

Kimmswick: A Clovis-Mastodon Association in Eastern Missouri

Abstract. Stone tools characteristic of the Clovis culture have been found in direct association with bones of the American mastodon at Kimmswick, Missouri. The vertebrate fauna from Clovis components suggests a deciduous woodland and meadow habitat. Such an environmental reconstruction provides a new perspective for Clovis adaptations and the ecological tolerances of *Mammut americanum*.

The association of man and the American mastodon *Mammut americanum* has been a frequent question in North American archeology (1). In recent excavations at Kimmswick, Missouri, two Clovis projectile points and other stone tools were found in stratified deposits in direct association with the bones of *Mammut americanum* and other fauna. This is firm evidence for the association of the American mastodon and the Clovis culture.

The Kimmswick site, approximately 32 km south of St. Louis, lies about 127 m above mean sea level on a terrace abutting a 20-m limestone bluff to the north. The terrace, occupying a small area at the confluence of Rock and Black creeks approximately 1.6 km from their confluence with the Mississippi, was formed from overbank alluvium from the two creeks and colluvium from the bluff to the north (Fig. 1). These types of late Quaternary deposits occur in similar microenvironments throughout the valleys of the central Mississippi and Missouri rivers and their tributaries.

At Kimmswick the basal terrace deposits (B₁ and B₂) contain Pleistocene vertebrate fossils, but preservation of bone is distinctly different from that in overlying deposits. The upper portion of the colluvial gravel (B₂) is pedogenically modified and contains an oxidized clay-rich horizon (E) with poor bone preservation. This 10- to 50-cm-thick horizon may represent a paleosol or a beta horizon (2) that formed in response to a textural interface and an alkaline environment at the top of the gravel. Laboratory analyses and field relations favor the latter interpretation, in which case the underlying colluvium may not be appreciably older than the overlying strata. However, it is also possible that the colluvium (B₂) is considerably older than the overlying deposits.

The upper surface of the colluvial gravel has several shallow basins that may have filled with overbank alluvium and colluvium. Three of these ponded basins have been discovered so far and partially excavated. All contain the remains of extinct megafauna, extant and extirpated microfauna, and artifacts. Diagnostic Clovis tools (Fig. 2) have been

removed from two stratified and superimposed pond deposits (C₁ and C₃). Absolute dates are not available for the pond deposits (3), and their overall relation to the late Quaternary dynamics and geochronology of the Mississippi River is not clear.

The ponded sediments lie beneath a tan layer of colluvium and alluvium (D). Stratigraphically, this unit appears correlative with early Holocene deposits in western Missouri and western Illinois (4). The stratum contains diagnostic chipped stone artifacts of Early or Middle Archaic age which are easily differentiated stylistically and stratigraphically from the Clovis tools (Fig. 2).

Two virtually complete Clovis lanceolate points, simple unifacial tools, a bifacial fragment, and hundreds of chert flakes were found in the upper pond deposit (Fig. 2). The two projectile points were 1.25 m apart horizontally and were vertically separated by less than 1.5 cm. One of these (K-L22-32) (Fig. 2) is large and steel-gray, with minor impact damage to the tip. This specimen was at least 14 cm below the highest mastodon bone, a pisiform, and lay horizontally among disarticulated foot bones of an adult mastodon and

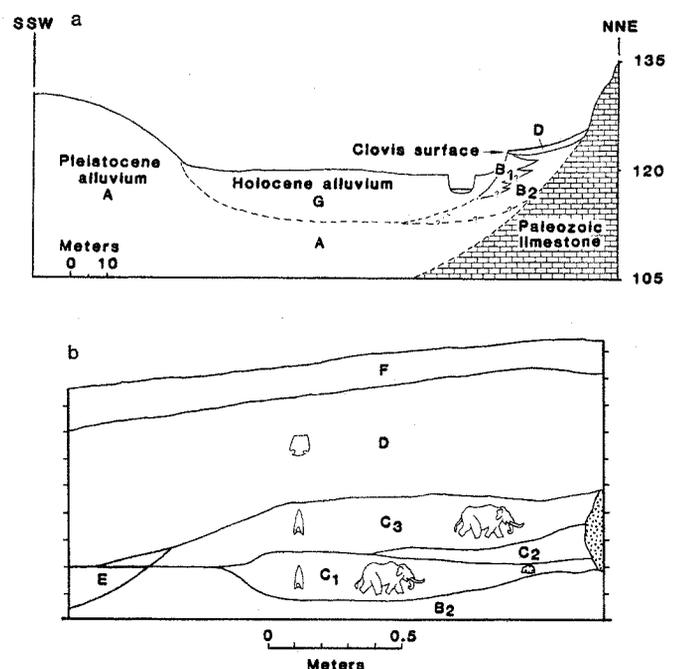
adjacent to a lenticular concentration of botryoidal manganese. Heavy coatings of manganese covered this point and other artifacts from the stratum.

