postcingulum is well separated from the protocone, does not tend to swing ventrally toward the apex of the protocone (*10*), and can carry a small hypocone. Molar trigonids exhibit a different style of inflation, involving marked swelling ventral and anterior to the metaconid. Talonid basins are open lingually by a deep notch and labial, basal cingula are better developed. Because of uncertainties concerning characteristics of primitive eutherian dentitions, differences in structure of P^4_4—presence of metaconid and postcingular development—cannot be clearly evaluated. Although they are possibly closely related, contrasting patterns of molar specialization suggest that *Purgatorius* probably was not derived from *Protungulatum donnae* or its descendants.

Gypsonictops, the only known latest Cretaceous leptictid insectivore, has been cited (*11*) as representative of the ancestry of Primates. Extensive molarization of P^4_4 and their functional relationships (*12*), sharp differentiation of postcingulum from protocone, and anteroposterior compression of high trigonids are specializations suggesting that known species of *Gypsonictops* are not involved in primate ancestry.

Latest Cretaceous palaeoryctid insectivores—*Cimolestes*, *Procerberus*, and particularly *Batodon* [considered an erinaceotan insectivore by some (*7*)]—have been posited as ancestors of Primates. Their dentitions, exhibiting modifications emphasizing puncturing and shearing, show no evidence of the trends toward more bunodont cusps and emphasis on crushing characterizing the evolution of early primate dentitions. Similarities appear to be common inheritances from the primitive eutherian tribosphenic dentition, which is characterized by: tribosphenic organization with sharp cusps and crests; a premolariform or submolariform P^4_4 [that is, lacking or with a poorly differentiated metaconid or metacone (*13*)]; pronounced difference in trigonid-talonid heights; M_3 talonid not distinctly elongated; and upper molars of transverse proportions, lacking hypocones or postcingula.

Recent speculations on origins of the Primates tend to ebb and flow toward favoring either a leptictid or palaeoryctid ancestry within Late Cretaceous Insectivora. Considerations of dental morphology as well as basicranial and bullar evolution suggest that the ancestry of Primates did not include latest Cretaceous members of these families. Fox (*14*) has demonstrated the presence of a third, erinaceotan insectivore lineage in latest Cretaceous faunas and this now appears to be a better candidate for the ancestral stock of the Primates.

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Holocene Stratigraphy and Archeology in the Middle Missouri River Trench, South Dakota

Abstract. *Shoreline erosion along man-made lakes in North Dakota and South Dakota has led to the discovery of stratified preceramic cultural remains in an area where previously few such materials have been found. One important exposure, the Walth Bay site, contains a 7000-year sequence of alluvial and eolian deposition capping an abandoned Missouri River terrace. Three distinct soil profiles are associated with successive Late Paleo-Indian, Plains Archaic, and Plains Village Tradition occupations.*

No other geographic area in North America has been the focus of so large a federal archeological salvage program, yet produced so little evidence of preceramic human activity, as has the Middle Missouri area in North Dakota and South Dakota (*1, 2*). This picture is suddenly changing, however, as a result of shoreline erosion along the series of man-made reservoirs spanning the middle Missouri River trench (*3*). Wave action and massive slumping of unconsolidated shoreline formations are exposing and destroying numerous sites (*4*); many undoubtedly contain Pleistocene and Holocene stratigraphic records and associated archeological remains (*2, 5*). One such important site is at Walth Bay on the eastern shore of the Oahe Reservoir in Walworth County, South Dakota. The Walth Bay site is on the western edge of a high terrace about 22 m above the preinundation level of the Missouri River (*6*).

Fieldwork was initiated in 1970 to test the intensive Extended Coalescent Variant occupation of the site (*1*, pp. 115–130). In 1971 several typologically and technologically early stone artifacts were found along the adjacent reservoir shoreline, apparently eroding from a number of subsurface cultural horizons exposed in the reservoir cutbank. Subsequent sampling included removal of a soil monolith from the cutbank for pedological and palynological analysis and excavation of two 1.52-m (5-foot) squares to the base of the cultural deposits, with all matrix waterscreened over 1.59-m (1/16-inch) square-mesh screen.

