same name, leading to total confusion. This was the situation that arose in the 1960s with the rat immunological and transplantation loci where three rival systems of nomenclature for the major histocompatibility locus (the H-1, Ag-B and R-1 systems) had become established, with different designations for the individual alleles, different type strains and different serological agents being used to identify the loci and alleles. The nomenclature was divisive and extremely confusing to any newcomer. Eventually, an international committee was established and after a substantial amount of hard work an entirely new unified system was developed which was independent of all previous systems. Energy can now be devoted to research rather than to defending a territory.

Guiding principles

Nomenclature systems need to be controlled by international committees which re often self-appointed initially, but eventually seem to evolve into democratically elected bodies. The committees are usually, but not always species-specific, though three is generally a considerable amount of cross-fertilisation among species.

The actual nomenclature used has to be a compromise between the need to convey information and the need to be simple, compact and understandable. There are examples where nomenclature has become too complex and has had to be abandoned because it is no longer widely used.

Nomenclature systems must also be dynamic, new situations are arising constantly. Visible mutants may be cloned and found to be alleles at a previously identified locus, so a name change becomes necessary. thus, lists of genes are in a constant state of flux.

Genetic nomenclature for laboratory mice

Genetic nomenclature for mice is the most comprehensive, and is the prototype for the nomenclature of all other laboratory mammals. Full details are given on the Jackson laboratory webs itt www.informatics.jax.org. Space only permits brief details to be given here.

Inbred strains

Inbred strains are produced by 20 or more consecutive generations of brothers x sister mating with all individuals tracing back to a single breeding pair in the 20th or subsequent generation they are almost like clones of genetically identical individuals, and are widely used in research (Festing, 1997; Festing, 1999).

Designations of inbred strains should be brief and should consist only of upper case letters, except for those strains which were already known by a designation involving numbers prior to the introduction of strain nomenclature in 1953. A few other exceptions are allowed. For example BALB, SJL and CBA conform to the rules, C57BL, 129 and C3H are exceptions. Note that BALB should never be written Balb.

Substrains

Substrains are regarded as having been formed when:

• branches of an inbred strain are separated before F40.
• In cases where a strain has been separated before F40, residual heterozygosity may be present so the two branches are assumed to differ genetically; or
• a branch has been maintained separately from other branches for 100 or more generations. The existence of differences arising by mutation is then highly probable; or
• genetic differences from other branches are discovered. Such differences could arise either as a result of residual heterozygosity or of new mutations.

Substrain symbols are appended to the strain name following a slanted line and may consist of a number, e.g., FL/ 1, or a laboratory registration code (see below) e.g., A.He, the Heston substrain of strain A. These codes have an initial capital letter, followed (where present) by lower case letters. A combination of the above is also allowed. Substrain symbols may be accumulated to show the history of the strain, though intermediate ones may be dropped if the designation becomes too cumbersome.

Genetic contamination as a result of a non-strain mating is likely to lead to numerous genetic differences. If contamination is thought likely, the strain should be renamed.

Strain 129 is widely used in the production of targeted mutations. Unfortunately, the strain has a very unfortunate history involving several outcrosses and even genetic contamination (Simpson et al., 1997) and the substrain designations had become so complicated that they were often incorrectly used. This strain has now been separated into a number of distinct, though related, strains (Festing et al., 1999).
Laboratory registration code

Differences in the phenotype of laboratory animals can arise as a result of both genetic and environmental influences. The composition of the diet, associated viruses, bacteria and parasites, and the physical environment can all change the characteristics of the animal. For this reason, it is important to be able to distinguish between animals of the same strain and substrain, but originating from different sours. This is achieved by appending a Laboratory Registration Code, following an @ symbol (to be read as "at"). This SJL@J indicates the colony of SJL mice bred at the Jackson Laboratory. Note that laboratory registration codes are not accumulated in the same way as substrain symbols. The list of laboratory codes is curated by ILAR: (http://www2.nas.edu/ilarhome/).

A list of inbred strains of mice and rats, with their phenotypic characteristics and with an indication of the major substrains is given on the Jackson Laboratory website (see previous page).

