refuse zone adjacent to structure 2-77. The second dates the upper surface of this zone and several cairns. The other nine dates are consonant, given statistical probability. The earliest date may be too early for Valdivia I, but the second date is in accord with those from another early Valdivia site, Loma Alta. A period around 3300 B.C. seems plausible for the appearance of Valdivia on the Ecuadorian Pacific coast.

After the identification of the original three carbon samples, the Real Alto carbonized materials were reexamined for fragments of dense carbon similar to the cotyledon fragments in the three original samples. Another sample, CS 93, also excavated in 1977, contained five such fragments. Sixteen other fragments were found in samples from the Valdivia I, Valdivia III, Valdivia IV/V, and Valdivia VI phases and nine fragments from as yet undated Valdivia features (*4*). This suggests that *Canavalia* was used during Valdivia I times and throughout the occupation of Real Alto. The possibility that *Canavalia plagiosperma* was present at Real Alto as a domesticate and was used as a food resource by the Valdivians is thus supported.

Other findings suggestive of the presence of agriculture during the Early Formative of Ecuador include phytoliths (silica bodies deposited in the leaves of certain plant families) identifiable as a maize type, which occur as early as Valdivia I at Real Alto and continue throughout the later Valdivia and Machalilla occupation (*3*, *4*). Beginning in Valdivia III, phytoliths identified as Cannaceae, the family of the edible cultivated achira *Canna edulis*, also occur. Since there are no native Cannaceae on the coastal plain of southwestern Ecuador, the introduction of cultivated *Canna* is a possibility.

The prehistoric occurrence of the South American domesticated *Canavalia plagiosperma* is known for coastal Peru beginning with the Late Preceramic (about 2500 to 1800 B.C.). *Canavalia* was recovered by Bird at Huaca Prieta in coastal Peru (*7*). Connections between Huaca Prieta and Valdivia have been suggested (*1*). The presence of the wild and possibly ancestral forms of *C. maritima* and *C. brasiliensis* in western Ecuador and of *C. maritima* extending into extreme northern Peru (*8*) indicates that this region was probably a site of early *Canavalia* domestication. The Real Alto data give chronological priority to a northern Ecuadorian origin.

One additional point is significant. *Canavalia* species are confined to humid areas. Irrigation in some form is necessary for growing the domesticated species in areas with short rainy seasons. Since the southwesternmost part of Ecuador is an area of marginal rainfall with a short rainy season, the presence of prehistoric *Canavalia* at Real Alto indicates a wetter area of origin for Valdivia, possibly the Colonche hills and the Guayas Basin of Ecuador.

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Microparticle Concentration Variations Linked with Climatic Change: Evidence from Polar Ice Cores

Abstract. *The microparticle concentrations in three deep ice cores reveal a substantial increase in the concentration of insoluble particles in the global atmosphere during the latter part of the last major glaciation. The ratio of the average particle concentration in the late glacial strata to that in the Holocene strata is 6/1 for the core from Dome C, Antarctica, 3/1 for the core from Byrd Station, Antarctica, and 12/1 for the core from Camp Century, Greenland. Whether this temporal correlation between increased atmospheric particle load and the lower surface temperatures is directly causal is unknown; however, the variations in these two parameters must be satisfactorily resolved in any successful hypothesis that addresses the causes of climatic change.*

The dry snow facies of the continental ice sheets and ice caps contain particulate material and isotopic species that provide information about the physical properties of the atmosphere at the time of precipitation formation and deposition. These data must be interpreted cautiously, as the complex relationship between particles (and gases) in the atmosphere and those in the associated precipitation is poorly understood (*1*). Nevertheless, a substantial increase in the quantity of material suspended in the global atmosphere should be recorded within the particle stratigraphy of the polar ice sheets.

The concentration and size distribution of insoluble particles within firn and ice cores are determined by the Coulter technique conducted within a class 100 clean room (*2*). Thus far, three ice cores encompassing at least the end of the last major glaciation (correlative with the Late Wisconsin or Würm stage) and the postglacial (Holocene) strata have been analyzed for microparticle concentration and the $^{18}O/^{16}O$ ratio ($\delta^{18}O$), a paleoclimatic indicator revealing the glacial-postglacial transition. These three cores are those from Byrd Station, Antarctica (2164 m) (*3*, *4*); from Camp Century, Greenland (1387 m) (*5*, *6*); and from Dome C, Antarctica (905 m) (*7–9*).