The soil monolith is in the group Ustorthent (*7*), which is basically a vegetation-supporting, structureless sediment exhibiting little or no alteration. Three distinct divisions of the monolith are made on the basis of color (wet), texture, and general information (Fig. 1A). With minor variations in thickness, general site stratigraphy parallels that in the monolith (Fig. 1C). Two recognizable A soil horizons (A_1 and IIA_{1B}/IIA_{3B}) exist throughout the site, and a third ($IIIA_{3B}$) is found locally in areas where it has not been removed by erosion (Fig. 1C).

Microscopic examination of quartz grains reveals little evidence of chemical solution of quartz particles. The decrease in the mean grain size of quartz between 1.94 and 1.36 m, and again between 1.30 and 0.42 m, is interpreted as a result of physical breakdown of quartz along microfractures.

Sediment in the monolith from the surface to 1.02 m is moderately sorted and silty, apparently of loessial origin. Sediment between 1.02 and 1.94 m is poorly sorted and extremely sandy, suggesting alluvial origin. The poorly sorted sediment below 1.94 m contains widely dispersed, glacially derived granite boulders. Petrographic analysis revealed no changes in total mineralogy of the monolith. Fluctuations in organic content were noted. Thus, sediments in the monolith are derived from the same basic source, irrespective of their alluvial or loessial origins.

Lacking sufficient charcoal, we submitted two bone samples for carbon-14 analysis of bone collagen. A small fragment of *Bison* tibia from horizon IIA_{3B} was dated at 8030 ± 1100 years before present (RL-308) and large mammal rib fragments (*Bison*?) from horizon $IIIA_{3B}$ were dated at 7010 ± 210 years before present (RL-309). Radiocarbon determinations on charcoal from the A_1/A_C horizon gave a date of 300 to 500 years before present for these deposits (Fig. 1C). Thus, the 7000-year record at Walth Bay is temporally equivalent to the Pick City and Riverdale members of the eolian Oahe Formation recently defined along the Missouri River in North Dakota (*8*), and with the uppermost units of the abandoned Missouri River terraces, Mt-1 and Mt-2, described in the Big Bend area 300 km to the south (*5*, pp. 319–325).

Usable data were derived from eight pollen test samples from zones producing cultural material (see Fig. 1B for provenance). No pollen was found in horizon C_2, and pollen in all other sam-

