A reader wonders why biomass was not covered in the 30 July Energy issue: "the potential for renewable liquid fuels from biomass should not be ignored." And a report of the discovery of *Australopithecus garhi* prompts a debate about the use of cladistic analysis to resolve questions about early hominid phylogeny: "Cladistics is the most objective method available for generating and testing hypotheses about phylogeny," says one group of researchers. "[A]ny powerful technique can be exploited by perfunctory misapplication," says another group.

Biomass in the Energy Picture

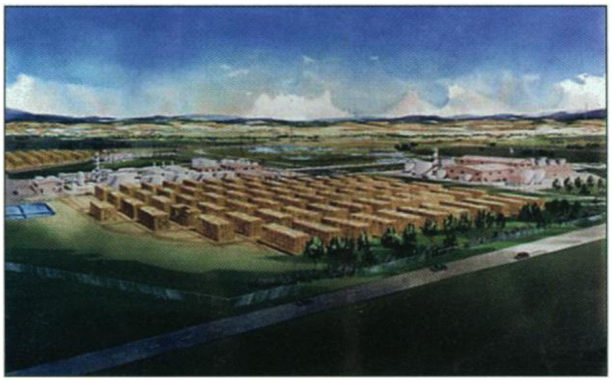
I was surprised that the 30 July issue highlighting renewable energy and fuel efficiency devotes so little attention to biomass energy. By my count, there are only three sentences mentioning biomass. One decries the pollution from incinerated biomass (K. S. Brown, News, p. 678), and two mention conversion of biomass to hydrogen (J. A. Turner, Viewpoint, p. 687).

Yet, according to the Energy Information Administration of the U.S. Department of Energy, biomass accounts for 43% of the renewable energy used in the United States, second only to conventional hydroelectric power (51%). Solar accounts for 1% and wind for 0.5%. Furthermore, the potential for renewable biomass, in the form of wood chips, grasses, and crop residues, is 5 times the current consumption (*1*), while Brown notes that conventional hydroelectric capacity is slated to be reduced because of environmental concerns.

In addition, biomass is the only practical source of renewable liquid fuel. A self-contained facility can convert green wood into methanol with an energy efficiency of 70% (*2*). The only by-product is the wood ash, which can be returned to the forest. And the estimated cost of the methanol is competitive with methanol from coal (*2*).

Methanol, which has an octane rating of 130, can be used directly in a vehicle or converted by means of a zeolite catalyst to high-octane gasoline with a 90% energy efficiency. Alternatively, a vehicle's exhaust heat can be used to reform methanol into carbon monoxide and hydrogen. This gas mixture contains 30% more energy than the methanol from which it is derived. Finally, the gas mixture can be burned in a very lean fuel-air mix when power requirements are low. All of these factors enable enhanced fuel efficiency.

By contrast, converting the same amount of biomass to ethanol would produce only 55% (by energy content) as much liquid fuel (*2*), and the opportunities for increased efficiency are substantially reduced.



Artists rendition of planned rice straw–to-ethanol plant near Sacramento, California.

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Despite these facts, the National Renewable Energy Laboratory's (NREL's) Web page lists only two renewable liquid fuel programs, the "Biodiesel Project" and the "Bioethanol Project." The former involves esters of biological fatty acids, which are produced with substantially lower energy efficiency than lignocellulose. And, as mentioned, the latter is not the most energy-efficient use of biomass feedstock.

Despite the NREL's emphasis, the potential for renewable liquid fuels from biomass should not be ignored.

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References

1. Office of Technology Assessment, *Energy from Biological Processes*, Vol. II, *Technical and Environmental Analyses* (052-003-00782-7, U.S. Government Printing Office, Washington, DC, September 1980). Also published commercially by McGraw-Hill and Ballinger.
2. T. E. Bull, in *Energy Sources: Conservation and Renewables* (American Institute of Physics, New York, 1985), chap. 26.

Response

The United States today generates about 10 gigawatts (GW) of electricity from biopower (biomass-to-electricity). This is divided into 7 GW from forest-product–industry residues and agricultural-product–industry residues, about 2.5 GW from municipal solid wastes, and 0.5 GW from other technologies, such as landfill gas. The majority of this power is used by the industrial sector primarily in the pulp and paper industry to supply their internal electrical needs. Overall, biopower represents a little more than 1% of U.S. electrical generating capacity.

Electricity costs for biopower range from $0.08 to 0.12 cents per kilowatt-hour, depending on the feedstock price (*1*). Current biopower plants use a mature electricity-generating technology that leads to low efficiencies for biomass-to-electricity conversion. This increases the sensitivity to feedstock price and gives higher costs for electricity. The U.S. Department of Energy has a number of programs to develop more efficient processes leading to lower costs for electricity (*2*). One of the most promising is conversion of biomass to syngas (a mixture of CO and hydrogen) and generating electricity by means of a fuel-cell system. The NREL maintains the Department of Energy's Office of Energy Efficiency and Renewable Energy Web site, where more information on all renewable technologies, including biomass, is available (*3*).

