Phylogenetic Analysis of the Evolution of Lactose Digestion in Adults

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Abstract In most of the world's population the ability to digest lactose declines sharply after infancy. High lactose digestion capacity in adults is common only in populations of European and circum-Mediterranean origin and is thought to be an evolutionary adaptation to millennia of drinking milk from domestic livestock. Milk can also be consumed in a processed form, such as cheese or soured milk, which has a reduced lactose content. Two other selective pressures for drinking *fresh* milk with a high lactose content have been proposed: promotion of calcium uptake in high-latitude populations prone to vitamin-D deficiency and maintenance of water and electrolytes in the body in highly arid environments. These three hypotheses are all supported by the geographic distribution of high lactose digestion capacity in adults. However, the relationships between environmental variables and adult lactose digestion capacity are highly confounded by the shared ancestry of many populations whose lactose digestion capacity has been tested. The three hypotheses for the evolution of high adult lactose digestion capacity are tested here using a comparative method of analysis that takes the problem of phylogenetic confounding into account. This analysis supports the hypothesis that high adult lactose digestion capacity is an adaptation to dairying but does not support the hypotheses that lactose digestion capacity is additionally selected for either at high latitudes or in highly arid environments. Furthermore, methods using maximum likelihood are used to show that the evolution of milking preceded the evolution of high lactose digestion.

The ability to digest lactose in adults is a genetic polymorphism inherited as a dominant genetic trait (Sahi et al. 1973; Johnson et al. 1977; Ransome-Kuti et al. 1975; Metneki et al. 1984). This trait is common in a few of the world's populations. The physiological cause of high lactose digestion capacity (LDC) in adulthood is the retention of high levels of lactase in the small intestine beyond infancy (lactase persistence), which contrasts with the standard mammalian developmental pattern of a steep decline in small intestine lactose levels after infancy (Flatz 1987).

The LDC of over 20,000 individuals worldwide has been tested. High frequencies (>70%) of adults with high LDC are found in northern Europeans and

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their descendants in North America and Australia and among some African pastoralist groups thought to have originated in North or East Africa. Intermediate frequencies (30–70%) of adults with high LDC are found around the Mediterranean, the Middle East, and in central and south Asia. Regions whose adult populations predominantly have low LDC include much of sub-Saharan Africa, east and southeast Asia, and the native populations of the Americas and Oceania. Patchy sampling in much of sub-Saharan Africa and in southern and central Asia necessitates caution in our overview of these areas, particularly because the distribution of adult LDC in these regions appears to be locally variable and complex.

Selective Pressures for Drinking Milk

There are three major hypotheses for the evolution of high adult LDC. The first hypothesis was independently proposed by Simoons (1969, 1970) and McCracken (1971). They observed that in regions where milk was not normally consumed until recently, adults mostly have a low capacity to digest lactose. Therefore it was hypothesized that lactase persistence in adulthood is an adaptation to millennia of pastoralism and milk consumption, a theory known as the culture-historical hypothesis (Simoons 1970a). This is a coevolutionary theory in which selection of a genetic trait is influenced by the cultural environment, the herding and milking of livestock. According to this hypothesis, the capacity to digest lactose has a selective advantage in adults in pastoralist populations. Individuals with a high LDC are able to derive a nutritional benefit from the lactose in milk, which is not available to individuals with low LDC. Individuals with low LDC may also suffer from symptoms of lactose intolerance when they consume fresh milk, including abdominal discomfort, flatulence, and diarrhea. It has been suggested that, because of these symptoms, milk could be nutritionally detrimental to individuals with low LDC, although this suggestion has been much debated (Scrimshaw and Murray 1988). Populations that keep livestock but do not milk them, for example, populations in China and southeast Asia and parts of sub-Saharan Africa (Murdock 1967; Simoons 1970), would not be expected to have evolved high adult LDC according to the culture-historical hypothesis (Simoons 1979).

The other two hypotheses refer specifically to the consumption of *fresh* milk. Milk is often processed into dairy products, such as cheese and yogurt, which have a reduced lactose content. Two specific selective advantages to drinking fresh milk, with a high lactose content, have been proposed. Flatz and Rotthauwe (1973) suggested that in high-latitude environments, where sunshine is limited, humans are at risk of vitamin D deficiency and rickets. The lactose in fresh milk, like vitamin D, promotes the uptake of calcium, also present in milk. This hypothesis could explain the high frequency of lactose digesters in northern European populations. Durham (1991) has used this hypothesis to explain the difference between northern Europe, where fresh milk is consumed in quantity and most adults have high LDC, and the Mediterranean, where milk is mostly eaten as cheese and the population has predominantly low LDC.

The third hypothesis, proposed by Cook and Al-Torki (1975) and Cook (1978), states that in highly arid environments the water content of fresh milk increases the survival chances of lactose-digesting milk drinkers among desert-dwelling nomadic pastoralists and also that diarrhea and consequent water depletion in lactose-intolerant members of the group cause selection against maldigesters. This hypothesis is supported by the high frequencies of adults with the LDC observed in pastoralist groups in hot areas, for example, the Middle East and North Africa, including the Bedouin, the Tuareg, and the Fulani (Table 1).

The evolution of adult lactase persistence has been modeled several times. Bodmer and Cavalli-Sforza (1976) estimated that a selection coefficient of 0.04 would be necessary for high LDC to increase from an initial prevalence of 0.001% to the levels observed today in northern European populations (estimated frequency of 0.5) within 290 generations (9000 years). If the initial frequency of the lactase persistence gene were 1.0%, a selection coefficient of only 0.015 would be required. This time scale is realistic for the Middle East, where livestock were first domesticated around 8000–7000 B.C. (Clutton-Brock 1987). Flatz (1987) estimated that for the gene to reach contemporary European levels in the 3500 years or less since the first known domestic livestock in northern Europe, starting from an initial frequency of 0.005%, a higher selection coefficient of between 3% and 7% would be required.