The second projectile (K-H22-83), made from olive-green chert and extensively reworked, was discovered directly beneath a large mastodon bone fragment. Inclined 34° from the horizontal with the tip down, the base was in contact with the bone. The projectile may not have entered the bone but does show minor damage to the tip; it could easily have been embedded in the animal's flesh next to the bone.

In the blue-gray silty clay pond deposit (C₁) beneath these finds were additional Clovis artifacts: the basal ear of a lanceolate point, a basal fragment of a projectile point preform, and chert flakes. These artifacts were also in association with the bones of mastodons and other extinct fauna, although they were stratigraphically separated from the olive-green clay by the sterile upper colluvial gravel. The basal ear is made from a chert identical to that of the Clovis point found at Kimmswick at the turn of the century (5); their basal grinding and fluting also correspond.

All the lanceolate points (Fig. 2) from the ponded sediments are consistent with type descriptions for Clovis (6), and one (K-L22-32) shows a striking similarity in size and flaking to two from the Blackwater Draw type locality and one from Naco (7). The Kimmswick points have straight to convex sides and concave bases with multiple flutes. The haft area, including the base and lateral edges, was extensively ground after flut-

Fig. 1. Schematic cross sections of Rock Creek Valley (a) and the Kimmswick excavation (b). A, fluvial silts and sands of high terrace (T-2); B₁, fluvial clays of intermediate terrace (T-1); B₂, colluvial limestone gravels of T-1; C₁, bluish-gray silty clay of lower pond deposit; C₂, brown, clayey, silty gravel of upper colluvial gravel; C₃, olive-green silty clay of upper pond deposit; D, brown clayey silt of tan colluvium; E, beta horizon developed in B₁ and C₃; F, organic matter-darkened zone of disturbed surface; G, fluvial silts, sands, and gravels of low terrace (T-0).



ing. All the specimens exhibit well-executed pressure flaking and, apart from differences in length due to reworking of the tip, are nearly identical.

The second bifacially flaked artifact from the lower pond deposit is a preform with a reverse hinge fracture (Fig. 2). It is both wider and thicker than the finished points and clearly illustrates end thinning, or "preform fluting" (8), executed prior to final lanceolate shaping. This technology is compatible with preform preparation at other Clovis sites (8, 9).

The stratigraphic relations of these finds are compelling evidence for an association between the Clovis culture and the American mastodon. There are also lines of evidence that make other interpretations most improbable. Krotovina

or other pedoturbational features that could displace artifacts were not encountered in excavations of the pond sediments. There is no evidence of edge damage to artifacts as a result of secondary deposition. Furthermore, the sedimentary environment of the clay matrix encasing the artifacts is not compatible with transport of these artifacts or bones.

Uniformity of the diagnostic artifacts denies the possibility that older bones were mixed with younger artifacts. Had this occurred, not only Clovis materials but also later artifacts would probably have been found in the pond sediments. This is not the case, even though artifacts are present in the Holocene deposits above the pond sediments. Also, the Holocene colluvial slope could not have

served as a source for mastodon bones being redeposited with Clovis artifacts.

Although few in number and kind, the Clovis artifacts do indicate that activity at Kimmswick involved more than the hunting and butchering of mastodons. Manufacture and maintenance of chipped-stone armatures are also evident. Furthermore, the fauna from the Clovis-age sediments suggests a diverse economy for the Clovis hunters—more than an individual mastodon kill. Thus, Kimmswick may represent a Clovis mastodon kill and processing site with limited occupation.

The mammalian fauna from the pond deposits contains species adapted to deciduous woodland with open grassy areas (*Sciurus*, *Marmota*, *Spermophilus*, *Geomys*, *Microtus pennsylvanicus*, *Synaptomys cooperi*). A similar reconstruction is also suggested by extrapolation of contemporary pollen data for southern Missouri, central Illinois, and western Tennessee (10). Such an environment is different from the spruce forest usually assumed to characterize the mastodon habitat and strengthens arguments favoring broader ecological adaptations for mastodons (11). Furthermore, this environment is markedly different from those encountered by Clovis hunters in the Great Plains and Southwest. Kimmswick therefore may illustrate another adaptive strategy of Clovis hunters: survival in the eastern woodlands.

