a linear regression of the right-hand side on the left-hand side. The 4000-m values of u and v between day 280 and day 480 are used with $\partial(f/h)/\partial x$ and $\partial(f/h)/\partial y$ as the unknowns determined from a least-squares fit. The left-hand side of Eq. 1 accounts for 60 percent of the variance of the right-hand side of Eq. 1, and the estimated bottom slopes are $\partial h/\partial x = 2.5 \pm 3.0 \times 10^{-4}$ and $\partial h/\partial y = -11.5 \pm 4.5 \times 10^{-4}$, with 95 percent confidence. From the digitized ocean topography, the respective values are estimated to be 4×10^{-4} and -13×10^{-4}. Hence, the wind-driven circulation is forced to flow zonally because of the Mendocino Escarpment.

These results are consistent with the time-dependent barotropic, linear vorticity equation provided that $(\omega/h\beta_e L) << 1$, where ω is the frequency of forcing, β_e is the equivalent potential vorticity gradient, and L is the scale of the wind stress (or bottom topography). Thus, for $\omega < 0.10$ cycle per day and $h\beta_e = 1.7 \times 10^{-11}$ m^{-1}sec^{-1}, motions with scales of $L \geq 450$ km are in Sverdrup balance. This scaling disagrees with the theoretical models (*4*), which suggest that Rossby waves are generated in this regime. There are two apparent reasons for this discrepancy. First, the wave-number spectrum of the winds for our observations could be quite different from the spectra used in those models. This would result in a scale mismatch between the atmosphere and the Rossby wave excitation band, leading to an inability of the atmosphere to excite the Rossby waves. Also, no specific theoretical computation has been made for the topographic regime of the eastern North Pacific. Second, a study of long-period tides (*17*) indicates that short-wavelength barotropic Rossby waves are dissipated much more quickly than had been assumed. Thus, any short-wavelength features would be rapidly damped and only the large-scale Sverdrup balance would remain.

Our results suggest that the northeastern Pacific Ocean has a much simpler dynamical response to atmospheric forcing at time periods from 10 to 100 days than has been argued. These measurements confirm that the ocean variability caused by atmospheric forcing is small compared with what results from fluid instabilities, such as those found in western boundary current regions.

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Anthropoid Origins in Asia? New Discovery of *Amphipithecus* from the Eocene of Burma

Abstract. *A new fossil of the primate* Amphipithecus mogaungensis *Colbert from the late Eocene of Burma shows that this species has a mandibular and molar morphology very similar to Oligocene and post-Oligocene higher primates. It has an exceptionally deep jaw. Its brachybunodont first and second molars have smooth enamel but lack hypoconulids. The shape of its second molar is nearly square—an advanced higher primate feature.* Amphipithecus mogaungensis *and related taxon* Pondaungia cotteri *Pilgrim are the earliest known higher primates. They suggest that Southeast Asia was an early theater of higher primate diversification.*

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Amphipithecus mogaungensis Colbert was first described 48 years ago (*1*). Despite the recovery of only one partial jaw of the type, there has been continued debate about whether *Amphipithecus* was an anthropoid primate, as argued by Colbert (*1*) and later by Simons (*2*), or a lemuriform primate, possibly an adapid, as Szalay (*3*) and Szalay and Delson (*4*) concluded. Our discovery of another jaw fragment elucidates some aspects of this controversy.

The new jaw fragment (Department of Geology, Mandalay University, primate specimen DGMU-P1) was discovered in September 1978 by a Mandalay Arts and Sciences University field party during a survey in Burma's Pondaung Hills. It had weathered from claystone beds of the Pondaung Formation about 2.4 km west of Mogaung Village in northwestern central Burma near the site where Barnum Brown collected the type specimen of this species in 1923 (*1*). Other primate jaws (*5, 6*) and an associated vertebrate fauna have also been collected here and are currently being studied.

The Pondaung fauna (*7*) correlates with later Eocene Asian faunas from Yunnan, Gaungxi, Henan, Shaanxi, and Nei Mongol in China and with similar faunas in Mongolia (*8*). Correlation with faunas assigned to the Uintan and Duchesnean mammal ages in North America and to the late Robiacian and Headonian mammal ages in Europe is more tenuous. The overlying Yaw Formation, south of the Mogaung district, has been correlated with the Bartonian Age of Europe (*9*). Extended correlations with radiometrically dated rocks (*10*) indicate that the Pondaung fauna lived between 40 and 44 million years ago. Thus the

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Pondaung primates of Burma pre-date the earliest known African anthropoids from the Fayum region of Egypt by at least 5 million years (*11*).