The examination of individual particles by light microscopy and scanning electron microscopy coupled with elemental analysis by an x-ray energy-dispersive system (XEDS) is a routine part of the microparticle analysis procedure (*10*). The Camp Century core particles are composed primarily of clay minerals (*5*, *11*), whereas both clay fragments and volcanic glasses were found in the Byrd core (*2*). These volcanic glasses are much more abundant in the late glacial sections of the Byrd core than in the overlying Holocene sections. The XEDS analyses are conducted only for particles with diameters greater than 5 μm, as the analysis of smaller particles is unreliable.

The particles in the Dome C core fall into two distinct classes according to size. The smaller particles (with diameters ≤ 2 μm) are more abundant by three or more orders of magnitude. The less abundant, larger particles (diameters be-

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tween 60 and 80 μm) are predominantly volcanic glass fragments which exhibit a much greater frequency of occurrence in sections below 500 m in this core. Those glasses that have been analyzed with the electron microprobe are nearly identical in morphology and chemistry to those found within several ash bands in the Byrd core and whose source has been suggested to be Mount Takahe, Antarctica (*12*).

The smallest fragments in the Dome C core are too small for quantitative chemical analysis and do not exhibit a distinguishable morphology. Their source or sources are unidentified. This insoluble material may represent a diverse mixture composed primarily of global stratospheric material brought to the surface by the descending motions over the Antarctic Plateau (*13*) and a smaller component of tropospheric material transported by cyclonic disturbances which periodically penetrate the plateau region.

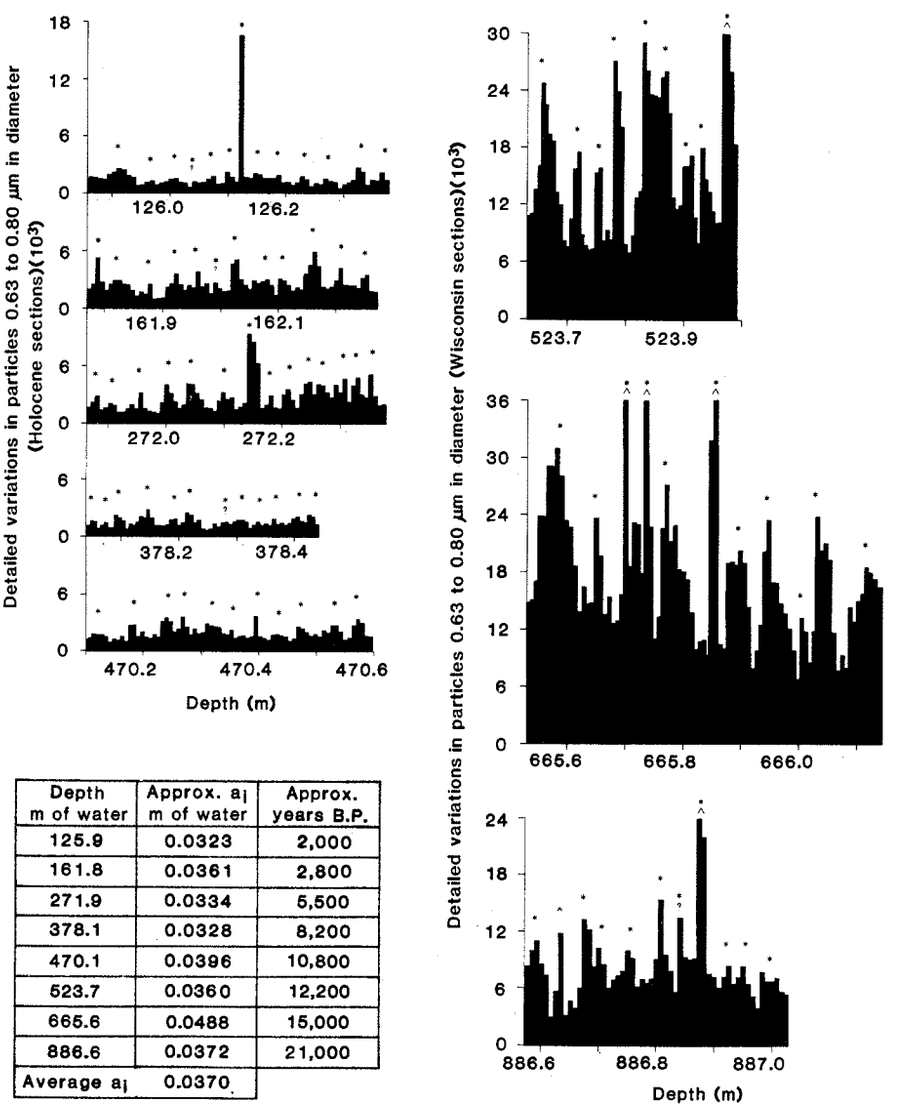
The 905-m core from Dome C, Antarctica (74°39'S, 124°10'E, 3240 m above sea level), was drilled as part of the International Antarctic Glaciological Program (*14*), and 51 sections provided by the French were analyzed for microparticle concentration and size distribution. The microparticle analysis of 5367 samples representing these 51 sections (averaging 0.76 m in length) comprises the most detailed microparticle record from any deep core. The average sample size of 0.0067 m of ice coupled with the annual accumulation of 0.035 m of ice (*15*) yields a resolution of 5.5 samples per accumulation year.