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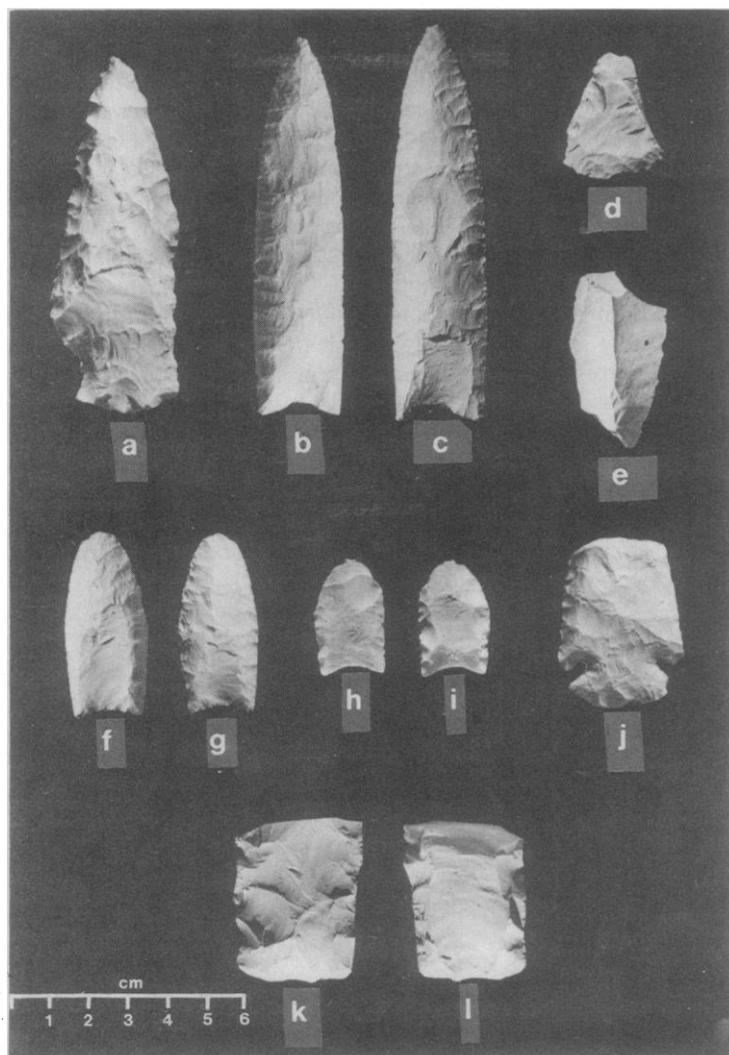


Fig. 2. Stone tools from Kimmswick. (a) Knifelike implement (FMNH 205527). (b and c) Obverse and reverse of Clovis projectile point (K-L22-32) from C₃. (d) Bifacial tool fragment from C₃. (e) Utilized flake from C₃. (f and g) Obverse and reverse of resharpened Clovis projectile point (FMNH 205526). Note impact fracture at tip in (g). (h and i) Obverse and reverse of Clovis projectile point (K-H22-83) from C₃. (j) Base of Saint Charles projectile point (K-P26-21) from D. (k and l) Obverse and reverse of "fluted" preform from C₁ with reverse hinge fracture. Specimens FMNH 205527 and 205526 were found at Kimmswick in the early 1900's, presumably in association with mastodon bones. However, specimen FMNH 205527 has D sediments still adhering to it (FMNH, Field Museum of Natural History, Chicago).

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12. Supported by National Geographic Society research grant 2234-80 and funds from the Missouri Department of Natural Resources and the St. Louis Academy of Sciences. Specimens from the Field Museum of Natural History were loaned to us by G. Cole. We thank F. B. King and M. A. Graham for technical assistance. This is contribution No. 56 of the Archeological and Quaternary Studies Program of the Illinois State Museum.

20 February 1981; revised 1 June 1981

Polymorphism in the 5'-Flanking Region of the Human Insulin Gene and Its Possible Relation to Type 2 Diabetes

Abstract. *The arrangement of the human insulin gene in DNA from 87 individuals was analyzed by the Southern blot hybridization technique with a cloned genomic human insulin probe. Insertions of 1.5 to 3.4 kilobase pairs in the 5'-flanking region of the gene were found in DNA from 38 individuals. These insertions occurred within 1.3 kilobase pairs of the transcription initiation site. In contrast, no insertions were observed in the region 3' to the coding sequence. The prevalence of these insertions in type 2 diabetes was significantly greater than in the other groups ($P < .001$). The limitation of this striking length polymorphism to a potential promoter region suggests that these insertions may play a role in insulin gene expression.*

Clinical diabetes includes a genetically heterogeneous group of disorders characterized by glucose intolerance (1). A higher concordance for diabetes in monozygotic versus dizygotic twins implicates genetic factors in the etiology of the disease, although the mode of inheritance is unknown. At present idiopathic diabetes mellitus has been divided into two major groups on the basis of family, twin, metabolic, immunologic, and HLA-association studies (2). Type 1 diabetes usually has its onset early in life, a strong association with certain HLA antigens, and a high prevalence of antibodies to islet cells. Type 2 diabetes generally develops in adults, bears no relation to distinct HLA haplotypes, and is not associated with antibodies to islet cells.

