

IMpRH Server: an RH mapping server available on the Web

Denis Milan¹, Rachel Hawken², Cédric Cabau¹, Sophie Leroux¹, Carine Genet¹, Yvette Lahbib¹, Gwenola Tosser¹, Annie Robic¹, François Hatey¹, Lee Alexander², Craig Beattie², Larry Schook², Martine Yerle¹ and Joël Gellin¹

¹Laboratoire de Génétique Cellulaire, INRA, BP27, 31326 Castanet-Tolosan, France and ²College of Veterinary Medicine, University of Minnesota, St Paul, MN 55108, USA

Received on December 15, 1999; revised and accepted on February 14, 2000

Abstract

Summary: The INRA-Minnesota Porcine Radiation Hybrid (IMpRH) Server provides both a mapping tool (IMpRH mapping tool) and a database (IMpRH database) of officially submitted results. The mapping tool permits the mapping of a new marker relatively to markers previously mapped on the IMpRH panel. The IMpRH database is the official database for submission of new results and queries. The database not only permits the sharing of public data but also semi-private and private data.

Availability: <http://imprh.toulouse.inra.fr>

Contact: milan@toulouse.inra.fr

Supplementary Information: Details can be found at <http://www.toulouse.inra.fr/lgc/pig/RH/help/help.htm>

Radiation hybrid (RH) clones are produced after irradiation of a cell of a species of interest and fusion to a cell of rodent recipient species. The PCR analysis of RH clones containing short DNA fragments of donor species, permits ordering of markers with a resolution 10–50-fold greater than genetic mapping. Following the production of radiation hybrid panels for the human genome, RH panels have been developed for various mammalian species like rat, mouse, porcine, bovine and dog (see <http://linkage.rockefeller.edu/tara/rhmap> for a list of available panels and of reference publications). Radiation hybrid mapping has thus become the tool of choice for mapping genes and markers, and even for ordering new microsatellite markers (Watanabe *et al.*, 1999). Availability of tools on the Web is a crucial point for a wide use of these panels. In humans for instance, the Stanford web site (<http://shgc-www.stanford.edu>) provides on line tools to map a new marker, whereas the RHdb web site (<http://corba.ebi.ac.uk/RHdb/index.html>) should be used to submit data.

For the pig genome, the INRA-Minnesota porcine Radiation Hybrid (IMpRH) panel has been developed

(Yerle *et al.*, 1998) and characterized (Hawken *et al.*, 1999) in collaboration between INRA and the University of Minnesota. For research groups that agree to submit their data to the IMpRH database, DNA could be obtained freely, at least at the time of publication. We have thus developed the IMpRH Server, accessible at <http://imprh.toulouse.inra.fr>, allowing the user: (1) to map porcine markers relative to a framework of previously mapped markers, (2) to submit data and (3) to query the database for official results.

Map a new marker This option is available for all users. The vector of result can be pasted onto the web page no matter which vector format is used (text with or without separator, selection of Excel cells, etc.), codes used for positive, negative and doubtful results can be customized. Users can then have access to the following outputs:

1. markers linked to the tested marker with a LOD score above a given threshold (Figure 1),
2. two-point distances relatively to all markers of a selected chromosome,
3. most likely multipoint locations (using minimum breakage criteria),
4. evaluation of all locations on a given chromosome.

In the first two options (two-point analysis) the list of hybrids in which breakage occurred can be displayed. In the last two options (multipoint analysis), the increase of the breakage number due to the mapping of tested markers is indicated. A drawing of the most likely map, including the tested marker, can be displayed (Figure 2).

Breakage probability, distances, and the corresponding LOD score are calculated for this panel, built using diploid cells according to Lange *et al.* (1995), as used in RHMAP 3.0 (Boehnke *et al.*, 1996).

