gish, the quenching of some of the tetragonal phase under pressure is not surprising. In order to determine the thermodynamic stability of the tetragonal phase, the samples prepared under high pressure were heated in air for 3 hours above 1200°C, and then quenched to room temperature. Subsequent x-ray analysis revealed only the monoclinic phase. The resultant microstructure was that of the conventional single-phase polycrystalline zirconium oxide. This back-transformation to the monoclinic phase is expected thermodynamically. Whitney (*7*) has calculated the thermodynamic stability of monoclinic and tetragonal zirconium oxide, and has determined that the equilibrium line runs from 1 bar at 1200°C to 36 kb at room temperature with a slope of -0.0302°C per bar. Above the line (higher pressure, given temperature) monoclinic zirconium oxide should be completely transformed to the tetragonal phase. Our experiments to quench the tetragonal phase have been in the predicted tetragonal region. With a "belt" apparatus, we have tried to "quench" the tetragonal phase at room temperature, at pressures of 36 to 90 kb, but have been unable to detect any tetragonal zirconium oxide in this manner.

Tetragonal zirconium oxide prepared under pressure seems to be stable at room temperature. After several weeks, it was still present in specimens prepared by the described technique.

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Molar Size Sequences and Fossil Taxonomy

Abstract. *Although relative molar size has been considered a major taxonomic criterion, separating the Australopithecines and some* erectus *fossils from* sapiens *man, the $M_2 > M_1$, or "fossil" size sequence is found in 33 percent of Ohio whites and Pima Indians, yet is not necessarily the major sequence in the chimpanzee.*

Considerable attention has been paid to the relative size of the first and second molar teeth as being distinguishing features between fossil and modern forms of man. Following Weidenreich (*1*), both Von Koenigswald (*2*) and Clark (*3*) consider the relative size of M_1 and M_2 as having taxonomic value within *Homo*. Clark characterizes Pithecanthropus as having the $M_2 > M_1$ size sequence in the upper jaw (*3*), while Von Koenigswald and others attribute this size sequence to the Australopithecines and the "older" of the *erectus* fossils (*4*). In similar vein, Coon observes that some of the Neanderthals had second molars larger than the first, while others exhibited the $M_1 > M_2$ size sequence said to be characteristic of modern man (*5*).

Table 1. Molar tooth size sequence in Ohio whites and Pima Indians.

Tooth size sequence	Ohio whites		Pima Indians	
	Sides *	Percent	Sides *	Percent
	Maxilla			
$M_2 > M_1$	114	32.7	54	35.5
$M_2 = M_1$	34	9.7	11	7.0
$M_1 > M_2$	201	57.6	90	57.5
	Mandible			
$M_2 > M_1$	32	10.9	34	18.5
$M_2 = M_1$	8	2.7	11	6.0
$M_1 > M_2$	254	86.4	114	75.5

* Because of asymmetries, sides were enumerated separately.

Studies on infrahuman primates do not confirm the reliability of relative molar size as a major taxonomic criterion; considerable individual variability is found in the Liberian chimpanzee. Nevertheless, M_1 more commonly exceeds M_2 in mesiodistal tooth diameter (*6*). In *Cercopithecus ascanius* and *Cercopithecus aethiops*, the size ratios of M_1 and M_2 are variable, particularly in the maxilla, indicating that the relative size of the first two molar teeth is not an absolute taxonomic guide (*7*).

In our studies, the $M_2 > M_1$ or "fossil" tooth size sequence has proved to be reasonably common in two groups of contemporary man. Among 201 Ohio whites, 33 percent are characterized by the size precedence of M_2 over M_1 ($M_2 > M_1$) in the maxilla. Using odontometric data on 91 individual Pima Indians (*8*) we can demonstrate a comparable (36 percent) incidence of the $M_2 > M_1$ crown size sequence as shown in Table 1. In the lower jaw of each group, the $M_2 > M_1$ size sequence is less common, occurring in 10 percent of Ohio whites and 19 percent of Pima Indians. Clearly, modern man does exhibit the $M_2 > M_1$ or "fossil" molar size sequence.

Actually, simple size superiority of one molar tooth over the other proves to be a poor way of expressing the ratio, because of the steep regression of M_2 on M_1. The size of the second molar tooth tends to exceed the first in large-toothed human beings, and is smaller than the first molar in individuals with small posterior teeth.

Nevertheless, if the relative size of the first and second molar teeth are alone taken into consideration, it is evident that the $M_2 > M_1$ size sequence is by no means restricted to fossils. Moreover, with the extent of individual variability shown to exist in *Homo*, *Pan*, and *Cercopithecus*, the $M_2 > M_1$: $M_1 > M_2$ size sequence does not appear to be a taxonomically useful criterion above the species level. However, the prevalence of the size polymorphism, the apparent differences between recent populations, and the obviously hereditary nature, as shown by sibling similarities, in the $M_2 : M_1$ ratio ($r = 0.39$ for 58 pairings) suggest that relative molar size may be useful at the species level and below (*9; 10*).

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