New Journal name, new section, new brief gene mapping report policy

Starting in 2002 the name of this Journal will be:

Cytogenetic and Genome Research

The name has been changed to more accurately reflect the types of papers that have been published in this journal in the past few years. When started in 1962 the name of the journal was *Cytogenetics*. In 1974 the words '*and Cell Genetics*' were added to reflect the increased number of papers that were being published in the then upcoming area of somatic cell genetics. We were aware that this name was actually a linguistic monstrosity in that it seemed to be saying the same thing twice – once in Latin and then again in English. But adding 'Somatic Cell Genetics' made the title too long and at the time it was clear to all investigators what the title meant. A Journal must keep up with the times and so the name must now be changed once more. We apologize to librarians and catalogers for the extra work, which such a change incurs.

The abbreviation to be used in citations will be: *Cytogenet Genome Res.*

New section:

Collaborative and interactive research projects

Who wants to _____? Who has _____?

With increasing frequency, investigators are in need of specific research materials, or need the assistance of colleagues with specialized expertise. In addition, investigators sometimes have data that is inadequate for a full report but which could be published when combined with data of other investigators. However, finding such materials and colleagues can be difficult. For these reasons, and on an experimental basis, we are adding a new section that we hope will meet these needs.

To give but some examples, this section will be devoted to requests for collaborators on specific research projects and requests for specific research materials such as molecular probes, sera, antibodies or other special reagents. Other examples are requests for subjects with certain types of diseases or specific mutant microorganisms, plants, animals, or rare animal species or tissues samples from such rare species.

In this issue the brief paper by M. Schmid (p. 111) is an example of such a proposal for an interactive project. The purpose of this paper on gene mapping in the frog *Xenopus laevis* is to stimulate interest in chromosome localization of genes and other DNA sequences in this important model organism. The author hopes that others interested in mapping *Xenopus* genes will either collaborate with him on this project or provide him with probes or other materials.

Another possibility would be for interested workers to form a consortium on frog gene mapping in amphibians and either jointly or independently publish their findings in this Journal. This could be similar to the reports of the Human Gene Mapping and other Workshops published periodically in this Journal, such as the *First Report on Chicken Genes and Chromosomes 2000* which appeared in Vol. 90, No. 3–4, pp 169–218 (2000).

As indicated, the foregoing are only some examples of the types of searches or requests for collaborative or interactive projects for which this section is designed. Suggestions for other types of communications that might be appropriate for this section will be welcomed.

All contributions for this section will be subjected to peer review like all other reports received by this Journal. However, an accelerated review procedure has been established for this section and every effort will be made to publish contributions to this section quickly. For these reasons these contributions should be as brief as possible. Very short requests of a few lines for specific materials, etc., will be acceptable. On the other hand, in cases where large bodies of data, figures, tables, graphs, or lengthy text are involved only a short summary will be published in the Journal. The authors should prepare this. The data and/or text will be posted on the *Cytogenetic and Genome Research* Internet site at www.karger.com/journals/cgr/cgr_col_inter.htm.

Contributions or suggestions for this new section can be sent to either of the undersigned in accordance with the submission policies of this Journal outlined in the 'Guidelines to Authors' section of each issue or at the Internet site: www.karger.com/journals/cgr/cgr_gl.htm.

New policy for brief gene mapping reports

The tremendous increase in the number of brief mapping reports we have received has forced us to reluctantly institute a new policy for this category of papers. We published such reports because it seemed important that authors of papers on gene map assignments should be able to publish the essentials of the materials and methods used and results obtained for the benefit of other investigators and to allow readers to evaluate the results. Something, which is not possible when assignments appear in a database. We still believe this to be true but can no longer devote the space that the many reports require.

Consequently we have instituted a new more space efficient procedure which should still meet the needs of researchers. In the Journal only the title, names of authors and affiliations of such reports will be published. **The text, figures and tables of the report will be posted on the Journal's Internet site** at: www.karger.com/journals/cgr/cgr_reports.htm. This is a free public site.

The title and authors of the report will also appear in the table of content of each issue and in the indexes of each volume. Illustrations may continue to be in color but **there will be no color plate fees. The processing fee will still be required.**

This policy will become effective with the first issue in 2002. **The previously published guidelines, which are also reproduced below, should still be adhered to** and authors should continue preparing such reports using the standardized format in the same way as they have in the past. These mapping forms are reproduced once more on the following pages. They are intended to not only to show the information that must be included but also the format in which it will appear. Authors need not format the text in double columns as shown but must set up the report with the topic headings and in the order shown. Electronic versions of the mapping forms may be obtained by email from: hklinger@aecom.yu.edu or they may be downloaded from: www.karger.com/journals/cgr/cgr_gm.htm.