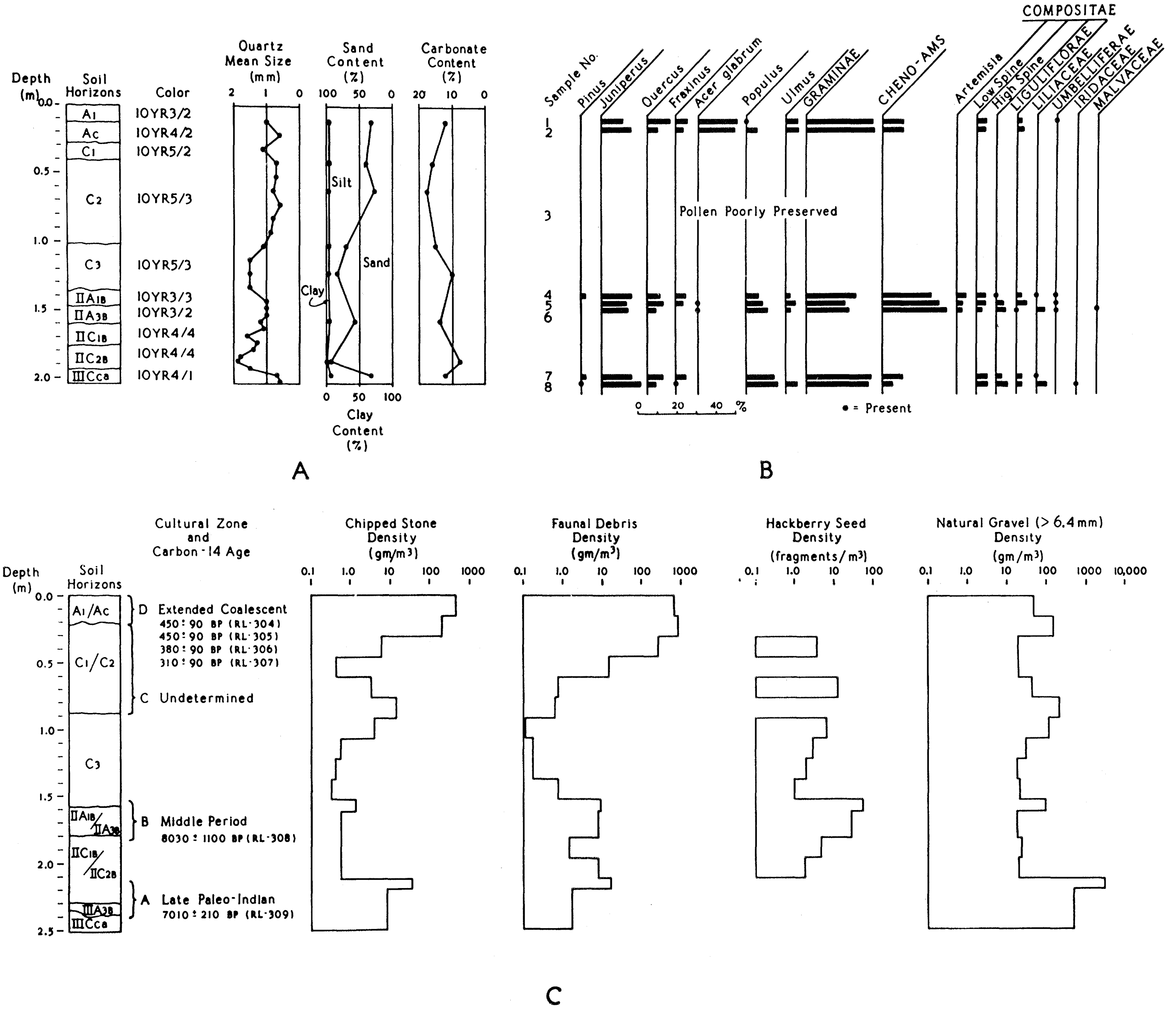

Fig. 1. Stratigraphic data from the Walth Bay site. (A) Monolith analysis, showing soil horizons and related information. (B) Pollen analysis, showing stratigraphic relationships of the test samples. Samples 1 and 2 are from an Extended Coalescent pit in cultural zone D. Sample 3 produced no pollen. Sample 7 is from horizon $IIIA_{3B}$, absent in the monolith but present in the test units. Samples 3, 4, 5, 6, and 8 are from the monolith. (C) Controlled excavation of 1.52-m square, showing the generalized stratigraphy, cultural zones, related soil horizons, and carbon-14 dates, and the debris densities derived from the waterscreen recovery technique.

ples was broken and eroded. The results (Fig. 1B) indicate that grass and herbaceous species dominate throughout, with juniper, *Populus*, and a number of arboreal hardwoods well represented. The high incidence of *Acer glabrum* in the Coalescent pit (samples 1 and 2) is probably due to aboriginal use of the storage facility, since smooth-maple pollen is transported by insects and has little wind dispersal (*9*). All samples represent a prairie plant community located near a river bottom woodland—conditions similar to the present ones. However, given the lack of pollen in the loessial sediments and the wide spacing of the samples, the homogeneity of the pollen percentages cannot be taken to indicate a lack of environmental change throughout the entire depositional sequence.