Order Primates Linnaeus, 1758
Suborder Haplorhini Pocock, 1918
Hyporder Anthropoidea Mivart, 1864
?Infraorder Catarrhini E. Geoffroy, 1812
Amphipithecus mogaungensis Colbert, 1937

Revised diagnosis [modified from (*1*)]. A gibbon-sized primate with a very deep and heavy mandible relative to cheek teeth size. It has a short, vertical, deepened symphysis with both an inferior and strongly developed superior transverse torus. The dental formula is two (?) incisors, one canine, three premolars (P) and three molars (M). The P_3 through M_2 on both sides of the jaw have smooth enamel crowns with faint or no buccal cingulids. All major cusps are about equal in height. The M_1 has a small and anterior placed paraconid near the tooth midline but has no hypoconulid. The M_2 has neither a paraconid nor a hypoconulid.

Range. The species is known from two localities in the upper part of the Pondaung Formation, late Eocene, Monywa District, northwestern Central Burma.

Description. The molars of the new jaw fragment of *Amphipithecus mogaungensis* indicate an adult animal (Fig. 1). The trigonid of M_1 is narrower transversely than the talonid. The metaconid and protoconid are about equal in size and height and the small paraconid is anteromedial. The trigonid forms a broad and low transverse lophid with only a small trigonid basin. Distally, there is a slight posterior closure of the talonid basin between the massive hypoconid and the more marginally placed but equally high entoconid. There is no hypoconulid on M_1.

The trigonid of M_2 on DGMU-P1 is composed of a relatively massive and bunodont metaconid and protoconid, separated by a smooth sulcus. A weak anteromedial rugosity, deep in the anterior part of the trigonid basin, is interpreted to be a remnant of an anterior cingulum, not a vestigial paraconid. The subpyramidal hypoconid is separated from the entoconid by a relatively deep sulcus, and, as with M_1, there is only slight closure of the talonid basin posteriorly. A hypoconulid is lacking. Also, as on M_1, cingulids are faint.

Discussion. The close metrical (*12*) as well as morphological similarity of the comparable parts of DGMU-P1 and the type specimen now make possible a reconstruction of the entire left mandibular corpus of *A. mogaungensis* (Fig. 2) showing the great depth of the jaw relative to molar-crown height, a strikingly anthropoid feature. This derived anatomy is associated with symphyseal fusion in the higher primates (*2, 13*). The strong development of mandibular tori in the type of *Amphipithecus* and the fracture of its jaw lateral to, rather than along, the symphyseal midline is another feature characterizing primates with fused symphyses. In lower primates, fusion of the symphysis is found only in several Malagasy subfossil lemurs (a clear case of convergence) and in a few Eocene adapids. However, adapids with fused symphyses lack the development of a superior transverse torus (*14*), a feature shared by *Amphipithecus* and later anthropoids (*1, 15*). Thus, the cited resemblances of *Amphipithecus* to Eocene adapids with fused symphyses (*3*) may be based, in part, on a comparison of nonhomologous structures.

The teeth of the new jaw fragment of *Amphipithecus* resolve some questions about dental morphology (*3*). Both Colbert (*1*) and Szalay (*3*) concluded that the M_1 of the type of *A. mogaungensis* had a small hypoconulid at the locus of a small nick in the enamel. Szalay argued that (i) the placement of this hypoconulid closer to the hypoconid than to the entoconid was a feature distinct among the primates and (ii) because *Amphipithecus* does not have a large cuspate and lingually placed hypoconulid as do the Fayum and later anthropoids, it cannot be considered a higher primate (*3, 4*). But, neither the M_1 nor M_2 of DGMU-P1 shows any sign of a hypoconulid (Fig. 1). An uninterrupted ridge connecting the entoconid and hypoconid can be seen rounding out the contour of the talonid of both molars. The absence of hypoconulids argues against the interpretation of