No change in policy for full gene mapping, cloning and characterization reports

Full descriptions of newly mapped genes will be accepted as in the past if they meet all the criteria outlined for the brief gene mapping reports (see below) and, in addition, present a reasonably full characterization of the gene. **These should not be expansions of brief reports but should constitute reasonably comprehensive, but not necessarily all inclusive, characterization of the mapped gene including, for example, information on its function, its gene expression characteristics, sequence, etc.**

Although no form is provided for these full reports authors are advised to consult the brief report instructions and forms to be sure that they include all the information shown on these forms to which they can add the additional information they consider appropriate. These reports should also be prepared in as concise a manner as possible. **All contributions for this section will be peer reviewed like all papers received by this Journal.**

*Harold P. Klinger
Michael Schmid*

Cytogenetic and Genome Research

Guidelines for preparing brief gene mapping reports

(These guidelines also apply to full gene mapping reports except that the latter should not be on the brief mapping report forms)

The title, authors and affiliations only of brief gene mapping reports are published in *Cytogenetic and Genome Research*. **The report itself is put on the Journal's Internet site at: www.karger.com/journals/cgr_reports.htm.**

In order to be able to disseminate the information on the increasing number of genes being mapped quickly and efficiently, and to provide a uniform format that will facilitate the retrieval of mapping data and assure the inclusion of all the essential information, we request that all brief gene mapping reports be prepared according to the format shown in the following pages. One of these forms is for genes mapped with in situ hybridization methods, the other when somatic cell hybrids are used. If both methods are used then the appropriate sections from each of these forms can be combined. When the in situ method is used a photograph should be included to allow the reader to verify the location of the signals. When somatic cell hybrids are used the authors should send photographs showing parental rodent, human, as well as cell hybrid phenotypes for verification by reviewers. **Mapping reports will be peer reviewed just like all papers processed by this Journal.**

Authors should provide all the information indicated on the form that is relevant to their report. All other items on the forms can be left off.

The name of the author who is prepared to answer inquiries about the report, his/her address, telephone and fax numbers, as well as e-mail address should be included. These should be entered where indicated at the bottom of the form. If this author is different from the one to receive proof and/or the reprints then the appropriate information should also be given in the letter of submission.

Authors must obtain or verify the official gene symbol of the gene(s) mapped. This can be accomplished for human genes by contacting the HUGO Gene Nomenclature Committee at: www.gene.ucl.ac.uk/nomenclature/ (The Galton Laboratory, University College London, MRC Human Biochemical Genetics Unit, Wolfson House, 4 Stephenson Way, London NW1 2HE UK; Tel: 44-270-679-5028; Fax: 44-270-387-3496), email: nome@galton.ucl.ac.uk.

Mouse and rat gene symbols can be obtained from Dr. Lois J. Maltais, Nomenclature Coordinator, The Jackson Laboratory, Bar Harbor ME 04609; Tel: (207) 288-6429; Fax: (207) 288-6132; e-mail: nomen@informatics.jax.org; MGD homepage: www.informatics.jax.org.

Authors must indicate in their covering letter that they have confirmed that the gene symbol(s) used is the official symbol.

Authors need not follow the double column format shown below but should maintain the same sequence of the items. All inappropriate items and instructions on the forms, including the Journal and form names at the top should be deleted.

Electronic versions of the forms on the following pages can be obtained from the Editorial Office in New York at: hklinger@aecom.yu.edu or they may be downloaded from: www.karger.com/journals/cgr/cgr_gm.htm.

The electronic version as well as two hard copies of **all mapping reports** should be sent to the Editorial Office in New York. (Please note that this is in contrast to other types of reports where authors in the Eastern Hemisphere of the world are requested to send their papers to Dr. Michael Schmid in Germany.) A processing fee of U.S. \$50 should accompany the report. If more than one report is sent at the same time an additional \$30 should be added for each report. (For specifics please see the *Guidelines for Authors* section of any issue of this Journal, or on the Internet at: www.karger.com/journals/cgr/cgr_gl.htm.)

Requirements that gene mapping reports must meet to be considered for acceptance:

1. The gene must be previously unmapped by any technique.

This means that papers of mapping confirmations will not be accepted. Relocations of genes incorrectly mapped within a major chromosome band, i. e., to a different subband, will not be accepted. However, genes that are relocated a significant distance from the one to which it had been assigned, or to another chromosome, will be accepted. The evidence for the new assignment must be obtained with two different methods.

2. Well-described flanking markers must be given for all mapping assignments.

The relative location of the flanking markers can be established by standard radiation hybrid or mouse backcross panels. For mapping by fluorescence in situ hybridization (FISH), the markers must be within 5 cM or 5 Mb of the gene or genes that have been mapped.