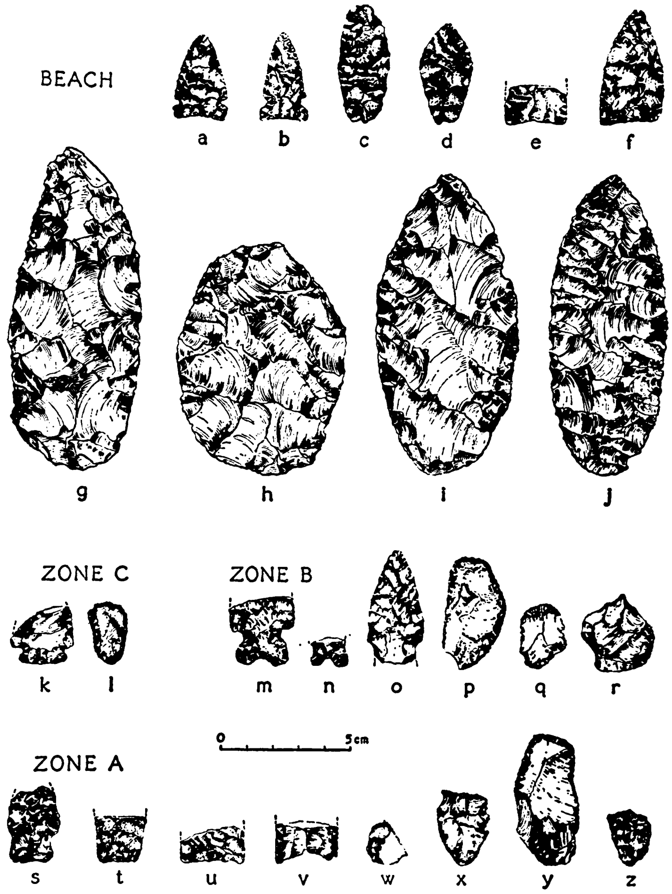

Fig. 2. Walth Bay preceramic chipped stone artifacts from mixed beach deposits (a to j) and cultural zones C (k and l), B (m to r), and A (s to z). (a to d, k, o, s, and t) Unnamed projectile points; (e, u, and v) Frederick points; (f) Frederick knife; (m and n) Hanna points; (g to j) bifacial preforms; (l, q, and z) end scrapers; (r and w) spurs; (x) beak; (p and y) retouched flakes.

Four definable cultural zones were observed during excavation and were supported by the debris density analysis (Fig. 1C). The lowermost, zone A, is represented by a concentration of chipped stone and faunal debris on or just above the erosional unconformity separating soil horizons IIC$_{2B}$ and the underlying IIIA$_{3B}$/IIIC$_{Ca}$. Cultural materials in zone B are concentrated in horizons IIA$_{1B}$ and IIA$_{3B}$. Charred and uncharred hackberry seeds are preserved in the deposit and are most dense in this zone. Cultural materials in zone C occur at various depths in horizons C$_1$ and C$_2$, depending on location within the site. Cultural zone D is confined to the uppermost horizons, A$_1$ and A$_C$. Unmodified gravels are of fluvial origin in zone A, and are likely the result of cultural activities or burrowing rodents in zones C and D. Rodent burrows have permeated all zones, particularly zone D and zone A.

A variety of projectile point fragments were found in situ in zone A, among them two Frederick-like specimens (Fig. 2, u and v). Frederick points (*10*) have been found in association with extinct bison at sites in Wyoming and Nebraska (*11*), and have been dated at 8600 ± 380 years before present (A-501) at Hell Gap, Wyoming (*12*). The projectile points and other stone tools in zone A (Fig. 2, s to z) are types normally made in varying frequencies by big-game-hunting Paleo-Indians of the late Pleistocene (*13*). Faunal debris in zone A was sparse (340 g), with a single *Bison* cuboid fragment identified.

Point typology and other chipped stone tools in zone B (Fig. 2, m to r) indicate that Middle Period (*14*) or Northern Plains Archaic peoples were responsible for this aggregate. Fauna in zone B was scarce (673 g); two *Bison bison* elements, ten elements of *Antilocapra americana*, and seven Geomyidae elements were identified.

Diagnostic cultural remains from zone C were sparse (Fig. 2, k and l); the single corner-notched projectile was found at the A$_C$/C$_1$ contact. Bone was also sparse (73 g), and no species were identified.

Cultural remains in zone D relate to intensive use of the site by more recent, sedentary, earth lodge-dwellers assigned to the Extended Variant of the Coalescent Tradition (*1*, pp. 115–130). The extensive material remains in this zone will be treated in some detail in future monographs (*15*).

Although no longer in situ, pre-Coalescent artifacts from the beach are significant (Fig. 2, a to j). Of note are typologically early side-notched projectiles made of heavily patinated clear chalcedony (Fig. 2, a and b) and a variety of lanceolate points (Fig. 2, c to f). Several large, thin, Knife River Flint bifaces (Fig. 2, g to j) are preforms, probably manufactured at a quarry site similar to those described in North Dakota (*16*). Slight patination on one face only suggests their original deposition in zone B, where in situ Knife River Flint artifacts show similar alteration.

The Walth Bay site is of unique importance; the environmental data, temporal depth, and cultural diversity of the site are presently unparalleled in the Middle Missouri area. The existence of sites such as Walth Bay was predicted more than a decade ago (*5*, pp. 326 and 327), but few have been recognized and none have been adequately studied. The transient archeological and geological resources at Walth Bay must not be lost to the waters of modern cultural advancement.