Accurate dating of ice cores is essential for interpreting any proxy data obtained from ice cores as well as for comparison of the core record with existing records. Dating of strata older than 100 years is a particular problem on the central Antarctic Plateau where accumulation rates are low (< 0.1 m/year) (*16*) and where the deepest cores, and hence the longest records, will be obtained. Cyclical variations in insoluble microparticle concentrations in the 101-m South Pole core were found to be annual features (*10*). The detailed analysis of the Dome C core sections revealed similar cyclical variations in particle concentration (Fig. 1). A Dome C pit study (*8*) and the net accumulation rates deduced from the microparticle variations in each core section (*8, 9*) support the annual character of these microparticle features.

Figure 1 presents the concentrations of small particles (0.63 μm ≤ diameter < 0.80 μm) (*C*) for five sections from the postglacial strata and three sections from the glacial strata of the Dome C core, respectively, and the average vertical layer separation (a_i) in water equivalent for each section. These estimates are in good agreement with the current estimate of net annual surface accumulation, 0.035 m of ice per year (density = 920 kg/m^3) or 0.032 m of water per year (*15*); these results suggest that these particle concentration peaks are annual. The problems that plague all stratigraphic interpretations (for example, missing years) are present here, but the solution must await the absolute dating of ice strata older than 100 years.

These annual features can be used to construct a relative time scale for the Dome C core as detailed in (*8, 9*). The maximum estimate for the age at the bottom of this core is 30,000 years, which is slightly older than the 27,000 years derived from Nye's model discussed in (*7*). Using an entirely different approach, Lorius *et al.* (*7*) estimated the age at the bottom to be 32,000 years. This older age was obtained by assuming lower accumulation rates at core depths greater than 381 m. On the basis of 51 sections of the Dome C core analyzed, no consistent or substantial reduction in net surface accumulation exists (*8, 9*).

In the Dome C core the largest increases in *C* are temporally correlated with the most negative $\delta^{18}O$ measurements (lowest temperatures). The Byrd and Camp Century cores also exhibit very substantial increases in particle concentration in association with more negative $\delta^{18}O$ values representing the last major glaciation (Fig. 2). The average concentration of particles (diameters



Depth m of water	Approx. a_i m of water	Approx. years B.P.
125.9	0.0323	2,000
161.8	0.0361	2,800
271.9	0.0334	5,500
378.1	0.0328	8,200
470.1	0.0396	10,800
523.7	0.0360	12,200
665.6	0.0488	15,000
886.6	0.0372	21,000
Average a_i	0.0370	

Fig. 1. Concentration of particles with diameters greater than or equal to 0.63 μm and less than 0.80 μm for five sections from the Holocene (upper 500 m) (left) and for three sections from the late glacial portion (lower 400 m) (right) of the Dome C, Antarctica, ice core; * indicates annual features, ? indicates questionable features, and ∧ indicates values exceeding the ordinate scale. At the lower left is listed the vertical layer separation (a_i) in meters of water equivalent for each of the eight sections illustrated.