3. The results from DNA sequence database searches must be given for the mapped gene(s).

The entire sequences should not be given, just the size, degree of the matches and their significance. If several sequences are involved, this should be presented in a concise table listing the standardized gene names as established by the HUGO Gene Nomenclature Committee (see above) and accession numbers of the matching sequences. The human chromosome reference sequences nucleotide position of mapped genes should also be given as they become available.

4. The following categories must be collected into a single publication if submitted from one group of investigators:

- (a) All cDNAs representing a single multigene family.
- (b) Genes located within a single chromosome band.
- (c) A series of orthologous genes when results of comparative mapping studies of mouse (or some other species) and human genes are reported.

5. Authors of both accepted and not accepted papers are encouraged to submit their data to mapping databases.

The Genome Database (www.gdb.org) is prepared to accept the data if presented in the short report format.

Form for submission of reports of gene mapping with somatic cell hybrids

(To gain space delete everything up to this point and the next two lines when you work with this form.)

Title of report (Please word as closely as possible to the text shown below and be sure to include all listed items.)

Assignment* of (1) to human (2) chromosome band(s) (3) with somatic cell hybrids

(Select one of the following)

*To our knowledge this is the first time this gene has been mapped.

*This is a more precise localization of a gene previously mapped to (region) by [as in foregoing]

*This report is discordant with a previous assignment of this gene to (region) by [as in foregoing]

(1) Full gene name followed by official symbol in parentheses (see instructions).

(2) Or other species.

(3) Chromosome number and band location.

Authors names and affiliations (Please put in style of this Journal and provide items listed in instructions.)

Rationale and significance

(In no more than 120 words indicate what gene does, why it was mapped, relationship to other important genes, and any other particularly significant items.)

Conditions:

(or) Insert size:

Vector:

Materials and methods

(Indicate if with PCR, Southern, Protein, or other methods. Reference an appropriate report and only note very important modifications, if any, very briefly.)

Probe/primer name(s):	Primer sequence(s):
1.	
2.	
etc.	

Amplicon:

Probe type:

Results

Regional mapping results

Hybrid designations	Chromosome region	Gene present (+) or not present (−)
(Hybrid No. 1)		(enter + or −)
(Hybrid No. 2)		(" " ")
(etc.)	(	" " ")

Regional mapping panel: (Give unique identifying designation of panel(s) or hybrids as appropriate.)

Nucleotide position in human chromosome reference sequences: (If available)

Table 1. Segregation of (gene) with human (or other species) chromosomes in somatic cell hybrids.

Gene/ chromosome	Chromosome numbers																							
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X	Y
+ / +																								
+ / −																								
− / +																								
− / −																								
% discordant																								
Hybrid panel reference:																								

Grant support or other acknowledgements:

Received ; manuscript accepted

(Above dates will be entered by the editors.)

Request reprints from (Please give corresponding author's name, full address, telephone and fax numbers, as well as email address.)

References

Use this size type (9 point), line spacing, and paragraph format like this paragraph (hanging indent).

Form for submission of reports of gene mapping by in situ hybridization

(To gain space delete everything up to this point and the next two lines when you work with this form.)

Title of report (Please word as closely as possible to the text shown below and be sure to include all listed items.)

Assignment* of (1) to human (2) chromosome band(s) (3) by in situ hybridization

(Select one of the following)

*To our knowledge this is the first time this gene has been mapped.

*This is a more precise localization of a gene previously mapped to (region) by [as in foregoing]

*This report is discordant with a previous assignment of this gene to (region) by [as in foregoing]

(1) Full gene name followed by official symbol in parentheses (see instructions).

(2) Or other species.

(3) Chromosome number and band location.

Authors' names and affiliations (Please put in style of this Journal and provide items listed in instructions.)

Rationale and significance

(In no more than 120 words indicate what gene does, why it was mapped, relationship to other important genes, and any other particularly significant items.)

Mapping by FL:

Number of chromosomes examined:

Mean location: Bands encompassed:

Range: Mean chromosome length (μm):

Standard deviation:

Materials and methods

(Indicate the methods used. Reference an appropriate report for details and only note major modifications, if any, very briefly.)

Probe name(s):

Probe type:

Insert size:

Vector:

Proof of authenticity:

Gene reference:

Results

Mapping data:

Most precise location:

Nucleotide position in human chromosome reference sequence:

(If available)

Number of cells examined:

Number of cells with specific signal:

1 (), 2 (), 3 (), 4 () chromatids per cell

Figure (Legend of figure(s) here. At least one figure is required but two may be used. Figure(s) must fit within the dimensions of the above rectangle after reduction.)

References

Use this size type (9 point), line spacing, and paragraph format like this paragraph (hanging indent).

Grant support or other acknowledgements:

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