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Elephant Seals: Genetic Variation and Near Extinction

Abstract. *Blood samples from northern elephant seals* (Mirounga angustirostris), *representing five breeding colonies in California and Mexico, were surveyed electrophoretically for protein variation reflecting underlying genetic differences. No polymorphisms were found among 21 proteins encoded by 24 loci. This uniform homozygosity may be a consequence of fixation of alleles brought about by the decimation of this species by sealers in the last century.*

What are the genetic consequences for a species of reduction in numbers to near extinction? We have approached this problem by examining genetic variation in the northern elephant seal (*Mirounga angustirostris*) whose numbers have varied enormously over the last 150 years.

In the mid-1800's, northern elephant seals were hauled-out by the thousands at numerous breeding rookeries along 2700 km of the coast of California and Baja California, Mexico (*1*). From 1820 to 1880 they were heavily exploited by man for oil. Because of a biological necessity to breed and give birth on land, the seals were more vulnerable than whales; hunters could quickly slaughter hundreds of adults and pups. The commercial harvest was so extensive and indiscriminate that by 1884 the species was considered virtually extinct (*2*). Only the most remote population survived—that on a nearly inaccessible beach on Isla de Guadalupe, 240 km west of Baja California (*3*). Estimates based on early census data indicate that this remnant population may have consisted of as few as 20 individuals in the early 1890's and the total number remained less than 100 individuals until at least 1900 (*4*). Under the protection of the Mexican and U.S. governments, the northern elephant seal slowly increased in numbers and, by the early 1930's, began to establish additional breeding colonies (*5*). Since then, the species has reoccupied its former breeding range and now numbers more than 30,000 (*6*). Thus the genetic reconstruction of this species was influenced by two factors: (i) the northern elephant seal suffered a severe "bottleneck" in numbers and (ii) its present genetic resources were derived from a single isolated population possessing but a fraction of the total variability of the predecimation species.

To assess the possible consequences of this species-wide decimation and subsequent recovery, we surveyed proteins electrophoretically for polymorphisms reflecting underlying genetic differences at structural gene loci (*7*). Blood samples were collected from 159 seals of both sexes at five rookeries: Año Nuevo Island ($N = 67$), San Miguel Island ($N = 24$), San Nicolas Island ($N = 20$), Isla de Guadalupe ($N = 25$), and Islas San Benito ($N = 23$) (*8*). Starch-gel electrophoresis was performed for 21 proteins encoded by 24 presumptive gene loci (*9*). No individual or populational differences were found; all proteins were monomorphic.

Is an apparent absence of genic heterozygosity unique to this species or is it also characteristic of other pinnipeds? For perspective we can look at the northern elephant seal's nearest relative, the southern elephant seal (*Mirounga leonina*), which is subantarctic in distribution. This species was also hunted extensively in the last century, but the effects were not as catastrophic as for the northern elephant seal (*10*). McDermid *et al.* (*11*) demonstrated five polymorphisms among 18 proteins examined electrophoretically in 42 individuals from Macquarie Island. From their data, we estimate genic heterozygosity at 0.028. Another population studied by Seal *et al.* (*12*) showed no variation in six proteins in 18 animals, but these proteins were among those found to be monomorphic by McDermid *et al.* (*11*).

The electrophoretic analysis of genic variation in pinnipeds other than *Mirounga* has been very limited (*13*). Multiple phenotypes of transferrin were demonstrated in 8 of 12 species of pinnipeds studied (*14*), and other polymorphic proteins include haptoglobin in 2 species, lactate dehydrogenase in another, and a rare variant of hemoglobin in a fourth (*15*).

Electrophoretic studies have convincingly demonstrated that a high level of genic variation is maintained as a normal equilibrium condition in most natural populations of plants and animals. In 22 species of vertebrates surveyed, genic heterozygosity averaged 0.0584 and the proportion of polymorphic loci ranged from 10 to 20 percent (*16*). The northern elephant seal apparently is genetically depauperate relative to its southern congener and other vertebrates, and indeed may be entirely monogenic. Whether this situation represents a reduction in genetic diversity from the level existing prior to the bottlenecking of the species is problematical. It is likely, however, that the genetic constitution of this species has changed as a consequence of decimation. It has been suggested that the magnitude of genetic change could be assessed by comparing means and variances of dimensions of museum specimens collected in the last century and more recently (*4*).

The roles of natural selection and random drift are complementary in bringing about a reduction in overall diversity in small and isolated populations. The uniformity of the marine environment throughout the range of the northern elephant seal provides little opportunity for the proliferation of genetic variability by natural selection. It is reasonable to assume that a rela-