More recently, attempts have been made to model the coevolution of a gene for lactase persistence and the cultural trait of milk drinking. Aoki (1986) estimated that for the selection of the gene for lactase persistence to increase from an initial prevalence of 0.05% to the prevalence observed in northern Europe today (estimated gene frequency of 0.7) within the time available since the advent of dairying (6000 years ago) and with an effective population size of 500, the selection coefficient must have been greater than 5%. Feldman and Cavalli-Sforza (1989) also found that a selection coefficient of greater than 5% was necessary for a gene frequency of 0.70 to be reached in 6000 years.

However, in these dual-inheritance coevolutionary models milk drinking is a cultural trait with a low initial frequency whose selection coefficient depends on the prevalence of the lactase persistence gene. The ethnographic evidence does not support this assumption, insofar as milk consumption apparently has been universally adopted by populations with predominantly low LDC, for example, the Mongols, the Herero, the Nuer, and the Dinka. Milk-based pastoralism may be the best means of subsistence, particularly in dry, marginal environments, even for lactose nondigesters. Milk processing and the consumption of fresh milk in only small quantities are cultural and behavioral means by which many lactose malabsorbers manage to consume milk products without suffering the symptoms of lactose intolerance. After milk-based pastoralism had been adopted as a means of subsistence, high LDC would have enabled adults to consume more fresh milk and to derive a nutritional benefit from the lactose component of fresh milk, and so be selected for. The initial frequency of the cultural trait of milk consumption may therefore be virtually 100%, which could reduce the selection coefficient required

Table 1. Data Used in the Analysis

Population and Ethnographic Atlas Code	*Number of Dry Months per Year*	*Global Solar Radiation (kcal/cm/yr)*	*Pastoralism as Proportion of Total Subsistence Activity (%)*	*Total Number of Individuals Tested in Each Population*	*Frequency of Low LDC (%)*	*Reference*
Apache (Nh17)	12	162	0	22	100	Johnson et al. (1978)
Australian Aborigines[a]	12	167	0	45	84	Brand et al. (1983)
Baggara (Habbania) (Cb13)	10	174	50.5	19	53	Bayoumi et al. (1981)
Baggara (Messiria) (Cb15)	10	174	70.5	20	60	Bayoumi et al. (1981)
Bedouin (Jordanian (Cj2)	10	162	80.5	162	24	Hijaki et al. (1983)
Bedouin (Saudi) (Cj5)	12	192	93	35	17	Cook and Al-Torki (1975), Dissanyake et al. (1990)
Beja (Amarar) (Ca35)	12	192	93	82	13	Bayoumi et al. (1982)
Beja (Beni Amir) (Ca36)	12	174	80.5	40	13	Bayoumi et al. (1982)
Beja (Haddendoa) (Ca43)			60.6	137	20	Bayoumi et al. (1982)
Beja (Bisharin) (Ca5)	12	192	80.5	22	14	Bayoumi et al. (1982)
Chippewa (Na36)	7	124	0	33	97	Newcomer et al. (1977)
Czechs (Ch3)	9	124	30.5	200	13	Madzarovova-Nohejlova (1974)
Dinka (Aj11)	5	144	50.5	213	76	Bayoumi et al. (1982), Elliott et al. (1973)
Egyptians (Cd2)	12	192	30.5	742	64	Hussein et al. (1982), Hussein and Ezzilarab (1994)
Eskimo (Greenland) (Na25)	8	79	0	119	85	Gudmand-Hoyer and Jarnum (1969), Gudmand-Hoyer et al. (1973), Asp et al. (1975)
Fijians (Ih4)	0	167	0[b]	12	100	Masarei et al. (1972)
Fulani (pastoralist) (Cb8)	7	174	80.5	9	22	Kretchmer et al. (1971)
Fulani (sedentary) (Cb22)	7	174	40.5	24	71	Kretchmer et al. (1971)

Ganda (Ad7)	0	144	10.5	27	96	Cook and Kajubi (1966), Cook and Dahlquist (1968)
Greeks (Ce7)	8	162	30.5	800	52	Kanaghinis et al. (1974), Ladas et al. (1982)
Hausa (Cb26)	7	174	30.5	17	76	Kretchmer et al. (1971)
Hazara Tajiki (Ea3)	10	162	50.5	79	82	Rahimi et al. (1976)
Herero (Ab2)	9	178	60.5	37	97	Currie et al. (1978)
Hopi (Nh18)	10	162	10.5	21	100	Johnson et al. (1978)
Hungarian (Ch8)	7	124	20.5	535	37	Czeizel et al. (1983)
Hutu (Ae10)	2	145	30.5	51	51	Cook and Kajubi (1966), Cox and Elliott (1974)
Igbo (Af10)	4	144	10.5	16	81	Elliott et al. (1973), Olatumbosun and Adadevoh (1971), Ransome-Kuti et al. (1975)
Iranian (Ie9)	12	162	30.5	40 (>12 yrs)	83	Sadre and Karbasi (1979)
Irish (Cg3)	0	94	40.5	50	4	Fielding et al. (1981)
Italians (South) (Ce5)	4	124	10.5	197	67	De Ritis et al. (1970), Burgio et al. (1984), Rinaldi (1984), Cavalli-Sforza et al. (1987)
Japanese (Ed5)	1	162	10.5	66	81	Nose et al. (1979), Shibuya et al. (1970), Yoshida et al. (1975)
Javanese (Indonesia) (Ib2)	1	144	20.5	53	91	Surjono et al. (1973)
Jordanians (Cj6)	10	162	30.5	204	75	Hijaki et al. (1983), Snook et al. (1976)
Lapps (Cg4)	8	79	60.5	519	41	Isokoshi et al. (1981)
Lebanese (Cj7)	5	162	20.5	225	79	Loiselet and Jarjouhi (1974), Nasrallah (1979)
Mongols (Eb7)	10	124	80.5	198	88	Wang et al. (1984)
Nama (Aa3)	9	178	50.5	18	50	Jenkins and Nurse (1976)
Northern Chinese (Han)[c]	8	162	20.5	314	88	Wang et al. (1984), Zheng et al. (1988)
Nubians (Midobi) (Cb11)	12	174	93	21	67	Bayoumi et al. (1981)
Nuer (Aj3)	5	144	50.5	23	78	Bayoumi et al. (1982)

