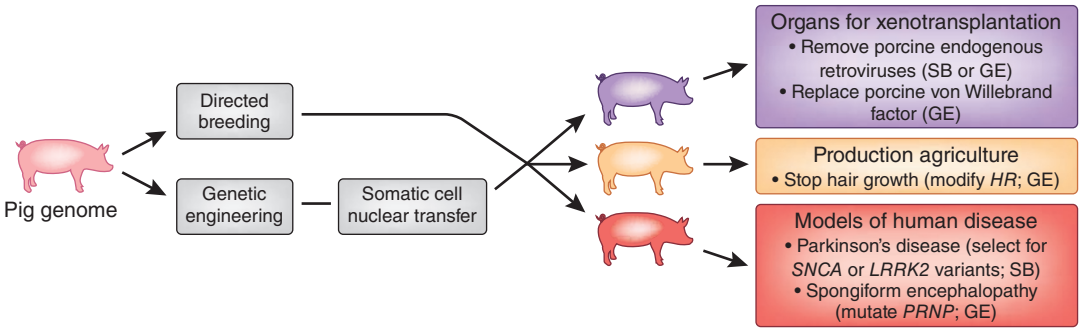

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Figure 1 Use of the swine genome for selective breeding and genetic engineering. Analysis of the swine draft reference genome sequence will identify genomic regions that may, through selective breeding or genetic engineering, improve porcine health and meat production, allow the creation of new models of human disease and lead to the development of organs suitable for xenotransplantation. Examples of genetic elements revealed by the genome sequence that may be relevant to these goals are indicated in the text boxes on the right; also indicated are whether these genetic elements would likely be selected for or against by selective breeding (SB), and/or be manipulated by genetic engineering (GE).

at the nucleotide level their identity to humans is three times higher compared with mice, and porcine-human synteny blocks are farther along the phylogenetic tree compared with those of mouse and human[4].

As swine are developed for disease modeling and for testing of new therapies, an application of particular interest is regenerative medicine studies using stem cells. A few existing lines of inbred pigs do not reject transplants from syngeneic donors, and efforts are underway to develop immunodeficient pigs (by disrupting genes such as *IL2RG* and *RAG2*) that could serve as universal hosts for cellular therapeutics[5].

Xenotransplantation of porcine organs has considerable potential to address the shortage of donor human organs. The major obstacle in this field is organ rejection by the human immune system[6]. The first stage of the rejection process, known as hyperacute rejection, is mediated in part by terminal α-1,3-galactosyl (Gal) epitopes on the surface of porcine cells, and promising results have been obtained by knocking out the gene encoding α-1,3-galactosyltransferase (*GGTA1*)[7,8]. However, more work is required. For example, mutating the gene encoding clotting factor von Willebrand factor (*VWF*) may help overcome post-hyperacute rejection[6]. It will also be important to better understand the risk posed by porcine endogenous retroviruses so as to eliminate any safety concerns related to zoonotic infection.

To build the new genome assembly, Groenen *et al.*[1] used a combination of existing bacterial

Goat genome sequence by optical mapping

With the report from Dong *et al.*[1] in this issue, the goat joins the pig, cow and chicken as major livestock species to have been sequenced. The authors assembled the genome *de novo* from short sequencing reads derived from a female Yunnan black goat.

A key limitation of genome sequencing using short reads is that the assembly usually consists of thousands of small fragments. Joining the fragments is a time-consuming, laborious process as it requires the generation of maps of markers throughout the genome. Dong *et al.*[1] have simplified this step by taking advantage of a method known as optical mapping[2]. The goat genome represents the first application to a large, mammalian genome of a commercial optical mapping technology, which provides raw whole-genome mapping data in a matter of hours.

The instrument images single DNA molecules cleaved by restriction enzymes and generates maps of the distances between restriction sites. Optical mapping has been applied to assess, refine and/or assemble the genomes of many microorganisms and of rice[3], maize[4], mouse[5] and human[6] by the group of David Schwartz, which pioneered the technique, but the goat genome marks a milestone with respect to commercialization of the technology.

Dong *et al.*[1] show that combining sequence data with optical mapping data yields 'super-scaffolds' that by a commonly used metric of genome assemblies (the N50 size) are >5 times longer than the scaffolds assembled from sequence data alone. These super-scaffolds represent a resource that should be valuable for gene mapping and marker-assisted breeding in goats. For example, the authors use their assembly to map RNA-seq data from hair follicle cells of cashmere goats, identifying candidate genes that may contribute to cashmere fiber production.

The commercial breeding infrastructure for goats is tiny compared with that of cattle[7]. Over 90% of the world goat population is kept in small herds by farmers in developing countries, and there are few systematic phenotyping and breeding efforts. However,

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China's status as the world's top producer of goats and the Chinese government's investment in agricultural biotechnology[8] could expedite practical applications of the goat genome sequence.

H. Craig Mak, Associate Editor, Nature Biotechnology

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