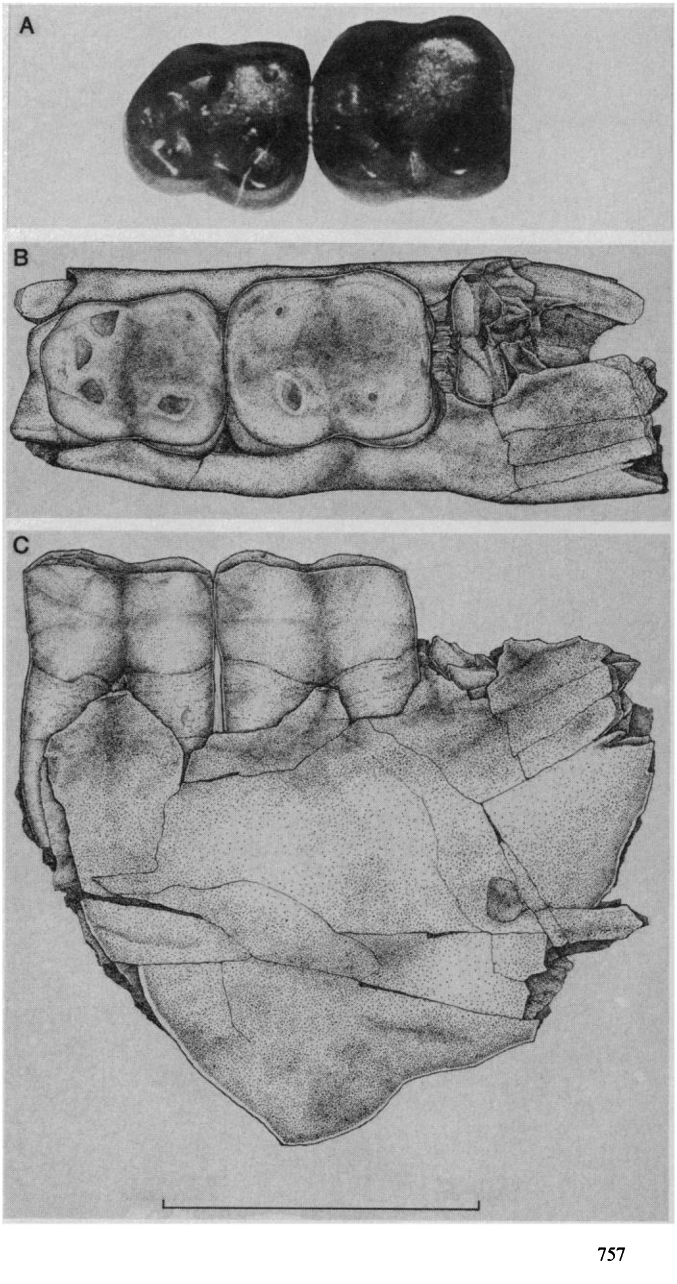

Fig. 1. *Amphipithecus mogaungensis*, left dentary showing the first and second lower molars of specimen DGMU-P1 from Mogaung West, Central Burma. (A) occlusal view (photograph); (B) occlusal view (drawing); (C) labial view (drawing). Scale bar, 10 mm. [The illustration is by Kyaw Min]

Szalay (*3*) and Szalay and Delson (*4*) but provides little support for the catarrhine affinities of *Amphipithecus*. Without a hypoconulid *Amphipithecus* is distinct among early Old World anthropoids, but among New World platyrrhines the absence of a hypoconulid on M_1 and M_2 is a common feature. In fact, Kay (*16*) has argued that the ancestral platyrrhine morphotype lacked this cusp. The absence of an M_1–M_2 hypoconulid in *Amphipithecus* and in ancestral platyrrhines might best be viewed as an anthropoid symplesiomorphy, a view also supported by Delson and Rosenberger (*17*).

Other cusp features used to support the adapid affinities (*3, 4*) of the type specimen of *Amphipithecus* are (i) the presence of a paraconid on M_1, (ii) the large size and the shape of the M_1 talonid, and (iii) the morphology of the P_3 and P_4. Specimen DGMU-P1 has a paraconid on M_1 but not on M_2. Presence of a paraconid on M_1 is indeed characteristic of lower primates, but this feature also occurs in several platyrrhines (*16*) and in the Fayum catarrhines *Oligopithecus* and *Qatrania* (*2, 18*). Furthermore, paraconids are present on the M_2 and M_3 of *Pondaungia* from the Eocene of Burma (*6*), a taxon that Szalay and Delson (*4*) place in the Catarrhini, *incertae sedis*. *Amphipithecus* has a relatively wide M_1 talonid. We agree with Szalay (*3*) that this lower primate feature is absent on the Fayum catarrhines except for *Oligopithecus* and *Qatrania*. However, the M_2 of DGMU-P1, unlike lower primates, is almost square because of an equally wide talonid and trigonid (*12*) (Fig. 1). The M_2 of *Amphipithecus* thus does resemble the M_2 of the Fayum and later catarrhines. Szalay (*3*) points out that the premolars of *Amphipithecus* are "mesiobuccally skewered [sic] like those of the Fayum genera," yet he finds the construction of the talonids to be dissimilar. He concludes that any similarity to the Fayum anthropoids must result from convergence rather than common inheritance. The jaw structure and cusp morphology of *Amphipithecus* as now known lead us to suggest that common inheritance is the more parsimonious interpretation.