≥ 0.6 μm) in all sections of the Camp Century core is 7.8 times that in the Byrd core and 5.7 times that in the Dome C core. This large concentration in the Camp Century core reflects the extensive particulate source areas in the Northern Hemisphere.

To obtain an estimate of past background levels of insoluble particles for comparison with $\delta^{18}O$ measurements, the average number of particles with diameters between 0.6 and 0.8 μm in the cleanest 10 percent of all samples ($\bar{C}_{10}$) is calculated for each core section and illustrated in Fig. 2b. A statistical examination of the relationship between $\delta^{18}O$ and $\bar{C}_{10}$ (*9*) indicates that the two variables are not independent at the 99.9 percent confidence level. Nevertheless, a cause-and-effect relationship cannot be assumed as the variation in both particle concentration and $\delta^{18}O$ could be produced by some as yet undetermined forcing function.

The ratio of the average particle concentration in sections representing the end of the last glacial to the average concentration for postglacial sections (Fig. 2a) is 6/1 for the Dome C core, 3/1 for the Byrd core, and 12/1 for the Camp Century core. This increase is probably due to a corresponding increase in atmospheric particle loading, a reduction in annual net accumulation, or some combination of these factors. In each core the particle concentration falls off rapidly during the transition into the Holocene (Fig. 2). Either the net accumulation regime at each site was rapidly altered, diluting the particles, or the particle source was rapidly diminished.

The increase in C in the late glacial sections of each core exceeds that expected merely from a reduction in net accumulation alone. In the Dome C core, for example, the sixfold increase in the average particle concentration for sections below 500 m far exceeds any concentration resulting from a 30 to 40 percent reduction in net accumulation as is suggested to have occurred (*7*). The accumulation data discussed above (see also Fig. 1) and presented in detail in (*8*, *9*) exhibit little variation within the 51 sections analyzed.

On the basis of these data, it is not likely that reduced accumulation can account for the increase in particles. It is more probable that a substantial quantity of additional material was added to the global atmosphere near the end of the last glaciation. Whether the material is volcanic or loess has yet to be determined. Nevertheless, the relationship between this increase in atmospheric particles and the reduction of global temperatures must be resolved satisfactorily in any successful hypothesis that addresses the causes of climatic change.