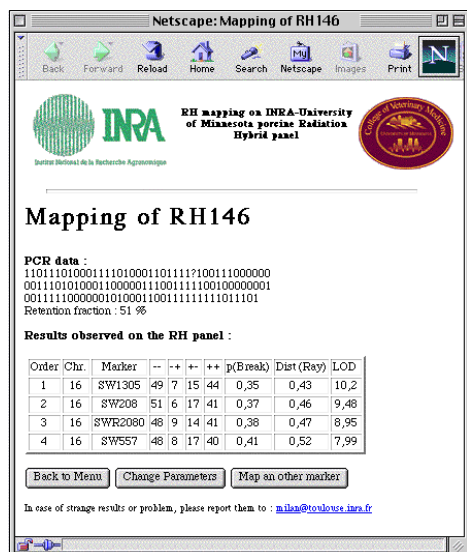


Fig. 1. Output showing markers linked to the submitted marker with a threshold LOD value of 5.

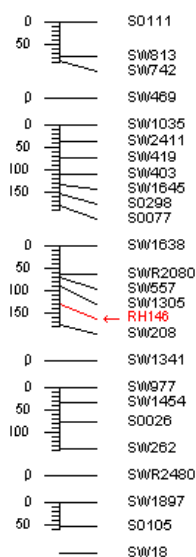


Fig. 2. Example of a map drawn by the IMpRH mapping tool. Such a map can be accessed using the multipoint mapping option. It shows the most likely location of 'RH146' on the framework of markers already mapped on chromosome 16.

Map a batch of markers The user may choose to map a batch of up to 100 markers in a single step. In that case the IMpRH mapping tool will return the closest marker (with distance and LOD score) of each tested marker.

Submit new marker(s) This option allows the user to submit a batch of markers to the IMpRH database. It can

be performed either interactively (for up to 100 markers in a single step) or by sending a file containing data for an unlimited number of markers. Users are requested to submit names of markers, primers and PCR conditions to be used, vector of results, and comments. At the time of submission, authors should specify whether all submitted information (public data), or name and location only (semi-public data), or location only (semi-public data), or name only (semi-public data), or no information (private data) can be made publicly available on the web. As an example, if only locations are made available, other users can identify that a new marker is available through the submitter (e-mail address is provided) at a given map location of interest. We think such an option can help to make information rapidly available to the scientific community.

Moreover, the user can decide to share information in the frame of a collaborative project. In that case private information will be considered as semi-private for members of the collaborative project.

Query the IMpRH database It is possible to query the database: on chromosome, possibly specifying a given interval; on submitter; on date of submission. The user may query the IMpRH database on public, semi-public or private data. Markers can be sorted by alphabetic order or chromosomal location.

Following a query, if vectors are available to the user they can be displayed in RHMAP 3.0 format for further analysis (two-point analysis with private markers or multipoint analysis).

General comments The IMpRH server has been developed using 4D software (ACI, <http://www.aci.fr>). Institutes interested in the establishment of a similar server for an other RH panel may contact the author. The server can run on Windows95 or 98, Windows NT, or MacOS platforms.

References

- Boehnke, M., Lunetta, K., Hauser, E., Lange, K., Uro, J. and Vanderstoep, J. (1996) RHMAP 3.0. University of Michigan, <http://www.sph.umich.edu/group/statgen/software/>.
- Hawken, R.J., Murtaugh, J., Flickinger, G.H., Yerle, M., Robic, A., Milan, D., Gellin, J., Beattie, C.W., Schook, L.B. and Alexander, L.J. (1999) A first-generation porcine whole-genome radiation hybrid map. *Mamm. Genome.*, **8**, 824–830.
- Lange, K., Boehnke, M., Cox, D.R. and Lunetta, K.L. (1995) Statistical methods for polyploid radiation hybrid mapping. *Genome Res.*, **2**, 136–150.
- Watanabe, T.K. *et al.* (1999) A radiation hybrid map of the rat genome containing 5,255 markers. *Nat. Genet.*, **1**, 27–36.
- Yerle, M., Pinton, P., Robic, A., Alfonso, A., Palvadeau, Y., Delcros, C., Hawken, R., Alexander, L., Beattie, C., Schook, L., Milan, D. and Gellin, J. (1998) Construction of a whole-genome radiation hybrid panel for high-resolution gene mapping in pigs. *Cytogenet. Cell Genet.*, **82**, 182–188.