If *Amphipithecus* is an early anthropoid, then from what lower primate stock were it and the Anthropoidea derived? Gingerich (*19*) argues that *Amphipithecus* along with *Pondaungia* and *Oligopithecus* are "transitional adapid-simiiform primates linking higher primates to an adapid origin." Szalay and Delson (*4*) conclude that *Amphipithecus* "does not seem far removed from a notharctine, or some other, unknown, primitive adapid. . . ." No one has argued explicitly that *Amphipithecus* is derived from an omomyid.

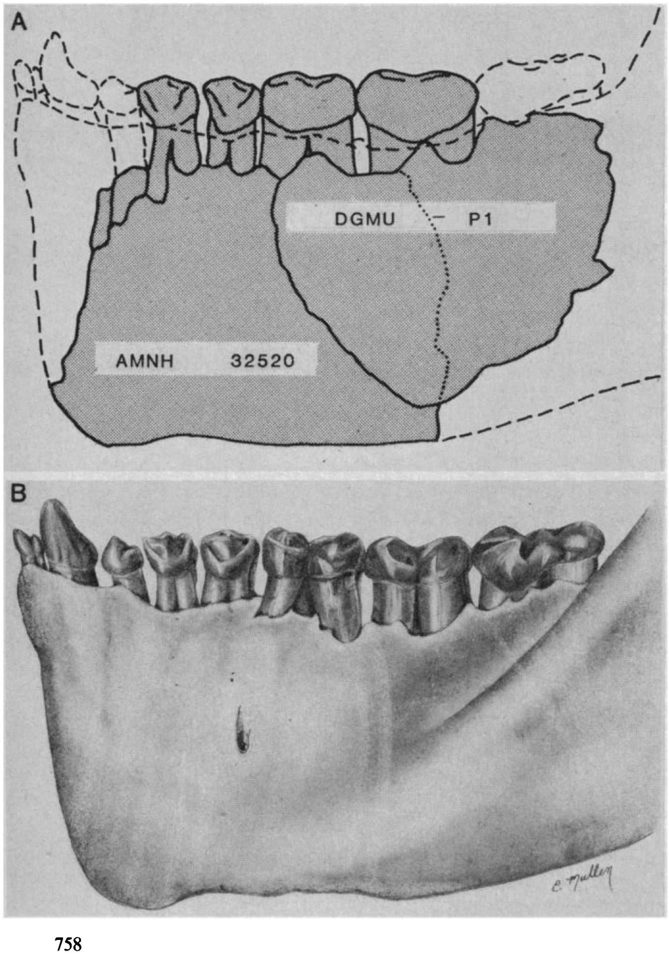

Fig. 2. Reconstruction of jaw of *A. mogaungensis* based on the type specimen (AMNH 32520) and new specimen (DGMU-P1) combined. (A) Labial view illustrating how the two specimens are combined. (B) Labial view of completed reconstruction based on fossil evidence and anatomical inference (*23*). [Drawing of (B) by Enita Mullen]

The apparent similarities shared by *Amphipithecus* and adapids are difficult to reconcile with the increasing body of evidence that anthropoids and *Tarsius* form a natural phyletic grouping. However, several critical studies of Eocene lower primates have questioned the traditional notion that omomyids and adapids are phyletically linked with living tarsiers and lemurs, respectively (*20, 21*). It now seems likely that the wide array of comparative anatomical, embryological, and biomolecular data (*22*) linking anthropoid origins with a "tarsiiform" ancestor have little bearing on the Eocene affinities of this ancestor. Thus the clade Haplorhini (*Tarsius* + anthropoids), supported by many shared derived characters documented among extant forms, is compatible with the derivation of this group (which now may include *Amphipithecus*) from an adapid-like ancestor (*21*).