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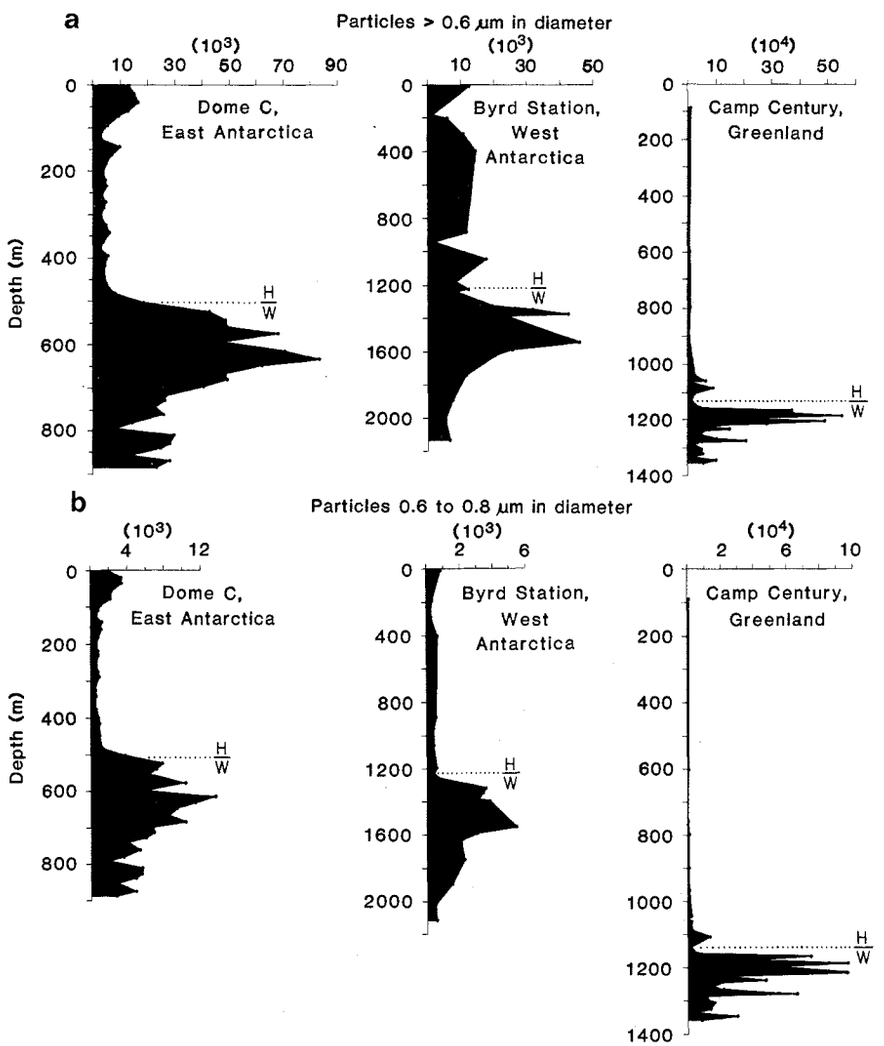

Fig. 2. (a) The average concentration of particles with diameters greater or equal to 0.6 μm for all samples in each section; (b) the concentration of particles with diameters between 0.6 and 0.8 μm in the cleanest 10 percent of the samples in each section of three deep ice cores encompassing the end of the last major glaciation. The transition into the Holocene (designated by *H*/*W*) is based upon the $\delta^{18}O$ record for each of the cores as compiled by Lorius *et al.* (*7*) for the Dome C core, Epstein *et al.* (*4*) for the Byrd Station core, and Dansgaard *et al.* (*6*) for the Camp Century core. To accommodate the high particle concentrations in the Camp Century core, the abscissa scale is increased by one order of magnitude.

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The Prolactin Gene Is Located on Chromosome 6 in Humans

Abstract. *The gene for prolactin has been located on chromosome 6 in humans. DNA fragments of 4.8 and 4.0 kilobases containing prolactin gene sequences were identified in human genomic DNA, whereas DNA fragments of 7.4, 3.6, and 3.3 kilobases containing prolactin gene sequences were found in mouse cells. In somatic cell hybrids of human and mouse cells the 7.4-, 3.6-, and 3.3-kilobase mouse fragments were always present, whereas the 4.8- and 4.0-kilobase human fragments were only present when human chromosome 6 was also present. We conclude that the prolactin gene resides on chromosome 6, a different location from those of the genes for the related hormones chorionic somatomammotropin and growth hormone.*

The polypeptide hormones growth hormone, chorionic somatomammotropin (placental lactogen), and prolactin belong to a common family (*1, 2*). Human growth hormone and chorionic somatomammotropin are composed of 191 amino acid residues and are closely related, with about 85 percent homology in their amino acid sequences (*3, 4*). Human prolactin is composed of 199 amino acid residues and is more distantly related, having only 26 percent homology with human growth hormone and 27 percent homology with chorionic somatomammotropin (*4*). The human growth hormone and human chorionic somatomammotropin messenger RNA's (mRNA's) have 92 percent homology, whereas the human prolactin mRNA has 42 percent homology with human growth hormone and 41 percent homology with chorionic somatomammotropin sequences (*4–6*). The genes coding for these three polypeptide hormones are believed to have originated from a common ancestral gene by duplication. Prolactin is thought to be the oldest member of this group (*4, 7, 8*). While the human growth hormone, chorionic somatomammotropin, and a third growth hormone–like gene have been located on chromosome 17 (*9*), the chromosome localization of the human prolactin gene (*prl*) was not known.