Table 1. (*continued*)

Population and Ethnographic Atlas Code	*Number of Dry Months per Year*	*Global Solar Radiation (kcal/cm/yr)*	*Pastoralism as Proportion of Total Subsistence Activity (%)*	*Total Number of Individuals Tested in Each Population*	*Frequency of Low LDC (%)*	*Reference*
Papago (Ni2)	10	162	0	14	93	Johnson et al. (1978)
Pathans/Pushtu (Ea2)	10	162	30.5	86	65	Rab and Baseer (1976), Rahimi et al. (1976)
Pima (Ni6)	10	162	0	62	95 (>4 yrs)	Johnson et al. (1977), Johnson et al. (1978)
Punjabis (Ea13)	5	162	20.5	384	56	Rab and Baseer (1976), Ahmad and Flatz (1984), Abbas and Ahmad (1983)
Russians (Ch11)	6	94	30.5	103	57	Lember et al. (1991)
San (!Kung and #hua)[d]	9	178	0	65	95	Jenkins et al. (1974), Nurse and Jenkins (1974)
Shilluk (Ai6)	10	144	20.5	8	63	Bayoumi et al. (1982)
Sindhi (Ea1)	11	192	30.5	45	42	Rab and Baseer (1976), Ahmad and Flatz (1984)
Sinhalese (Eh6)[e]	0	144	30.5	158	73	Senewiratne et al. (1977)
Sotho (Ab8)	5	178	30.5	23	65	Segal et al. (1983)
Spanish (Ce6)	5	162	30.5	265	15	Pena Yanez et al. (1971, 1972)
Swazi (Ab2)	4	192	20.5	12	75	Segal et al. (1983)

Tamils (Eg2)[e]	0	144	20.5	31	71	Senewiratne et al. (1977)
Thai (Ej9)	4	174	10.5	339	98	Flatz and Saengudom (1969), Flatz et al. (1969), Keusch et al. P(1969), Rotthauwe et al. (1971)
Tswana (Ab13)	6	178	40.5	24	83	Segal et al. (1983)
Tuareg (Aulliminden) (Cc8)	8	144	60.5	118	13	Flatz et al. (1986)
Tunisians (Cd16)	8	162	20.5	43	83	Filiali et al. (1987)
Turks (Ci5)	6	162	40.5	470	71	Flatz et al. (1986)
Tutsi (Ae10)	2	145	40.5	59	7	Cook and Dahlquist (1968), Cook and Kajubi (1966), Cox and Elliott (1974), Elliott et al. (1973)
Xhosa (Ab11)	3	178	30.5	17	82	Segal et al. (1983)
Yoruba (Af6)	4	144	10.5	100	91	Kretchmer et al. (1971), Olatunbosun and Adadevoh (1971), Ransome-Kuti et al. (1975)
Zulu (Ab12)	3	178	40.5	32	81	Segal et al. (1983)

a. *Ethnographic Atlas* not used. Subsistence practices and longitude and latitude taken from Brand et al. (1983).

b. 6–15% dependence on livestock, but pig-based livestock economy.

c. Shantung Chinese, Murdock (1967) ref. Ed10, cluster 163, used.

d. Nyae Nyae Kung, *Ethnographic Atlas*, ref. Aa1, used.

e. Longitude and latitude of Sri Lanka used, instead of using *Ethnographic Atlas*.

for the lactase persistence gene to reach observed frequencies in the time available. In this case these traits would not be truly coevolutionary, because selection for milk consumption would not depend on the gene for lactase persistence.

Materials and Methods

One way to test the three hypotheses would be to regress the relevant environmental variables (pastoralism, sunshine intensity, and aridity) against the prevalence of adult LDC in different populations worldwide. However, the relationships between environmental variables and LDC are highly confounded by the shared ancestry of many human groups. Shared ancestry of several variables can either produce a spurious, apparently functional relationship between variables or obscure a real association between variables (Mace and Pagel 1994).

For example, the association between high latitude and high LDC in Europe could be parsimoniously interpreted as the result of northern European populations sharing a relatively recent common ancestral population in which high LDC was prevalent. It is not necessarily correct to count each case of high prevalence of LDC in northern European populations (e.g., in the Irish, British, Danes, Norwegians, and Finns) (Sahi 1994) as an independent evolutionary adaptation, providing independent statistical evidence for the correlated evolution of high LDC capacity and living at high latitudes.

Alternatively, many sedentary Arab populations in North Africa and the Middle East have predominantly low LDC, although livestock were originally domesticated in this region about 10,000 years ago (Table 1). These populations present a challenge to the hypothesis that adult LDC is an evolutionary adaptation to keeping domestic livestock. However, if these populations are viewed historically, it is clear that they share a recent common ancestor (Figures 1 and 2). A parsimonious interpretation of the prevalence of low LDC in sedentary Arabs is that low LDC was prevalent in a common ancestor of these populations. This reduces the challenge that is presented by these populations to the culture-historical hypothesis if they are all counted separately.

Phylogenetic comparative methods overcome these problems by placing all the populations on a phylogeny and by measuring the amount of *change* along the branches of the tree (Felsenstein 1985). Regression analysis is done on independent occurrences of change in the relevant variables along the branches of the phylogeny, known as contrasts, rather than just on the branch tips, or populations as they are seen today (Pagel 1992).

