

Editorial

Génolevures – a novel approach to ‘evolutionary genomics’

This special issue of *FEBS Letters* is a series of 21 consecutive reports on the outcome of Génolevures. This program, conducted by investigators from seven French laboratories, was the genomic exploration of 13 species selected from the Hemiascomycetes yeasts. A prerequisite was the development of a special approach to obtain sufficient sequence information from genomes of these closely related species, and the result of this effort would answer basic questions concerning molecular evolution. The extensive comparative analysis yielded a wealth of information on the conservation of synteny, on genetic redundancy, and on functional classification of genes. These results culminated in the conclusion that speciation could result from a limited reshaping of the genetic repertoire and that an entire genome duplication is not a prerequisite to explain the structure of the *Saccharomyces cerevisiae* genome and other species of the *Saccharomyces sensu stricto* group. The sequencing was performed near Paris at Génoscope, the French center for large scale sequencing projects. Thus, the designation Génolevures is a composite word, with *géno* referring to the sequencing center and the aim of the project, and *levure* being the French word for yeast.

When referring to ‘yeast’, which in every day language is synonymous for *S. cerevisiae* (the name created for a yeast strain observed in malt in 1837), one is immediately reminded that this species is probably the oldest domesticated organism. It lives on sugars and was used for beer brewing in Sumeria and Babylonia, already in the year 6000 B.C. In parallel, *S. cerevisiae* strains were used with grape cultivation in Georgia and for dough leavening in Egypt. *Levure* goes back to the latin word *levare*, and *leaven* is a word simultaneously used for both dough and yeast, an organism that anaerobically releases CO₂ during the baking process. The German word *Hefe*, and very much so the English *yeast*, like Dutch *gist*, are derived from a west-Germanic expression, *haf-jon*, meaning the potential to leaven. The Greek *zymi* (ζυμι) is used simultaneously for yeast and dough and occurs as a root in words related to beer or fermentation. Thus the modern expression ‘enzymes’ (*en zymi*=in yeast) has been created to designate the compounds derived from yeast that are able to ferment sugar. In fact, this observation dates back to the first studies of Louis Pasteur (Études sur la bière) in 1857, which he carried out during his time at Strasbourg University. The unique properties of the yeast *S. cerevisiae* (one of approximately 700 yeast species representing a subgroup from 700 000 different fungi) have been exploited for many thousands of years, and, in more recent years, have also made it a preferred organism for research. Moreover, *S. cerevisiae* and other yeasts have yielded a vast majority of industrial and medical applications beneficial to human life.

Around 1970, *S. cerevisiae* was introduced as an experimental system for molecular biology. As early as 1980, yeast was

used to produce the hepatitis B vaccine. In 1996, yeast was the first eukaryotic organism in which the complete genomic sequence was established. Following their tradition with yeast research, French scientists had an important role in this endeavor. In the 4 years that followed, yeast became a useful reference against which sequences of human, animal or plant genes, and those of a multitude of unicellular organisms under study could be compared. Moreover, the ease of genetic manipulation in yeast opened the possibility to functionally dissect gene products from other eukaryotes in the yeast system. In the ‘post-genomic era’, yeast was again at the forefront of functional genomics.

Despite the fact that numerous gene functions in yeast have been established, we still are uncertain about the actual number of active genes or the significance of gene redundancy. These problems are pertinent to all other genomes as well. The ‘Génolevures’ project will provide some insight into these questions, but at the same time may contribute to the improvement of industrial applications in yeasts, which have the potential to live under particular conditions, using extraordinary food sources, or have a pathogenic potential.

Upon examining the cover of this issue, the reader will immediately realize which yeast strains have been selected for this project. The rationale of the approach and the criteria used to select the set of species are described in the first paper. The second paper documents details of data generation and processing, while the third paper presents the evaluation of the sequences, i.e. methods and strategies used for sequence analysis and annotation. As all data are interpreted with reference to *S. cerevisiae* as an ‘internal standard’, it was necessary to try to define its ‘common’, ‘maverick’ and ‘Ascomycetes-specific’ genes (paper 4). The series of papers to follow (papers 5–17) describe characteristics of the strains of each single species used in this project and the results of genomic comparisons using the instruments developed in the third paper. The four ‘summary’ papers cover particularly interesting aspects in the synopsis of the Hemiascomycetes yeasts: comparative analysis of chromosome maps and synteny with *S. cerevisiae* (paper 18); ‘Ascomycetes-specific’ genes (paper 19); evolution of gene redundancy compared to *S. cerevisiae* (paper 20); and comparative functional classification of Hemiascomycete genes (paper 21).

Along with the authors, I am confident that similar approaches will be applicable to related species of other organisms. As with this novel approach, knowledge of entire genomic sequences is not necessary, and such an approach will successfully contribute to the faster development of ‘evolutionary genomics’.

Horst Feldmann
Munich, November 2000

The Génolevures network

The genomic exploration of Hemiascomycetous yeasts, or Génolevures, is the result of a collaborative network between six French laboratories and Génoscope. The authors would like future papers referring to the contents of this special issue to cite this directory. The authors' affiliations appear in the following 21 papers.

Jean-Luc Souciet, Michel Aigle, François Artiguenave, Gaëlle Blandin, Monique Bolotin-Fukuhara, Elisabeth Bon, Philippe Brottier, Serge Casaregola, Jacky de Montigny, Guillemette Duchateau-Nguyen, Bernard Dujon, Simone Duprat, Pascal Durrens, Chantal Feynerol, Claude Gaillardin, Fabien Jovelin, Marc Lemaire, Andrée Léplinge, Bertrand Llorente, Alain Malpertuy, Roland Marmeisse, Christian Marck, Robert Montrocher, Cécile Neuvéglise, Huu-Vang Nguyen, Odile Ozier-Kalogéropoulos, Arnaud Perrin, Serge Potier, Catherine Robert, William Saurin, Claude Scarpelli, Catherine Spohner,

Marie-Laure Straub, Emmanuel Talla, Fredj Tekaia, Michel Termier, Claire Toffano-Nioche, Jean Verdier, Virginie Vico, Micheline Wésolowski-Louvel, Patrick Wincker, Jean Weissenbach.

The authors would like to express thanks to Horst Feldmann and André Goffeau for their helpful advice, discussions and comments on this set of manuscripts.

This comparative sequencing program was supported by the Ministère de la Recherche et de la Technologie (MRT), the Centre National de la Recherche Scientifique (CNRS), the Institut National de la Recherche Agronomique (INRA) and each host institution: the Institut National Agronomique Paris-Grignon (INA-PG), the Institut Pasteur, the Université Bordeaux II, the Université Lyon I, the Université Paris VI, the Université Orsay-Paris XI, the Université Louis Pasteur-Strasbourg I.