Concerning the conversion of biomass to methanol, the current spot price of methanol (derived from natural gas) is about $0.30 per gallon (*4*), whereas methanol from coal and biomass would probably be $0.80 to $1.20 per gallon. While one may be able to convert green biomass to methanol with an efficiency of 70%, photosynthesis was only 1% efficient in turning sunlight into the biomass, giving an overall energy efficiency for solar-to-methanol of 0.7%. And this does not account for the energy required for harvesting and processing the biomass. Hydrogen can be generated with a solar-to-hydrogen efficiency of at least 10%, and that can be combined with CO_2 to make methanol with an energy efficiency of 70%. This gives an overall solar-to-methanol efficiency of 7%, an order of magnitude higher. If we have to cover land area to collect solar energy, it only makes sense to use the most efficient renewable energy converters available.

When it comes to renewable energy, we have a lot of choices. A variety of chemicals as well as electricity can be made from biomass, depending on how it is processed. For maximum impact of renewable energy, we must match the renewable technology with regional resources and local and national needs.

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References and Notes

1. "Renewable energy technology characterizations" (EPRI Topical Report TR-109496, Electric Power Research Institute, Palo Alto, CA, December 1997), at http://erendev.nrel.gov/power/techchar.html, "Overview of Biomass Technologies."
2. See www.eren.doe.gov/biopower.
3. www.eren.doe.gov.
4. See www.methanol.org/methanol/fact/methhistpr.html.

Cladistics and Early Hominid Phylogeny

Two recent reports (B. Asfaw *et al.*, 23 Apr., p. 629; M. A. McCollum, 9 Apr., p. 301) (*1*, *2*) are skeptical about the utility of cladistic analysis to resolve questions about early hominid phylogeny. Although we disagree with aspects of these studies (*3*, *4*), it is true that phylogenetic analyses would benefit from studies of character variability and integration. However, this does not mean that current analyses are without value. Cladistics is the most objective method available for generating and testing hypotheses about phylogeny. Even if future studies are able to improve the quality of the character data, analyses of presently available data sets can still provide a legitimate baseline for discussions about early hominid phylogeny.

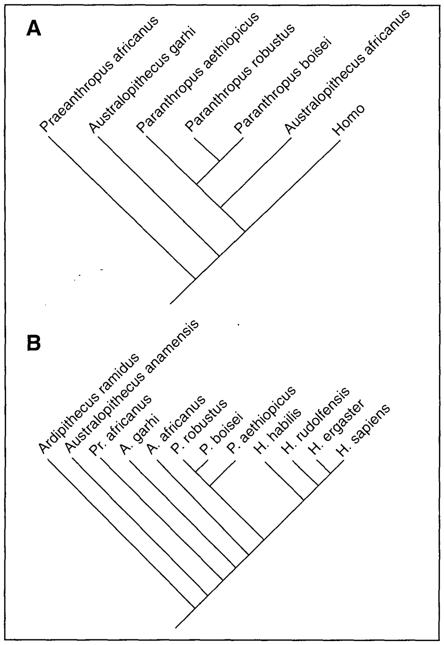

Fig. 1. Early hominid cladograms. Most parsimonious cladograms supported by (A) the trait list of Asfaw *et al.* (*1*), when characters were ordered and free to reverse their states [*Pan troglodytes* was added as an outgroup; tree length, 94; consistency index (CI), 0.73]. (B) The updated trait list (*9*) of Strait *et al.* (*6*), after the addition of *A. garhi*, *Ardipithecus*, and *A. anamensis* (tree length, 214, CI, 0.58). The only difference between A and B (aside from the number of taxa) concerns the relationships of *A. africanus*, which is positioned as either the sister taxon of the "robust" australopithecines (A) or as the sister taxon of a *Homo* + *Paranthropus* clade (B). In both trees the "robust" australopithecines are attributed to the genus *Paranthropus*, and the species usually referred to as *A. afarensis* is subsumed within *Praeanthropus africanus* (*5*, *6*).