Both genetic and cultural phylogenies were used as models of the historical relationships between populations, because both genetic and cultural transmission might be implicated in the evolution of high LDC since lactase persistence is a genetic trait, whereas pastoralism and milk drinking are cultural traits. The phylogenies used here represent only estimates of past relationships between populations, but they are assumed to be better approximations of the past than would be obtained without a phylogenetic model. Not explicitly using a phylogeny implicitly

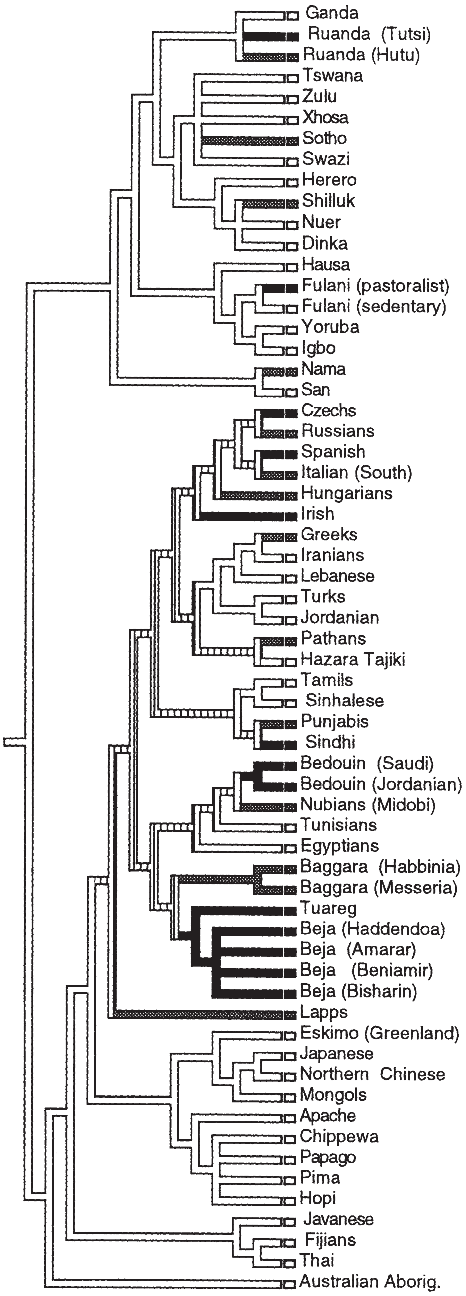

Figure 1. First genetic tree of populations used in analysis, using Cavalli-Sforza's F_{ST} linkage tree (Cavalli-Sforza et al. 1994, p. 78), showing frequencies of lactose malabsorption in these populations. Lactose malabsorption frequencies are grouped into three levels here for illustrative purposes only: black, 0–30%; shaded, 30–70%; white, >70%.

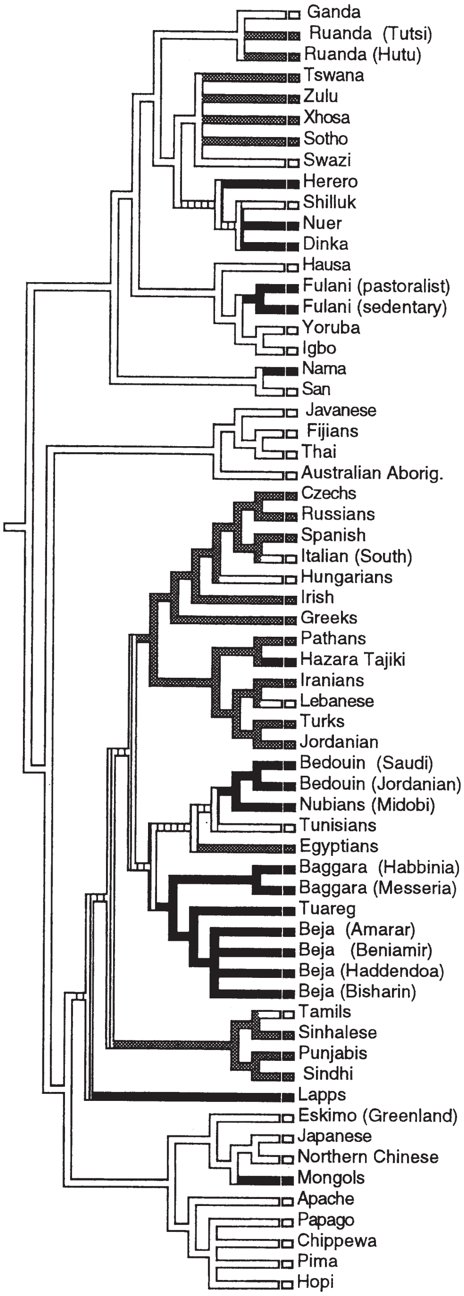

Figure 2. Second genetic tree of populations used in analysis, a modified Nei linkage tree (Cavalli-Sforza et al. 1994, p. 78), showing percentage of dependence on pastoralism in these populations. Dependence on pastoralism is grouped into three levels for illustrative purposes only: black, >50% dependence; shaded, 30–50% dependence; white, 0–30% dependence.

assumes that all populations are equally related to one another, which is certainly a less accurate representation of the past than the models used here.

An analysis using a maximum-likelihood method (Pagel 1994) was also performed. This method gives information about the direction of evolutionary change, that is, about which variable changed first in the course of evolution.

Data. The data used in this analysis were selected from comprehensive reviews by Simoons (1978), Flatz (1987), and Sahi (1994) and from a literature search of the *Science Citation Index* from 1981 to 1996 using the terms "lactose absorption" and "lactose malabsorption." Except where stated in Table 1, only samples from adults were included.

The comparative method employed in this analysis requires that all the populations be placed on a genetic and linguistic tree to model the historical relationships between populations. All populations included are found in Cavalli-Sforza et al.'s *History and Geography of Human Genes* (1994) and therefore can be placed on a world genetic tree. Cavalli-Sforza et al. (1994) include only aboriginal populations, defined as populations present in their current locations before 1492. Recent migrant populations were excluded, including all nonnative Americans and non-Aboriginal Australians. All samples of emigrant populations were also omitted here to decrease the probability of recent genetic admixture in the data set. Samples from populations recognized to have mixed ancestry in the original studies were excluded. Because a linguistic tree was also used in this analysis, all samples are also from populations whose language or language group is listed in Ruhlen's *Guide to the World's Languages* (1991). A number of language synonyms were found in Voeglin and Voeglin's (1977) book.

