

Landsat reveals China's farmland reserves, but they're vanishing fast

Sir — We have compared the official estimates of agricultural land and rates of agricultural land conversion with those derived from Landsat thematic mapper satellite images for 10 counties in the Pearl River Delta, which is one of the fastest-developing regions in China. Ground-based field assessments verify the high accuracy of our techniques in estimating the area of agricultural land and its change through time^{1,2}.

Our results indicate that there is significantly more agricultural land than reported in official statistics³. Although this under-reporting is well documented⁴, particularly using coarse resolution (1-km) satellite data sets⁵, our study is the first to use high-resolution satellite imagery to quantify this bias.

Satellite-derived estimates of total agricultural area in the ten counties for 1990 is 6,724 km² — this is 115% greater than the 3,119 km² reported in government yearbooks (Fig. 1a). Similarly, satellite-derived estimates for the total area of agricultural land converted to other uses between 1990 and 1996 is about 11% greater than the 789 km² reported in statistical yearbooks (Fig. 1b).

One interesting effect is that while the satellite-based method estimates more overall conversion of agricultural land, the fraction of the agricultural land converted is smaller than official estimates.

With the world's largest population and one of the fastest-growing economies, China's ability to feed itself has important domestic and international implications. Agricultural self-sufficiency is a concern because economic development is rapidly converting China's small per-capita stock of agricultural land to other uses^{6,7}. Analyses of the severity of this problem are based largely on official statistics for the stock of agricultural land and its rate of conversion, but these statistics may be biased by institutional factors.

Starting with the Great Leap Forward in 1958, Chinese farmers have had strong incentives to understate the extent of their agricultural land. Grain quotas were based on agricultural acreage, so understating agricultural area reduced the quota a farmer was expected to provide.

Although this production quota has been eliminated, farmers still have incentives to understate their agricultural land. A 1985 moratorium in the region limited the amount of agricultural land converted for other uses. This directive, together with a desire to evade taxes on land leased for

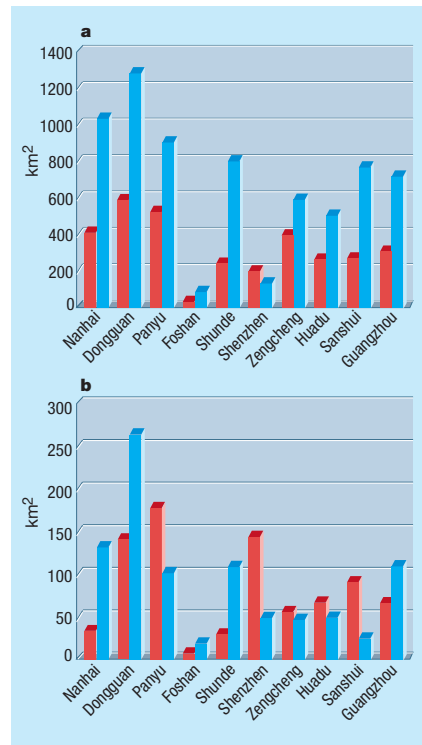


Figure 1a, Estimates of agricultural land in 10 counties of the Pearl River Delta, 1990, derived from satellite imagery (blue) and official yearbooks (red). **b**, Estimates of agricultural land conversion from 1990 to 1996 in 10 counties of the Pearl River Delta, derived from satellite imagery (blue) and official yearbooks (red).

commercial purposes, causes farmers to understate the area of agricultural land that has been converted to other uses.

Despite this under-reporting, we are not suggesting that the satellite-derived estimates are unbiased. Remote-sensing estimates may overestimate the amount of agricultural land because the resolution of the imagery (30 × 30 m) is too coarse to differentiate among small irrigation ditches, dirt paths and the other types of land use that co-exist with agriculture. Moreover, remote-sensing and government classification regimes of agricultural land may differ.

Our conclusion that there is more agricultural land than reported does not eliminate concern about the loss of agricultural land associated with rapid rates of economic development. Indeed, our results indicate that more agricultural land is being converted than reported.

Our results do, however, indicate that analysts must exercise caution when they use official statistics of agricultural land area and rates of loss to assess future rates of agricultural production in China.

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Please don't downgrade the sequencers' role ...

Sir — As representatives of the funding agencies that support the large-scale genome sequencing of parasites and related genomic research, we disagree with Colin Macilwain's description in the News report "Biologists challenge sequencers on parasite genome publication" (*Nature* **405**, 601–602; 2000) of the spirit of collaboration among the sequencers, funders and research scientists involved.

The data-release policy of these genome projects is for each sequencing centre to release unfinished sequence and assembled 'contigs' to a publicly accessible website. The policy encourages investigators to use the sequence data for gene-by-gene discovery. Already, in the case of the malaria parasite, more than a dozen peer-reviewed publications have used the preliminary sequence data and acknowledge the source of the sequences.

The sequencing centres and their collaborators need to keep responsibility for the computational analysis of unpublished sequence data on a chromosome or genome scale, for various reasons. First, the data are preliminary, and analyses will need correcting or completing as new data are added and existing data are modified. Second, the sequencing investigators and their collaborators should be allowed to confirm their research and publish the initial analysis of the data they have worked hard to generate.

Unfortunately, a few researchers view scientists at sequencing centres as service providers. In reality, they are conducting cutting-edge research, such as developing strategies for dealing with genomes with unusual base composition (*Plasmodium falciparum* is 80% A–T), including new methods to close difficult gaps in the sequence. In addition, they have designed and modified computer algorithms to identify and more accurately predict parasite genes and intron–exon boundaries.