Locus names and symbols

Gene loci should have a name which describes as succinctly as possible the character by which it is recognised. Names should not include special symbols, Greek letters or Roman numerals and should be limited to a total of 40 characters. Where a mouse gene is homologous to a gene in another species (particularly humans) it should, as far as possible be given the same name and symbol, the first letter of which should be the same as the locus name with subsequent letters being lower case. Symbols are shown in italics, e.g., Lep is the symbol for the leptin locus. Loci which are members of a series are designated with a number, e.g., Es3 is the designation of the third esterase locus. Anonymous loci, i.e. those defined only in terms of DNA sequence, the function of which is unknown, are designated by the symbol D for (DNA) followed by an integer to show the chromosomal location and a two to three letter code representing the laboratory or scientist who described it. Finally a unique serial number is appended, e.g., D14Pas23 designates the twenty third such sequence on that chromosome.

Alleles are defined by the gene symbol and an allele symbol following the gene symbol, e.g., Hbb² is the allele at the haemoglobin locus that gives a single band following electrophoresis. Sometimes the superscripts are descriptive (as above), and sometimes they are designated after a type strain such as "b" for C57BL or a "d" for DBA/2. Allele designations may be quite complicated, particularly with targeted mutations. For example, an insertional mutation in the hotfoot locus is designated ho(14kbp)wg.

See below for a full explanation.

Congenic, coisogenic and segregating inbred strains (Mutations maintained on an inbred genetic background)

Where a mutation is maintained on an inbred genetic background, either as a result of several generations of backcrossing or due to a mutation or knockout within an inbred strain, the strain name is given, followed by a hyphen, then the gene symbol. For example, C3H/ N- +Wv is the designation for strain C3H, substrate "N", with the dominant spotting gene Wv maintained in a heterozygous condition, the wild-type allele being indicated by the + sign. More details are given in the official nomenclature rules. There is special nomenclature for congenic strains carrying immunologically defined loci. The rules for naming transgenes were formulated by a cross-species nomenclature committee in 1992 (Committee on Transgenic Nomenclature, 1992).

The basic format is: TgX(YYYYYY)####Zzz

Where TgX is the mode, with the X being replaced by an N for non-homologous insertion, R for insertion via infection with a retroviral vector and H for homologous recombination. The nature of the insert is indicated by no more than eight letters. It should identify the inserted sequence and indicate important features. There are a number of standard abbreviations that can be used, such as An for an anonymous sequence, Ge for a genomic clone, Rp for a reporter sequence, etc., Finally, the ######Zzz is a laboratory assigned number and the laboratory code.

Some examples are:

C57BL6j-TgN(CD8Ge)23jwg

The human CD8 genomic clone (Ge) inserted into C57NI/6j by microinjection; the 23rd mouse screened in a series by Jon W. Gordon (jwg).

Crl:ICR-TgN(SVDhfr)432jwg

The SV40 early promoter driving a mouse dihydrofolate reductase (Dhfr) gene; a 4-kilobase plasmid; the 32nd mouse screened by Jon W. Gordon (wg). Outbred ICR mice were from Charles River Laboratories (Crl).

TgN(GPDHIm)1Bir

The human glycerol phosphate dehydrogenase (GPDH) gene inserted into zygotes retrieved from (C57BL/6J x SJL/J) F1 females: the insertion caused an insertional mutation (Im) and was the 1st transgenic mouse named by Birkenmeier (Bir). No strain designation is given because the mutation is on a segregating genetic background.
The names of transgenes can be abbreviated by omitting the insert, so TgN(GPDHIm)1Bir can be written TgN1Bir. The full designation should be used in the materials and methods section of a paper, but the abbreviated version could then be used.

Note that in the case of transgenic mutations induced by homologous recombination, the nomenclature should be in accordance with the guidelines for gene nomenclature for that species. The mutant Mbp\textsuperscript{mlDn} would be used to denote the first targeted mutation of the myelin basic protein (Nbp) by Muriel Davisson (Dn).

References


Committee on transgenic nomenclature (1992) Standardised nomenclature for transgenic animals. ILAR News 34:45-52.