For example, Asfaw *et al.* (*1*) propose a phylogenetic hypothesis that is testable using cladistic analysis. They suggest that *Australopithecus garhi* may be ancestral to *Homo* (*5*), with the caveat that the exact relationships of that species are unknown. Cladograms consistent with this hypothesis would place *A. garhi* as the sister taxon of *Homo*. We tested this hypothesis with two cladistic analyses. The first examined the trait list and taxa presented in table 1 of Asfaw *et al.* (*1*). The second analysis built on a previous study (*6*) by adding to it new taxa (*A. garhi*, *A. anamensis*, and *Ardipithecus ramidus*) (*1*, *7*, *8*) and new characters taken from Asfaw *et al.* (*1*, *9*). The most parsimonious trees found by the two analyses (Fig. 1) both reconstruct *A. garhi* as the sister taxon of a clade that includes *A. africanus*, *Paranthropus*, and *Homo* (*10*).

The relationships presented here must be considered preliminary given the small sample sizes of the three newly described species, as well as the fragmentary nature of the fossils themselves. As is always the case in paleontology, future fossil finds may necessitate a revision of these results. However, on the basis of current evidence (*11*), a hypothesis in which *A. garhi* is ancestral to *Homo* should be rejected. *A. garhi* shares no synapomorphies (shared, derived features) with *Homo*, and it is more distantly related to that genus than is the geologically older *A. africanus*. This means that the clade containing *Homo*, *Paranthropus*, and *A. africanus* must have originated at least 500,000 years before the known appearance of *A. garhi*. Although it is possible that an early member of the *A. garhi* lineage gave rise to the clade that includes *Homo*, a more likely explanation is that *Praeanthropus africanus* [more commonly known as *A. afarensis* (*5*, *6*)] independently gave rise to that clade and to *A. garhi*. *Australopithecus garhi* was probably, therefore, a side branch of hominid evolution that evolved postcanine megadontia in parallel with *Paranthropus*. The ancestor of *Homo* remains surprisingly elusive.

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References and Notes

1. B. Asfaw *et al.*, *Science* **284**, 629 (1999).
2. M. A. McCollum, *ibid.*, p. 301.
3. McCollum (*2*) posits that the many derived features shared by "robust" australopithecines (*6*) can be conflated into only four complexes, and thus she doubts that the "robust" species are monophyletic. However, the hypotheses underlying the complexes are untested, and characters within each of those complexes appear to be poorly integrated: (i) *A. garhi* indicates that postcanine megadontia can be independent of enamel thickness and tooth cusp position (*1*); (ii) on the basis of alveolus size, *P. aethiopicus* possessed fairly large incisors (*6*), even though it exhibits derived clivus morphology; (iii) the chewing muscles do not insert on the lateral face of the mastoid process and thus are not obviously related to inflation; and (iv) *Homo sapiens* and the "robust" species share some, but not all, derived subnasal features (*2*), indicating that the features are partially independent. Thus, it is likely that several independent characters or complexes support "robust" australopithecine monophyly.
4. If the variability of the characters described in (*1*) is sufficiently understood to allow the discrimination of *A. garhi* from other species, then arguably those characters (except for autapomorphies) should be adequate for use in phylogenetic analysis. Character correlation is a more serious problem, but can be dealt with by eliminating descriptively redundant characters (*6*) and by testing patterns of integration [D. S. Strait, thesis, SUNY at Stony Brook (1998)].
5. Note that Asfaw *et al.* (*1*) use *H. habilis* and *H. rudolfensis* to represent the genus *Homo*, but there is some uncertainty as to whether those species belong to the *Homo* clade [B. Wood and M. Collard, *Science* **284**, 65 (1999)].
6. D. S. Strait, F. E. Grine, M. A. Moniz, *J. Hum. Evol.* **32**, 17 (1997).
7. T. D. White, G. Suwa, B. Asfaw, *Nature* **371**, 306 (1994).
8. M. G. Leakey, C. S. Feibel, I. McDougall, A. Walker, *ibid.* **376**, 565 (1995).
9. A description of the trait list employed in the second cladistic analysis is available at www.gwu.edu/~hogwash/dataset.html.
10. *A. garhi* was the sister taxon of *Homo* in trees that were, respectively, eight and five steps longer than the most parsimonious cladograms (Fig. 1).
11. An appropriate test of the relationships presented here would be to examine character variability and integration in all of the traits in the two data sets and then repeat the analyses.
12. We thank B. Wood, D. Lieberman, M. Collard, O. Pearson, B. Richmond, and R. McCarthy for helpful discussion and advice. Supported by the Henry Luce Foundation.

Response

We are fully cognizant of the strength and power of cladistic methods. These are not at issue. However, any powerful technique can be exploited by perfunctory misapplication, and such is clearly the case with Strait and Grine's "analysis." The traits employed in constructing cladograms must be biologically relevant. Without such pertinence, they cannot contribute to a resolution of phylogenetic relationships. It is more than obvious to most students of human evolution that many traits commonly employed in formal descriptions of hominid specimens are merely a convenient means of delineating elementary anatomical features. A blind compilation of such