Amphipithecus is found alongside *Pondaungia* in the Eocene of Burma. These Burmese primates were specialized as deep- and heavy-jawed animals with bunodont cheek teeth. *Amphipithecus* had smooth enamel on its cheek teeth but *Pondaungia* featured corrugated enamel. These two genera present a mosaic of "lower" and "higher" primate characters with the latter predominant, indicating that by later Eocene times in southern Asia the anthropoid adaptive zone had been entered. The current knowledge of Old World paleogeography in the later Eocene presents no insurmountable obstacle to the existence of early anthropoids in both Asia and Africa. Therefore, when consideration is given to their morphology, geographic position, and 40-million-year-old age, *Amphipithecus* and *Pondaungia* document the earliest record of primates that were adaptively anthropoids, raising the possibility that the origin of the Anthropoidea could have been in southern Asia.

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Genomic Diversity of Human T-Lymphotropic Virus Type III (HTLV-III)

Abstract. *The DNA genomes of human T-lymphotropic virus type III (HTLV-III) isolated from 18 individuals with AIDS or who were at risk for AIDS were evaluated for evidence of variation. Although all of the 18 viral DNA's hybridized throughout their entire genomes to a full-length cloned probe of the original HTLV-III isolate, each of the 18 isolates showed a different restriction enzyme pattern. The number of restriction site differences between isolates ranged from only 1 site in 23 to at least 16 sites in 31. No particular viral genotype was associated with a particular disease state and 2 of the 18 patients had evidence of concurrent infection by more than one viral genotype. Propagation of three different viral isolates in vitro for up to 9 months did not lead to detectable changes in their restriction patterns. These findings indicate that different isolates of HTLV-III comprise a spectrum of highly related but distinguishable viruses and have important implications regarding the pathogenicity of HTLV-III and attempts to develop effective diagnostic, therapeutic, and preventive measures for this virus.*

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Human T-lymphotropic virus type-III (HTLV-III), also referred to as lymphadenopathy-associated virus (LAV) and AIDS-related virus (ARV), is the etiologic agent of the acquired immune deficiency syndrome (AIDS) and related immunological disorders (*1, 2*). Diversity, or heterogeneity, in the genomes of different isolates of HTLV-III was first noted by our laboratory in the course of our initial characterization of the virus (*3*) and subsequently by the comparison of the nucleotide sequences of four different AIDS virus isolates (*4–6*). The latter studies also suggested that the extent of divergence between isolates could be minor (1 to 2 percent among BH-10, BH-5/8, and LAV-1A) or more extensive (7 percent between BH-10 and ARV-2) but, because so few isolates had been examined, the extent of variation among AIDS viruses was unclear. Thus, to gain more information on the extent and nature of genomic variation in the HTLV-III group of viruses, we analyzed by Southern hybridization the viral DNA from 17 consecutively studied patients with either AIDS or AIDS-related complex (ARC) and one subject at risk for AIDS but with no apparent clinical disease.

Virus from nine patients with AIDS or ARC and one healthy subject was transmitted to established neoplastic T-cell lines (H4, H9, or JM) or to normal peripheral blood lymphocytes (PBL) (*1, 7*). Primary tissues (lymph node or brain) from the eight AIDS or ARC patients were examined directly (Table 1). DNA from cultured cells or primary tissues was digested with a panel of restriction enzymes and analyzed by Southern hybridization to 9-kb cloned HTLV-III probe (BH-10) (*3*). DNA bands constituting an entire genomic complement were detected by this probe for each of the viruses under high stringency hybridization and wash conditions indicating that a high degree of homology exists among all of the isolates (Fig. 1). Despite this overall conservation in sequence homology, a striking degree of restriction enzyme site polymorphism was found among the isolates. For example, Sst I generated three predominant genotypic patterns: a 9.0-kb fragment (isolates RH, RF, and TM), 5.5- and 3.5-kb fragments (isolates HW, JS, and SC), and 5.5-, 1.8-, and 1.7-kb fragments (isolates MN and SL). The cell line H9/HTLV-III_B (Fig. 1, lane IIIB), which was derived from the HT line that was infected by virus from several different patients (*8*), contains both the 9.0-kb and (5.5 + 3.5)-kb Sst I genotypes. Although all 18 isolates that we examined contained one of the three Sst I patterns described above, digestion of these isolates with three other enzymes (Bgl II, Hind III, and Pst I) yielded overall restriction patterns different for each of the viruses. It should be noted that the interpretation of restriction site differences between HTLV-III isolates is complicated by the simulta-