We report here that the prolactin gene is not on the same chromosome as the growth hormone gene, the chorionic somatomammotropin gene, and the growth hormone–like gene; rather it is located on chromosome 6 in humans. Somatic cell hybrids of human and mouse cells containing all the mouse chromosomes but lacking certain human chromosomes have been used to determine this chromosome localization. These cell hybrids were constructed, maintained, and analyzed as previously described (*10*).

Large-molecular-weight DNA was isolated from cultured mouse cells, human cells, and human-mouse cell hybrids and was digested with the restriction endonuclease Eco RI. The digested fragments were then separated by electrophoresis on agarose gels and transferred to nitrocellulose filters (*9, 11*). Restriction fragments containing the prolactin genes were analyzed by hybridizing the filters with labeled prolactin complementary DNA (cDNA) probes. The cloning of DNA complementary to both rat and human prolactin mRNA has been reported (*4, 12*). ^{32}P-Labeled prolactin probes were prepared by nick translation or by random priming with calf thymus DNA primers (*9, 11*). Specific activities greater than 10^8 cpm/μg were routinely obtained. The hybridization of these probes with filters containing human, mouse, or human-mouse cell hybrid Eco RI restriction fragments and the washing of the filters to remove nonspecifically bound probe were performed as described (*9, 11*).

In the control mouse line, the rat prolactin probe hybridized with three fragments of 7.4, 3.6, and 3.3 kb (Fig. 1, channel i). The rat prolactin probe did not cross-hybridize with human DNA under these hybridization and washing conditions (Fig. 1, channel j). Similarly, the human prolactin probe did not cross-hybridize with mouse DNA sequences (Fig. 1, channel a). In the control human cell line and in all the human cell lines used in this investigation, the human prolactin probe hybridized with two fragments of 4.8 and 4.0 kb (Fig. 1, channel b).

The mouse 7.4-, 3.6-, and 3.3-kb DNA fragments were present in all cell hybrids, while the human 4.8- and 4.0-kb

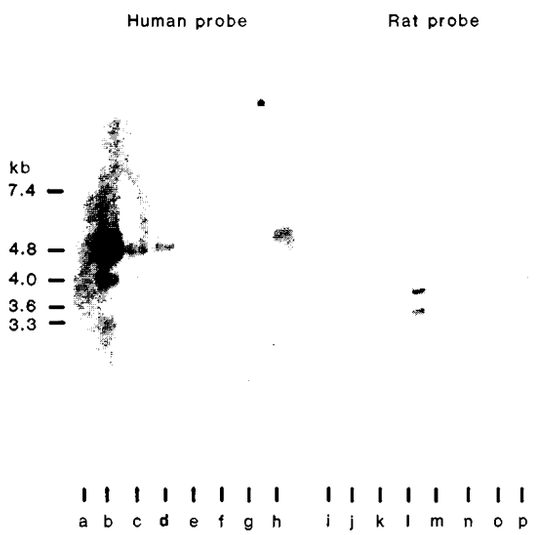

Fig. 1. Analysis of human and mouse prolactin DNA sequences present in Eco RI restriction digests of mouse, human, and human-mouse cell hybrid DNA. Isolation, digestion, and transfer of DNA to filters and hybridization were as described (*1, 11*). Labeled DNA bands were detected by exposing the filters to x-ray film for 2 to 10 days in the presence of an intensifying screen (Dupont Lightning Plus). Channels a through h were hybridized with human prolactin probe, while channels i through p were hybridized with rat probe. Prolactin hybridization patterns are shown for (channels a and i) mouse RAG cells; (channels b and j) human T cell lymphoblasts; (channels c and k) hybrid ALR-2; (channels d and l) hybrid TSL-2; (channels e and m) hybrid TSL-5; (channels f and n) hybrid TSL-6; (channels g and o) hybrid WIL-3; and (channels h and p) hybrid WIL-6. Fragments of Hind III–digested lambda phage DNA (New England Biolabs) were used as markers for molecular size. Hybrids ALR-2, TSL-2, and WIL-6 contained the human prolactin DNA sequences.

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