

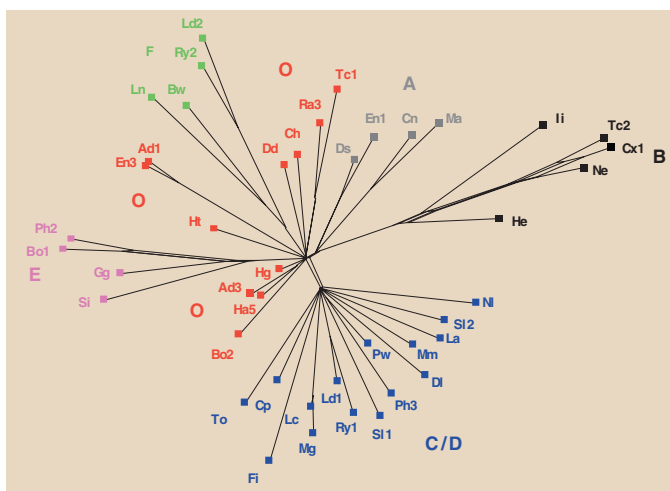
# The phylogeny of *The Canterbury Tales*

Geoffrey Chaucer's *The Canterbury Tales* survives in about 80 different manuscript versions<sup>1</sup>. We have used the techniques of evolutionary biology to produce what is, in effect, a phylogenetic tree showing the relationships between 58 extant fifteenth-century manuscripts of "The Wife of Bath's Prologue" from *The Canterbury Tales*. We found that many of the manuscripts fall into separate groups sharing distinct ancestors.

Manuscripts such as these were created by copying, directly or indirectly, from the original material (written, in the case of *The Canterbury Tales*, in the late fourteenth century). In the process of copying, the scribes made (deliberately or otherwise) changes, which were themselves copied. Textual scholars have developed a system for reconstructing the relationships between textual traditions by analysing the distribution of these shared changes, and have constructed family trees (stemmata) on the basis of the results, with the ultimate aim of establishing precisely what the author actually wrote. This analysis is carried out manually and is feasible only for a few manuscripts of short texts. The sheer quantity of information in a tradition the size of *The Canterbury Tales* defeats any system of manual analysis.

However, the principle of historical reconstruction is similar to the computerized techniques used by evolutionary biologists to reconstruct phylogenetic trees of different organisms using sequence data. We therefore applied phylogenetic techniques to *The Canterbury Tales* using the 850 lines of 58 surviving fifteenth-century manuscripts of “The Wife of Bath’s Prologue”. We believe this to be the first full tradition of a major work to be analysed in this manner.

It may be inappropriate to impose a tree-like structure on such data sets, so we used the method of split decomposition implemented in the program SplitsTree<sup>2</sup>, in addition to the cladistic analysis of PAUP<sup>3</sup>. Figure 1 shows a SplitsTree analysis of 44 of



**Figure 1** SplitsTree analysis of 44 manuscripts of "The Wife of Bath's Prologue" from Chaucer's *The Canterbury Tales*<sup>4</sup>. The two- or three-character codes indicate individual manuscripts, whereas the large capitals indicate groups of manuscripts, which are coloured the same.

the 58 manuscripts. Very similar results were given by PAUP (not shown). Several manuscripts form groups (A, B, C/D, E and F), each descended from a single and distinct common ancestor. The remaining 14 manuscripts were removed from the analysis shown in Fig. 1, as they were likely to have been copied from more than one exemplar, either by deliberate conflation of readings or by changing the exemplar during the course of copying. These manuscripts were identified by comparison of the trees generated with different regions of the text, which showed that their position in the analysis varied dramatically depending on which region was used. The central point is likely to represent the ancestor of the whole tradition. The manuscripts grouped as O are particularly crucial; their position near to the centre suggests that they all descend from Chaucer's original, and may therefore contain crucial evidence about this original. However, most of them have been ignored by scholars.