All the samples used here come from populations represented in the *Ethnographic Atlas*, a cross-cultural database originally written by Murdock (1967) and currently in the process of being revised and computerized by P. Gray (personal communication). Data on pastoralism and geographic location were taken from this source. The *Ethnographic Atlas* code for each population is included in Table 1. The Australian Aborigines are an exception. They are not a single *Ethnographic Atlas* culture, but they are a genetically monophyletic group [according to Cavalli-Sforza et al. (1994, p. 78)] who were traditionally hunter-gatherers without domesticated livestock.

In total, 7905 individuals from 62 distinct cultures (as recognized in the *Ethnographic Atlas*) were included in the data set. The greatest loss of individual samples resulting from the selection criteria was from the nonaboriginal populations of the Americas and Australia. More important for the aims of this study, a number of samples from anthropological populations were unable to be used because these populations are not known genetically or are not included in the *Ethnographic Atlas*. Anthropologically interesting populations that could not be included were the hunter-gatherer Khants from western Siberia (94% lactose maldigesters; Lember et al. 1995) and several other groups from the former Soviet Union (Sahi 1994), the pastoralist Kasakhs (Wang et al. 1984), the Roma

(Gypsies) (56% lactose maldigesters; Czeizel et al. 1983), and various Indian groups (45% lactose maldigesters in North India, 67% in South India; Tandon et al. 1981). The inclusion criteria applied here, however, had the advantage of allowing all populations to be compared using the same source of variables, such as pastoralism, which had been previously quantified by an independent researcher. It also allowed the use of different trees as models of human evolution, with the same data set of populations in each tree.

The longitude and latitude of each population were taken from the *Ethnographic Atlas*.

The *Ethnographic Atlas* estimates the percentage of dependence on livestock in each population's total subsistence activities. Pastoralism in this analysis is a quantitative cultural trait, not a qualitative category. The midpoint of the *Ethnographic Atlas* estimate was used as a measure of pastoralism here (e.g., where Murdock coded a culture's reliance on livestock as 3, that is, 26–35% of total subsistence activities, this was counted as 30.5% dependence here). Pastoralism is used here only in reference to livestock capable of being milked, thus permitting the evolution of LDC if the culture-historical hypothesis is correct. The *Ethnographic Atlas* also states the main type of livestock kept and whether or not milking was traditionally practiced. If the main type of animals kept was recorded as pigs or small domestic animals (e.g., dogs), the society is recorded as nonpastoralist here (0% dependence). The analysis was repeated twice, firstly including and then excluding pastoralists who traditionally did not milk their animals. Populations that kept livestock but did not milk them are found in China and southeast Asia and in parts of sub-Saharan Africa (Murdock 1967; Simoons 1970).

No distinction is made in this analysis between populations that consume predominantly processed, low-lactase forms of milk and populations that consume significant amounts of fresh milk, with a high lactose content. Ethnographic evidence suggests that milk-processing technologies are present in all dairying or pastoralist groups today. In hot climates such as Africa and the Middle East milk is soured naturally if it is left to stand. It seems probable that milk-processing technologies were present early in the history of milking domestic animals. It is therefore assumed here that all pastoralists have had equally effective milk-processing technology, whether they lived 6000 years ago or more recently. This assumption contrasts with Durham (1991), who interprets the high frequencies of high LDC in some present-day North African pastoralists as the outcome of their adopting a pastoralist mode of subsistence early on, before the full development of milk-processing technologies.

An estimate of aridity was taken as the number of months per year with less than 50 ml of rainfall in the area inhabited by each population (Pearce and Smith 1993). Other measures of aridity were tried, including average annual rainfall and average rainfall in environments above 30°C, but this made no difference to the outcome of the analysis. The sunshine experienced by each population was estimated from the global solar radiation for land at that longitude and latitude (Kessler 1985).

Statistical Methods. Correlated evolution of high LDC was tested with the following quantitative traits: dependence on pastoralism (%), solar radiation, and (alternatively) dry months per year and average rainfall. Independent contrasts (which are measures of change at each branch of the tree) were generated by following the method of Pagel (1992), which is implemented in the computer program CAIC (Purvis and Rambaut 1995). Regressions on the contrasts are through the origin (Pagel 1992). We assume that all the branch lengths on the trees are equal. LDC was used as the special variable to resolve unresolved nodes.

Two alternative genetic trees were tested, both taken from Cavalli-Sforza et al. (1994). These two trees were constructed using different methods of calculating genetic distance. The first is an F_{ST} linkage tree by Cavalli-Sforza (Figure 1). The second was constructed using Nei's modified method of calculating genetic distance (Figure 2). The cultural descent of populations was modeled using a language tree based on the classifications of Ruhlen (1991) and assuming a monophyletic origin of language (Figure 3). On a worldwide scale language groups show a broad correspondence with genetic relationships (Cavalli-Sforza et al. 1988). The world language phylogeny used here is less resolved than the genetic trees because of the lack of resolution above the language phylum level. Because language evolves much more rapidly than genes do, similarities resulting from deep historical relationships are generally considered completely obscured after 10,000 years of divergence [although see Cavalli-Sforza et al. (1988) and Ruhlen (1991) for an opposing argument]. Because of the lack of resolution back through time, using the language tree was rather similar to using a test involving only the tips of the genetic trees. The genetic and linguistic trees in Figures 1 through 3 were drawn using the software MacClade. The variables were traced onto the branches of each tree using parsimony (Maddison and Maddison 1992).

