ETHICS WATCH

Bioterrorism and the right to research

A basic tenet of scientific freedom has been the right to research any topic and to publish the results. But that freedom is now under pressure as awareness grows that biological research could be misused to create bioweapons that are directed at human beings, staple crops and livestock[1]. Balancing scientific freedom and public security has become an important challenge for both the scientific community and society.

In reconciling those interests, it is helpful to recall that in most countries there is no clear set of legal rights that protect what scientists may do. In the United States, for example, the rights to free speech protect a scientist's choice of research topic and the publication of results, but they leave room for government restrictions in the methods that are used and the projects that are funded. The right to research and publish does not include the right to use any method to achieve this goal, such as the use of human subjects without their consent, or the use of chemicals or pathogens that pose a high risk of harm. Funding agencies can also set limits on the topics that can be pursued, the methods that can be used and what may be published[2].

Against this backdrop, the attempts of governments to reduce the chance that biological research could be used to produce bioweapons raise issues of policy more than of rights. The main question is whether the burdens on free inquiry and exchange are justified by the threats or dangers that they might pose. The scientific community has made clear its willingness to cooperate in minimizing threats to security[3]. For example, the editors of 20 leading scientific journals have announced that they will weigh the potential harm of publication against the scientific benefits of an article, and make the decision to modify or to publish on that basis[4]. It is essential that the government be also sensitive to the needs of science.

Of special concern in the United States is the maintenance of the longstanding policy that ensures that the results of nonclassified funded research may be published. The scientific community has strongly opposed the creation of a new category of "sensitive, nonclassified research" to restrict publication. Such a category is inherently vague and would probably be administered by nonscientists who are less sensitive to the needs of scientific research[5] .

Also of concern are restrictions on who may work with certain "select agents" that recent security laws now require to be registered and inventoried. Should past drug use, consultation with a psychiatrist, or having been born in certain countries disqualify individuals from working with those materials?

The halcyon days of scientific research that was unfettered by larger concerns about how results might be misused are now over for microbiologists and molecular biologists, as has long been the case for the scientists involved with nuclear energy. Inquiries into the genomic and protein structure of viruses and other microorganisms must continue, but scientists must also act responsibly in publicizing techniques that could yield bioweapons.

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Diptych: 'Yin/Yang lilac', by Jacques Deshaies (2002) (detail).

EVOLUTIONARY GENETICS

Chromosomal barriers to sex lifted

Many millions of years ago, two yeast cells became unable to have productive sex with each other. These eventually gave rise to separate species, or what we now know as *Saccharomyces cerevisiae* and *Saccharomyces mikatae* respectively. But how did the original barrier to mating arise in these yeasts, and how has it been maintained for all this time? In studying such speciation events, geneticists have been limited to retrospective studies that infer what might have happened. Now that has changed — in the 6 March issue of *Nature*, Delneri *et al.* actually 'do the experiment' to test the effects of chromosomal translocations on speciation.

The genomes of *S. cerevisiae* and *S. mikatae* are known to vary by at least two reciprocal chromosomal translocations, which disturb the collinearity of the two genomes. If these yeast species attempt to mate, sterile progeny result — presumably from the inability of the two rearranged genomes to complement each other to produce viable spores. We do not know what initiates the speciation process, but it has been speculated that genome rearrangements between protospecies reinforce their reproductive isolation.

Delneri *et al.* effectively backtracked in evolution by engineering laboratory strains of *S. cerevisiae* to the *S. mikatae* state at the translocation breakpoint. The popular Cre/loxP system was used to create large reciprocal translocations, resulting in a new strain with a genome that is more collinear with that of *S. mikatae*. When these engineered strains were mated to *S. mikatae*, viable progeny resulted. Even so, the matings were not 100% fertile, which indicated that the translocation is not the only important genomic difference between the two species. Further important variations might exist at the single-gene scale, which would only be discovered by sequencing both genomes — projects to sequence multiple yeast species are well underway.

Interestingly, the viable hybrid spores that were recovered were often extensively aneuploid, retaining chromosomes from one parent more often than should be the case, and having two copies of many chromosomes. The likely explanation is the duplication of one parental genome followed by some chromosome loss, but future experiments will be needed to discover the details. With this work, Delneri *et al.* have provided a new approach for further exploring these evolutionary mysteries. Although we still do not know what led to the divorce of these two yeasts, we now know what keeps them from reconciling.

Chris Gunter, Associate Editor, Nature

References and links

ORIGINAL RESEARCH PAPER Delneri, D. *et al.* Engineering evolution to study speciation in yeasts. *Nature* **422**, 68–72 (2003)
FURTHER READING Wolfe, K. Speciation reversal. *Nature* **422**, 25–26 (2003)
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