From this analysis and other evidence, we deduce that the ancestor of the whole tradition, Chaucer's own copy, was not a finished or fair copy, but a working draft containing (for example) Chaucer's own

notes of passages to be deleted or added, and alternative drafts of sections. In time, this may lead editors to produce a radically different text of *The Canterbury Tales*. These results also demonstrate the power of applying phylogenetic techniques, and particularly split decomposition, to the study of large numbers of different versions of sizeable texts.

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## Green-wave phenology

Phenology, the traditional study of seasonal plant and animal activity driven by environmental factors, has found new relevance in research into global climate change<sup>1–4</sup>. Global phenology research so far has concentrated on measurements obtained by satellites, downplaying connections of these measures to information obtained on the surface<sup>1,4</sup>, perhaps because of a lack of conventional, surface-based phenological data. However, an integration of conventional

and satellite-derived measures is needed to understand better the mid-latitude spring onset of photosynthesis, known as the ‘green wave’ or ‘green-up’<sup>5–7</sup>. Here I show how a surface-based green-wave model can extend the monitoring of climatic variability back to 1900, providing a longer-term context for the more limited, recent data obtained from satellites.

Simple events, such as flower blooms or insect hatchings, offer clues to the workings of complex processes<sup>8</sup>. The spring green wave signals the start of the growing season and profoundly influences subsequent

productivity<sup>7</sup>; plant activity is more responsive to spring weather than to other seasons. Thus, indices that measure the onset of the green wave are ideal biological measures of climatic variability. Despite these attributes, traditional phenological studies are typically local-scale agricultural projects, rarely involving ecosystem- or global-scale processes. In contrast, satellite remote sensing has been widely used for biospheric monitoring, including for phenology<sup>1,2,4,9</sup>.

The daily global coverage by satellites makes them essential to investigations of green-up. However, remote-sensing data

extend back only to about 1982, are limited by cloud cover, and may not distinguish between overstorey (the dominant trees in the forest) and understorey (shrubs and herbaceous plants on or near the forest floor) phenology in forests<sup>2,5</sup>.

Other biospheric phenomena have been assessed globally through strategic combinations of satellite and surface measurements<sup>3</sup>. The above limitations of remote-sensing 'phenology' highlight the complexity of the green wave, and suggest the need for a similar strategy here. What the satellite senses and what is observed on the ground are both integral parts of the green wave. Conventional phenological data — carefully selected according to species, and globally distributed — should play a crucial role in global green-wave research. As global-scale phenological networks do not yet exist, empirical green-wave models can partly fill the void.

Models that simulate phenology using meteorological data offer several advantages, if based on appropriate plants<sup>10,11</sup>. They allow reconstruction of green waves back through the period for which instrumental records of weather are available, providing a context for short-interval satellite data. Also, models serve as 'anchor points', binding together commonalities among records for native species in adjacent biomes and remote-sensing observations. Empirical models (spring indices) can closely mimic actual plant first-leaf and first-bloom events, correlate with native-species data, and reveal changes in lower-atmospheric processes at the ecosystem scale<sup>5,6,10,12,13</sup>, illustrating their potential use in longer-term studies (Fig. 1).

As an example, I studied green-wave changes in eastern North America<sup>5</sup> from 1900 to 1995 (Fig. 2). Meteorological data were from the Historical Climatology

Network Daily Temperature and Precipitation Data (CDIAC, Oak Ridge National Laboratory). I calculated several indices for each year for all stations over their respective periods of record. All indices showed considerable year-to-year variation, without striking long-term trends, but with significant shorter-period changes. For example, from 1978 to 1990, first-leaf spring index dates became earlier at a rate of about 1 day per year (trend adjusted  $r^2 = 0.43$ ,  $\alpha$ -level = 0.009; Fig. 2).

The tendency of global phenology research to concentrate on satellite-based measurements makes this approach fundamentally incomplete. Satellite measurements provide broad areal coverage but reveal only one aspect of green-up. All measures — empirical models, native-species phenology, and appropriately calibrated satellite indices — need to be understood and interconnected for maximum effectiveness<sup>5,6</sup>.