Statistical tests using independent contrasts depend on inferring, by parsimony, a single set of values at the internal nodes of the genetic tree. Where characters evolve rapidly and repeatedly, as is likely to be the case with cultural traits, parsimony methods may give unreliable answers. Pagel (1994) describes a comparative method for analyzing binary discrete characters that does not require inferring a particular pattern of changes at internal nodes. This method finds evidence for correlated evolution in two discrete characters by considering all the possible transitions among traits on a phylogeny. The method can test hypotheses about the extent to which the evolution of one trait is likely to be correlated with the evolution of another and can also test hypotheses about the direction of evolutionary change.

The test begins by fitting two alternative statistical models to a data set. The model of independent change allows the two binary variables to evolve independently of each other along each of the branches of the tree. The model of dependent change makes the probability of change in one variable dependent on the state of the other variable. We are interested in whether the dependent variable LDC is more likely to change from low to high if the dependent variable milking is present. The independent and dependent models of change are fitted

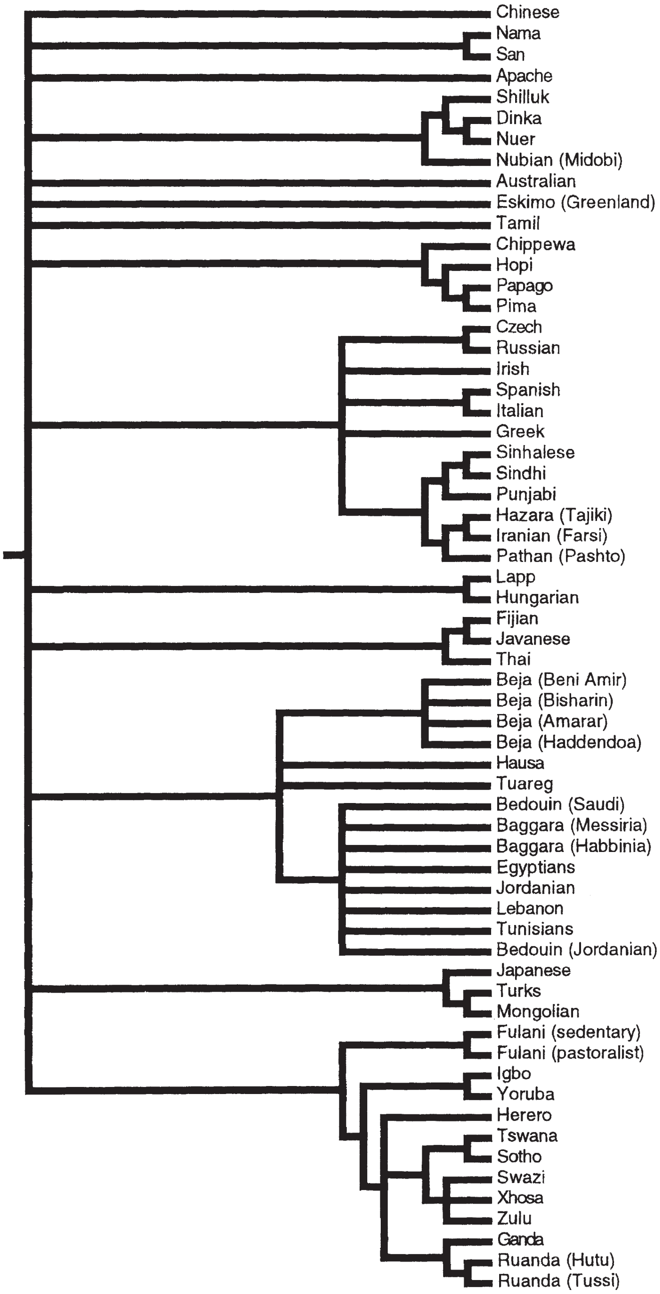

Figure 3. Linguistic tree for populations used in analysis, based on Ruhlen (1991), assuming a monophyletic origin of language.

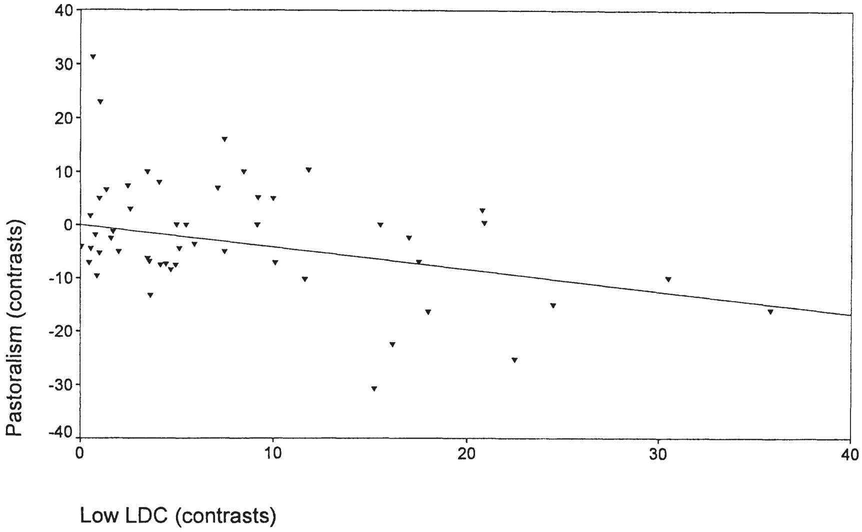

Figure 4. Independent contrasts in LDC and pastoralism, using the F_{ST} genetic tree. The x axis is a measure of *low* LDC (hence the negative relationship with pastoralism). The regression is through the origin. The appearance of this plot using the Nei genetic tree is virtually identical.

to the data by a technique known as maximum likelihood, which chooses a set of values for the parameters (rates of character change) of both models that make the observed data more likely, given the phylogenetic relationships between populations. This can determine whether the model of dependent change fits the data better than the model of independent change. The test statistic compares the log-likelihood (a measure of goodness of fit) for the model of independence with that for the model of dependence. The method is implemented using the computer program DISCRETE (available from M. Pagel, Department of Zoology, Oxford University).