Sequence data are no different from other types of biological data, and their generators deserve the same rights — to do an initial analysis and to publish the results — that other researchers have traditionally enjoyed. These data and their analysis should be published in peer-reviewed journals as quickly as possible. Until then,

the sequencing centres and their collaborators are seeking ways to provide added value to the unpublished sequence data.

At a meeting of the malaria genome project in June at the Wellcome Trust Genome Campus in Hinxton, UK, the sequencing centres agreed that a first-pass annotation would be added to their websites, including posting the results of blast hits for all the open reading frames. Participants in the malaria genome project have agreed on the development of the PlasmoDB database (<http://plasmodiumdb.cis.upenn.edu>), a web-accessible relational database facilitating the analysis of various genome-related data. With support from a grant from the Burroughs Wellcome fund, this database is being developed by David Roos and his colleagues at the University of Pennsylvania and by Ross Coppel at Monash University.

Contrary to your News report, the PlasmoDB team is not supported for, or engaged in, any effort to annotate the genome. Discussion is under way, however, to determine the extent of automated annotation that will be provided through PlasmoDB for unfinished sequence available from the sequencing centres.

WHO's programme for research and training in tropical diseases (see below) is to provide support for a 'help desk', in addition to the current distribution of data through a CD-ROM version of Malaria Information Resource, to help investigators who lack the computational resources to access and analyse the data.

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... when public-interest science needs solidarity

Sir — As a member of the small community of people working on malarial parasites, I am a constant user of sequence databases from the consortia at Sanger Centre, TIGR and Stanford (*Nature* **405**; 601–602; 2000). I am deeply grateful to these centres, which release all the data freely on the Internet, even in raw form, as soon as they are available.

According to the data-release policy of these three consortia, “these data will assist colleagues in their research, particularly in the search for genes and the studies of the genes’ biological function” and “provide investigators with information that may jump-start biological experimentation”. New perspectives are being added to virtually all the ongoing research projects and many more projects will start, as well as other ‘brute force’ approaches such as roteomix and SAGE (serial analysis of gene expression). All these data together will be integrated by bioinformaticists into more sophisticated and complete databases.

I sympathize with those who say that a period of “non-hypothesis science” has started, but I don’t agree with them. Good scientists will go on making good hypotheses, and the vastness of available data will only eliminate time-consuming and painstaking benchwork. As things stand, much laboratory work contributes to the efforts of the sequencers by providing clues for annotation and function. In the near future, many other hints will help to clarify the fine structure of the sequenced regions, for example when introns and exons are present that are too small to be revealed by the currently used algorithms, or when regulatory regions need to be identified.

For these reasons, I found the quarrel between the sequencing consortia and laboratory researchers reported in your News article very worrying. It would of course be wrong for a tribe of ‘annotators’ to develop, exploiting raw data only for their own publications instead of helping the sequencers. But, again, the release policy states that any investigator should ask permission of the consortia to publish data based on the content of the databases, and referees should easily be able to distinguish between a genuine contribution and data piracy. In this regard, the PlasmoDB database of Roos and colleagues represents an important tool for all of us and cannot be described simply as an “Internet portal” or connected with the concept of “piracy”.

Scientific careers are largely based on the amount and quality of publications, but it would be impossible for every new chromosome of every organism to be published in the highest-impact journals such as *Nature* and *Science*. Perhaps an online journal or supplement dedicated to sequencing and annotation work should be launched.

The most serious aspect of this situation is, however, not mentioned in the malaria article but is well put in another News report on the same pages: “Drive for more genomes threatens mouse sequence” (*Nature* **405**; 602–603; 2000).

Craig Venter of Celera Genomics is quoted as stating that the mouse genome is almost correctly assembled, directed by the blueprint of the human genome — that is,

by fundamental work done by public enterprise and non-profit consortia. In spite of this, Venter says Celera’s mouse genome will be restricted to subscribers.

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The search continues for Kármán’s St Christopher

Sir — It is nice to see fourteenth-century Bolognese frescoes getting a bit of well-deserved publicity in the *Science* in Culture article “St Christopher and the vortex”¹. However, if Theodore von Kármán was inspired by the beautiful San Domenico fresco of St Christopher to conceive of his ‘vortex street’, his powers as a psychic would be at least as remarkable as his achievements in the physical sciences.

True, the fresco in the church of San Domenico was painted during the late fourteenth century (to a formula much used by Tomaso da Modena and his associates²) and Kármán was born in 1881. But it had been hidden since 1728–31 behind a staircase built up to an organ loft. It was only revealed during repairs in 1979.

So what was the painting that Kármán reported had inspired him? Mizota and his partners are surely correct in seeing fourteenth-century painting style in Kármán’s water-flow representation, but today remarkably few examples of St Christopher survive in Bologna itself: the grandest, in San Petronio, by Giovanni da Modena (circa 1410–20), has been cut off at the ankles. Tomaso da Modena painted a similar image in San Francesco, Treviso, around 1350. A pupil of his painted another in the next chapel; similar accumulations probably occurred in churches in Bologna, but were lost during the Counter-Reformation.

The representation of St Christopher that Kármán is most likely to have seen is the triptych by Jacopo di Paolo from the 1390s that has long been shown in various rooms of the outer cloisters of San Stefano³ — but this comes nowhere near the San Domenico fresco in the clarity with which it shows water flowing.

We might deduce from this that von Kármán was sufficiently sensitive to painting style to have read the appropriate patterns into what he saw, from his own knowledge of both art and water, in his moment of inspiration.

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