Global-scale plant phenology networks should be established to strengthen this research strategy. However, empirical models offer a way to reconstruct past green waves, and allow regional comparisons. Although imperfect and of limited geographical application, these models provide one of the few independent comparisons available for satellite measurements of plant activity<sup>9</sup>. Connections between conventional phenology and remotely sensed greenness measures at the ecosystem level are being confirmed, and further studies are underway<sup>4</sup>. It is encouraging that a satellite-derived change in green-up<sup>9</sup> (earlier by  $8 \pm 3$  days over the 1981–91 period) is consistent with the trend, over roughly the same period, that I describe here (ten days earlier during the 1980–90 period, inferred from the 1978–90 regression line). But this short period appears unremarkable when compared with the overall first-leaf spring

index variability in eastern North America (Fig. 2).

My results endorse empirical models as useful partners for satellite-derived green-wave measures. Studies of other regions, especially those with long-term warming trends, can provide a context for evaluating satellite measurements that indicate earlier greenness onset over large areas. Energy budget analyses coupled with surface and satellite phenology (for example, examination of phenological effects on the exchange of latent and sensible heat between the surface and the atmosphere) should also prove rewarding in further understanding and monitoring spring plant–climate interactions.

**Mark D. Schwartz**

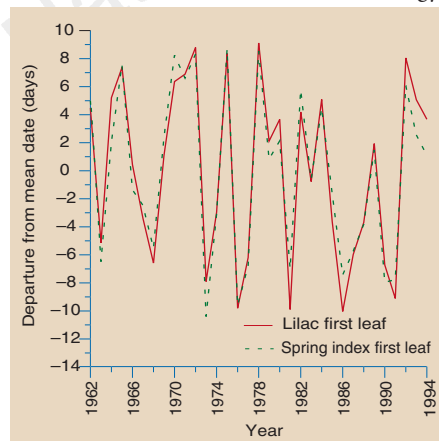
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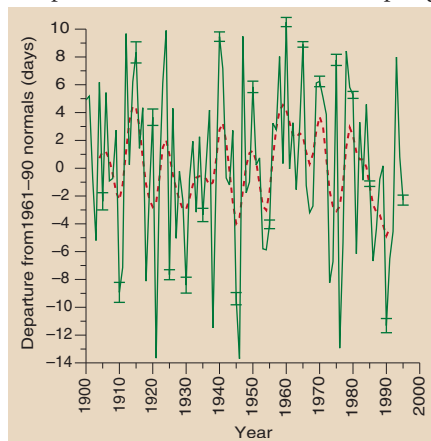
## A posteriori teleportation

The article by Bouwmeester *et al.*<sup>1</sup> on experimental quantum teleportation constitutes an important advance in the burgeoning field of quantum information. The experiment was motivated by the proposal of Bennett *et al.*<sup>2</sup> in which an unknown quantum state is 'teleported' by Alice to Bob. As illustrated in Fig. 1, in the implementation of this procedure by Bouwmeester *et al.*<sup>1</sup>, an input quantum state is 'disembodied' into quantum and classical components, as in the original protocol<sup>2</sup>. However, in contrast to the original scheme, Bouwmeester *et al.*'s procedure necessarily destroys the state at Bob's receiving terminal, so a 'teleported' state can never emerge as a freely propagating state for subsequent examination or exploitation. In fact, teleportation is achieved only as a postdiction.

Bouwmeester *et al.* used parametric down-conversion from two sources (SI, SII in Fig. 1) in an attempt to teleport the



**Figure 1** Comparison of annual departures from the mean of spring index first-leaf dates (derived from an empirical model) and of *Syringa chinensis* 'red rothomagensis' (lilac) first-leaf dates (derived from actual data), 1962–94 (details of the network of the 183 stations with relevant data, and methods, are available from the author).



**Figure 2** Eastern North American<sup>5</sup> departures from the mean of spring index first-leaf dates, 1900–95, with  $\pm 1$  standard error bars, and smoothed trend produced by a nine-year, moving average, normal curve filter (dotted line) (details of the network of the 465 relevant stations, and methods, are available from the author).