The phylogeny used for the analysis using DISCRETE was the F_{ST} genetic tree, slightly modified to create a completely resolved tree, which this method requires (Figure 4). Resolution was achieved by resolving multiple genetic nodes on linguistic relatedness where possible (Ruhlen 1991). The Beja groups and the Zulu, Ngoni, and Swazi were pooled. These groups had no variation in the relevant variables. It was assumed that all the branch lengths are equal. The tree used is shown in Figure 5. Because this method analyzes discrete variables, LDC was divided into a high LDC/low LDC discrete variable, following its binomial distribution in the populations included in this analysis (Figure 6). Populations with high LDC have >70% prevalence of high LDC. Milking (traditionally present or absent; data from the *Ethnographic Atlas*) was the variable used to measure

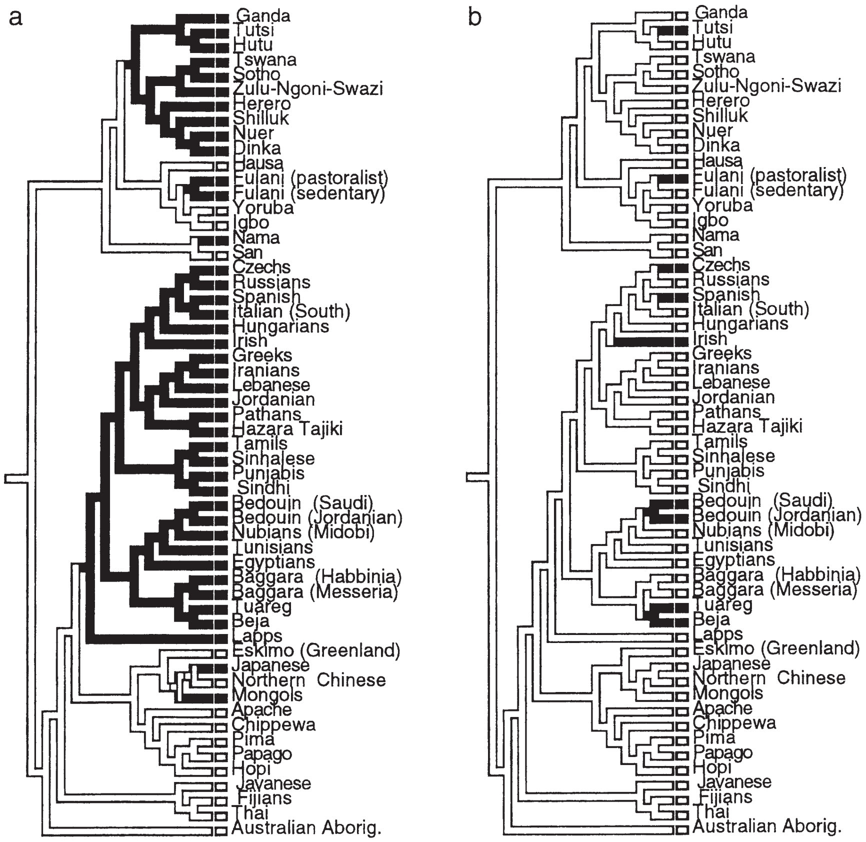

Figure 5. (a) Tree used for the maximum-likelihood analysis, using DISCRETE, based on the F_{ST} genetic tree. Black indicates milking populations, and white indicates nonmilking populations. (b) Tree used for the maximum-likelihood analysis, using DISCRETE. Black indicates high LDC populations, and white indicates low LDC populations, following the bimodal distribution of this trait seen in Figure 7.

pastoralism in this analysis, because it is a discrete variable. The distribution of milking and high LDC are shown in Figure 5.

Results

Figures 1 and 2 show the two alternative genetic trees used in the analysis. Figure 1 also shows the variation in LDC in populations throughout the world, divided into high, medium, and low prevalences of low LDC for illustrative purposes. High prevalences of high LDC are mostly clustered within the Indo-European–North African clade. Apparently, independent instances of evolution of high LDC are scattered throughout the sub-Saharan African clade. As expected

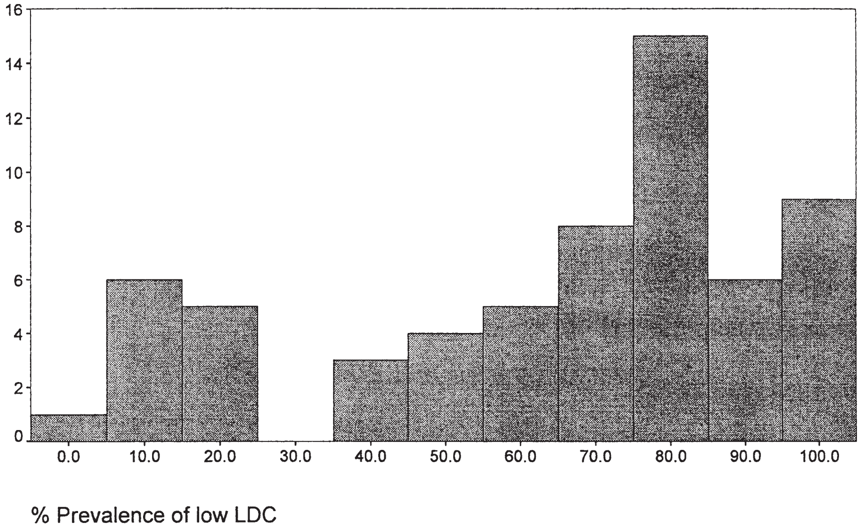

Figure 6. Bimodal distribution of LDC phenotypes in the populations in this analysis, showing prevalence of low LDC phenotypes (%) in the study populations. (High LDC populations are on the left of the histogram.)

from the geographic distribution of this trait, high LDC is virtually absent in the southeast Asian, east Asian, and native American clades.