The two groups differ with regard to endogenous insulin production (3). In type 1 diabetes, because of destruction of pancreatic beta cells, there is absolute insulin deficiency, whereas in type 2 some ability to synthesize insulin is maintained. A relative insulin lack depends in part on the extent of coexistent insulin resistance (4). This feature is analogous to the deficient globin production in the various thalassemias (5) in which the α - and β -globin gene complexes give evidence of molecular defects. In the present studies we have examined

the insulin gene in diabetics to determine whether alterations similar to those found in the thalassemias could be responsible for impaired insulin production.

Structural studies of the human insulin gene in diabetics have become possible as a result of recent advances in recombinant DNA technology. A total of 19 kb [kilobase (pairs)] of human DNA was cloned, and 1430 bp (base pairs) containing the insulin gene were sequenced (6). In addition, 5650 bp on the 5' side and 11,500 bp on the 3' side of the gene were

analyzed by restriction endonuclease mapping. The entire region was shown to be single-copy DNA except for 500 bp of repetitive DNA located 6 kb 3' to the gene (6). There is no evidence for more than one nonallelic insulin gene in humans (6). We have used the cloned human insulin gene probe to study the arrangement of the human insulin gene in type 1 and type 2 diabetics and compared it with the gene in nondiabetics by the Southern analysis (7) of DNA from 87 individuals.

High molecular weight DNA was prepared from peripheral blood leukocytes or human placental tissue (8). Leukocytes were isolated from 10 to 25 ml of whole blood by centrifugation at 500g at 22°C through a Ficoll-Hypaque gradient (9). In some instances, a crude nuclear fraction was obtained according to the method of Cordell *et al.* (10). Placenta obtained fresh at birth and stored at -70°C until use was pulverized on Dry Ice and lyophilized before DNA extraction. The DNA was purified essentially as described (8, 11). After isolation, the DNA was precipitated with ethanol, dissolved in 10 mM tris, 1 mM EDTA, pH 7.5, and dialyzed extensively against 1 mM tris, 0.1 mM EDTA, pH 7.5, usually for 5 to 7 days. Typical yields included 200 to 400 μ g of DNA per 10 ml of blood, and 1 to 2 mg of DNA per gram of placenta.

Restriction endonucleases were used according to the manufacturers' specifications (New England Biolabs and Bethesda Research), except that 2.5 to 3 units of enzyme were added to the reaction mixture per microgram of DNA. Completeness of digestion was monitored by adding 1 μ g of lambda DNA to the reaction mixture. The samples were then subjected to electrophoresis through 0.8 to 1.5 percent agarose gels in

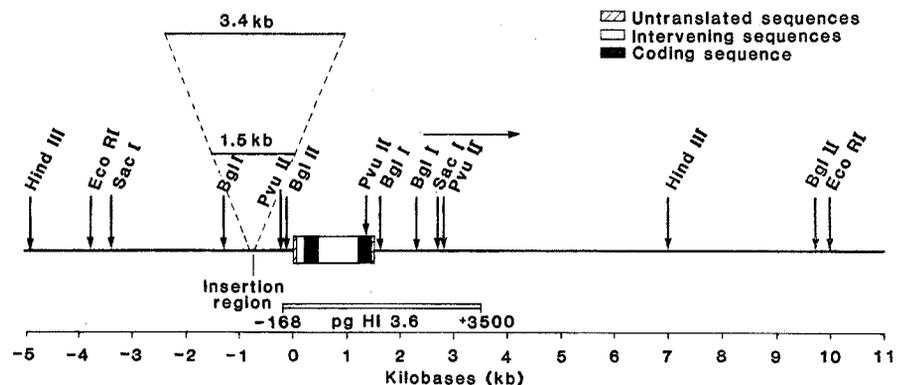


Fig. 1. Human insulin gene restriction map. The restriction sites were determined after single and multiple enzyme digests. The sites presented in this figure are only those used in our study. For a more complete map see (6). The insertion region falls somewhere between the Bgl I site (-1300) and Pvu II site (-259). The size of the insertions varied between 1.5 kb and 3.4 kb. The direction of transcription of the gene is shown by the arrow.