Lister *et al.* perceived the work that is necessary for definitive conclusions, and it is precisely what our study has provided: "This study needs to be enlarged by accruing larger domestic samples of accurate pedigree (using both [mitochondrial DNA] and microsatellites), and by further pursuing those ancient specimens which gave indications of DNA preservation..." (*2*, pp. 276–277).

Molecular evidence from both modern and ancient wild horses is providing clues to the origins of domestic horses.

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Moreover, the fact of high genetic diversity alone, as found by Lister *et al.* and other authors before them (*3*), is not sufficient to suggest a widespread origin of modern horse lineages. Large populations can have substantial genetic diversity. In this sense, sampling of a large diversity of modern horses coupled with sequences from late Pleistocene horses from Alaska that we examined is a necessary prerequisite to definitive conclusions. Our study represents the first attempt to characterize the genetic diversity in a wild horse population before domestication. The limited diversity we observed in this ancient population suggests that multiple populations of wild horses were likely involved in the origin of domestic horses.

We agree with arguments by Lister *et al.* that archaeological discoveries are fundamental to an understanding of the domestication process. However, early domestic horses likely were indistinguishable from their wild counterparts (*4*); hence, the timing and location of domestication are not easily revealed by a morphologic study. DNA analysis of archaeological specimens might assist in this regard if population-specific markers could be found. However, DNA is not readily isolated from material in areas where horses were likely first domesticated, as indicated by Lister and co-authors' inability so far to genetically characterize some of these horses. Specimens from the Arctic permafrost, where the likelihood of DNA preservation is high, or more recent archaeological sites might offer our only perspective into the genetics of ancient horses. This is the approach that we chose to take.

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Networked Research: An EC Model for U.S.?

THE EUROPEAN COMMUNITY (EC) HAS FOUND ways to systematically benefit underrepresented minorities and less research-intensive regions through the distribution of re-

search funds. Raising the level of research performance and excellence across Europe is a criterion for receipt of awards from the European Union, where research networks rather than individual research units have become the basis of research funding. Researchers from the preeminent centers seek out colleagues from less renowned centers for inclusion in research proposals, and chances of success in receiving funds improve if a research group from southern Europe, a declining industrial region, or a rural region is included in the project. In turn, the research performance of relatively excluded groups is positively influenced and upgraded through their association with leading researchers, and these groups gain experience in managing networked research projects, accumulating connections that can help them initiate their own collaborations.

In the United States, women and underrepresented minorities and research groups from less research-intensive regions are often still excluded from the informal and formal networks that are crucial to advancement in science (*1*). A "networked research" funding initiative could provide incentives to leading researchers to collaborate with relative outsiders; for example, points could be added to proposal ratings for projects that included non-elite research groups.

Access to networks of social relationships or "social capital" is as important in the conduct of science as obtaining research funds or financial capital. Programs such as EPSCoR (The Experimental Program to Stimulate Competitive Research) focus primarily on addressing state funding rather than national inclusion inequities. The EC's experience allows us to imagine what the United States might do if it had to design our system of research funding from the ground up to promote the best science, build capabilities, increase diversity among scientists, and evaluate costs and benefits across these objectives. Creating a networked funding scheme, superimposed on the present system, could broaden the capacity of institutions from different parts of the country, expand human resources, and create stronger research networks.

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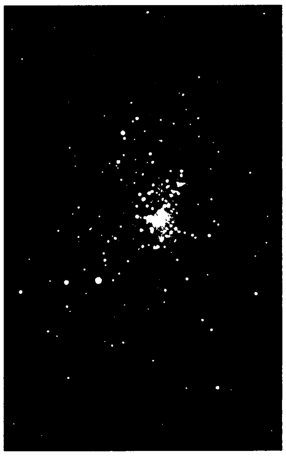
CORRECTIONS AND CLARIFICATIONS

PERSPECTIVES: "Orion sheds new light on star and planet formation" by J. Kastner (5 Jan., p. 57). Regarding the figure, the legend did not refer to the rectangular box in the wide-field image of the Orion Nebula, which indicated the region studied by C. Briceño *et al.* (their *Science* report was discussed in the Perspective). Also, the wrong image was used for the enlarged region of the figure. It was not of the Orion Nebula, as stated in the legend. An appropriate image of Orion is shown here. [Atlas image obtained as part of the Two Micron All Sky Survey (2MASS), a joint project of the University of Massachusetts and the Infrared Processing and Analysis Center/California Institute of Technology, funded by NASA and the National Science Foundation.]



Short Course in Computational Molecular Biology

Washington University in St. Louis
SCHOOL OF MEDICINE

Eric P. Newman Educational Center
Washington University in St. Louis

July 9-13, 2001

Objectives: The faculty of Washington University's computational molecular-biology program joined by Michael Zuker (Professor for Mathematical Sciences at Rensselaer Polytechnic Institute) offers a challenging, intensive course covering material from our regular graduate course on computational biology in a format that is accessible to working scientists. Participants will become familiar with the theory and practice of molecular sequence analysis and are offered sessions on programming in PERL. Participants should be accustomed with basic molecular biology and mathematics to the level of college calculus, but do not require programming skills or higher-level computer science. The course is targeted to students at the level of a first or second year doctoral candidate and addresses professional scientists in molecular biology or biotechnology. The aim of the course is to provide an appreciation for how and why different analytic approaches are used, their capabilities and their limitations. We emphasize the use of public domain software tools rather than focusing on a specific commercial package.

Syllabus: 5-day course with 6 hours of lectures each day (3 hrs. in the morning and 3 hrs in the afternoon).

- Probability and statistics, model based data analysis, HMMs, gene modeling and gene finding
- Protein models, threading, dynamic programming, optimal and suboptimal RNA alignment and folding
- Information measures, Karlin-Altschul statistics, Sum statistics, gapped BLAST, database searching
- Multiple sequence alignment, Generalized dynamic programming, Phylogeny and molecular evolution
- Physical mapping, Data clustering, and the inference of classifications, Expression data analysis

One of the two offered PERL programming sessions is targeted to professional software developers and the other one to scientists with a limited background in computer programming. All participants are encouraged to bring a laptop computer (Windows/Intel) for use in the programming sessions. A CD-ROM containing course lecture notes, problem sets, programming exercises, public domain software and reference material will be distributed.

Instructors:	David States (course master)	Center for Computational Biology
	Warren Gish	Department of Genetics
	Volker Nowotny	Center for Computational Biology
	Gary Stormo	Department of Genetics
	Michael Zuker	Mathematical Sciences, Rensselaer Polytechnic Institute

Graduate students from the Center for Computational Biology will fill in as Teaching Assistants.

The course (BME-72-537A) is offered through the Washington University Summer School and carries two units of graduate credit. Additional information and registration materials may be obtained from our website:

http://www.ccb.wustl.edu/shortcourse2001.html

Early application is advised, as the number of participants for this course has to be restricted.

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