Dependence on livestock in populations throughout the world is shown in Figure 2. A comparison of Figures 1 and 2 shows that the pattern of livestock dependence is broadly similar to the distribution of LDC but that the distribution of livestock dependence is more widespread than that of LDC. The root of the Indo-European–North African clade shows a moderate to high dependence on livestock (the ambiguity represented by the shading in the figures indicates that it is uncertain whether this dependence was high or moderate), which is consistent with archeological evidence of the antiquity of domestic livestock in the Middle East and North Africa (Clutton-Brock 1987; Sherratt 1980). In sub-Saharan Africa the root of the Bantu-Nilotic clade shows a moderate to high dependence on livestock, but pastoralism is absent from deeper nodes within the sub-Saharan part of the tree.

Using a phylogenetic analysis, whichever phylogeny is used, the percentage of reliance on pastoralism today explains the greatest amount of variance in LDC between populations worldwide (Table 2). Neither solar radiation nor number of dry months per year is significantly associated with the variation in the frequency of LDC in any of the regressions.

It did not make a significant difference to the results whether the populations that traditionally kept livestock but did not milk their animals were counted as pastoralists or not. Counting these populations as nonpastoralist slightly increased

Table 2. Multiple Regressions Through the Origin Using Independent Contrasts and Three Different Trees and Showing Changes in Lactose Digestion Capacity (Measured as Low LDC) as a Dependent Variable of Pastoralism, Sunshine, and Aridity[a]

	F_{ST} Genetic Tree		*Nei's Genetic Tree*		*Language Tree (60 Populations)*	
Variable	*Coefficient*	*Significance*	*Coefficient*	*Significance*	*Coefficient*	*Significance*
Pastoralism	–0.464	0.0016	–0.456	0.0015	–0.661	0.0034
Solar radiation	0.113	n.s.	0.062	n.s.	–0.322	n.s.
Aridity	0.0598	n.s.	0.291	n.s.	–1.199	n.s.
Overall significance of multiple regressions						
Multiple *R*		0.45		0.45		0.52
R^2		0.20		0.20		0.27
Significance (*F*)		0.0131		0.0109		0.024

a. No interactions were significant.

the association between pastoralism and high LDC, as the culture-historical hypothesis predicts, but the significance level of the result was not changed. These populations formed a small proportion of the populations included here.

The maximum-likelihood independent model yielded a log-likelihood of −41.46. The model of dependent change had a log-likelihood of −37.04. These numbers are logarithms of probabilities, and the more strongly negative numbers represent probabilities closer to 0. The dependent model is therefore more likely. To assess whether the difference is significant, we used the likelihood ratio statistic, defined as

$$\mathrm{LR} = -2 \log[I/D] = -2[\log(I) - \log(D)], \tag{1}$$

where *I* and *D* represent the independent and dependent models, respectively. The software generates a probability distribution similar to a chi-square distribution, which is used to measure the significance of the likelihood ratio statistic. In this case the probability that there is a relationship between the evolution of high LDC and milking, LR = 8.83, is significant at $p < 0.05$.

This finding corresponds with the finding from the analysis by independent contrasts that the evolution of the two traits is highly correlated. However, the maximum-likelihood method also gives us information about the direction of evolutionary change. Figure 7 shows all the possible pathways of evolutionary change. Which particular pathways of change are most likely to have occurred can be established by comparing the full dependent model with a model in which the probability of one of the rates of transition has been set to 0. If a model where one pathway has been set to 0 is much less likely to have occurred than the full model, then this pathway of evolution is likely to have been important. Conversely, if the likelihood ratios of the two models are not significantly different, then it is unlikely that there has been much evolutionary change in this direction. The significance of

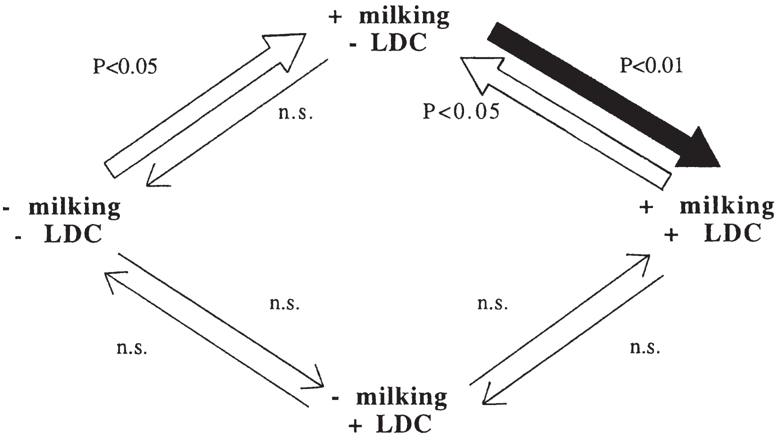

Figure 7. Direction of evolution of high LDC, estimated using maximum likelihood. Milking evolves first, and evolution of high LDC is highly dependent on milking. According to this model, some populations that evolved high LDC may also have lost it again.

each evolutionary transition is shown in Figure 7. From an ancestral condition of no milking (− milking in Figure 7) and low LDC (− LDC in Figure 7), milking (+ milking in Figure 7) probably evolved first, followed by the evolution of high LDC. In some cases some milking populations that evolved high LDC may have subsequently lost high LDC. It appears that high LDC never evolved without the prior presence of milking. This further supports the hypothesis that high LDC is an adaptation to dairying.

Discussion

The results of this analysis support the culture-historical hypothesis that adult LDC evolved in populations that kept livestock. These results do not support Flatz and Rotthauwe's (1973) hypothesis that fresh milk consumption and LDC are additionally selected for in high-latitude, low-sunshine environments. Cook and Al-Torki's (1975) arid environment hypothesis, which would predict an increase in LDC in drier environments, was also not supported in this analysis. The analysis using a maximum-likelihood method shows that the evolution of high LDC is strongly associated with the presence of pastoralism and further that pastoralism is always adopted before high LDC evolves.

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