

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

## High-priority genomes announced

ArticleInfo		
ArticleID	:	4579
ArticleDOI	:	10.1186/gb-spotlight-20020913-02
ArticleCitationID	:	spotlight-20020913-02
ArticleSequenceNumber	:	245
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	3
ArticleHistory	:	RegistrationDate : 2002-9-13 OnlineDate : 2002-9-13
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

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The addition of two of humanity's favorite mammals to the high-priority list for complete genome sequencing had been expected for some time, and has been announced Thursday by the [National Human Genome Research Institute](#) (NHGRI). But an organism's ascension to the high-priority list is only a kind of triaging, "not a permanent designation or a commitment to begin sequencing," noted Harvard's William Gelbart, who chairs NHGRI's genome selection committee. NHGRI director Francis Collins underscored Gelbart's cautionary note, saying that the priority list "is not yet a commitment to sequence the genomes of these organisms."

Organisms on the high-priority list are not ranked and the order in which they will feed into the US's large-scale sequencing capacity, or whether they will overtax it, is undetermined. Along with the [first group of new genome projects decided in May](#), the 'to-do' list now includes nine high-priority and two moderate-priority organisms.

Start dates for these projects are unknown and will depend on sequencing capacity becoming available. Researchers recently received NHGRI permission to begin sequencing some genomes from the May list, including chimp and chicken.

The NHGRI priority list does not include a host of other federally funded genome projects already underway, such as human (still under construction), mouse, rat, a second fruit fly, fish, a frog, plants and many microbes. A new plan setting out NHGRI's long-range genome research priorities is scheduled for release next year, and how the priority list will meld with that plan remains unclear.

Securing project funding is also a separate process and may involve other federal agencies. The cow project, for example, is likely to be supported in part by the [US Department of Agriculture](#) (USDA), and officials at NHGRI and USDA are discussing the possibility of sharing the financial burden for other livestock as well.

Two tinier and far more obscure creatures also found favor in the latest round of genome selection. The macronuclear genome of *Oxytricha trifallax*, a ciliate with a remarkable two-genome biology and scads of telomeres is now a high-priority sequencing project. The metazoan *Trichoplax adhaerens*, which possesses the smallest known animal genome, has been accorded "moderate" priority.

The dog and cow projects are considered especially valuable because *Homo sapiens* has been breeding both *Canis familiaris* and *Bos taurus* selectively - and keeping good records - for centuries, amassing vast amounts of pedigree information. This storehouse includes not only data about inheritance of physical characteristics such as size and vulnerability to disease, but also about the genetics of behavioral traits.

In a [white paper](#) advocating the dog project, the international consortium known as The Canine Genome Mapping Community, led by Elaine Ostrander of the [Fred Hutchinson Cancer Research Center](#) in Seattle, emphasized the dog's relevance to human biomedicine, including complex disorders such as cancer, heart disease, deafness, blindness, motor neuron disease, skin disorders and several autoimmune disorders.

The cow will also be a boon to the study of complex traits, according to Harris Lewin, director of the [W.M. Keck Center for Comparative and Functional Genomics](#) at the University of Illinois at Urbana-Champaign, a partner in the cattle genome project. Because of the animal's enormous economic importance, cattle researchers have done substantial work on quantitative trait loci in the past several years, he said.

All the organisms are expected to help in annotating the human genome sequence, and they are all considered interesting as experimental organisms. In addition, there is a desire to sample widely from the tree of life, according to NHGRI's Adam Felsenfeld. "They are all reasonable and valuable targets that can teach us about what the human genome means in the annotation sense, but also about basic biology - which of course is critical for understanding human biology," he noted.

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