

populations using a series of cranial measurements. These cranial measurements generally assess group identity through morphometric comparisons using multivariate and biological distance statistics (Howells 1989, 1973, 1969). The resulting groups, or clusters, reflect some degree of relationship or lack of relationship. There is an assumption that those populations displaying the most similarities, or affinity, are most closely biologically related. That is, groups that are closely related tend to share similar features and dimensions (measurements).

The lack of comparable data is particularly problematic when dealing with Paleoamerican (late Pleistocene to early Holocene-11,350-8,000BP) materials as there are only approximately 21 known skeletons from North America older than 8,500 BP (Powell & Steele 1992:59). Due to the limited number of ancient materials available, there are relatively few metric and/or non-metric morphological analyses (Bretemitz et al. 1971, Fenton 1998, Green et al. 1998, Jantz & Owsley in press-2000, 1998, 1997, Neves & Blum 2000, Owsley & Jantz 1999a,b, Ozolins 1999, Ozolins et al. 1997, Powell 1999, Powell & Neves 1999, Powell & Rose 2000, Powell & Steele 1992, Steele 2000, Steele & Powell 1999, 1994, 1993, 1992). Studies are often based on different measurements due to the fragmentary or incomplete nature of the material. Most ancient remains do not resemble contemporary Native Americans nor each other. "Specifically, the early skulls consistently have longer, narrower faces; longer, narrower braincases; a more projecting, mid-facial region; and cheekbones that slope to the rear," (Steele 2000:61) than Northern Asians and contemporary North American Indians. Jantz and Owsley (1998:128), in a study on 11 ancient crania, found that "...it is critical to recognize the marked heterogeneity among early American crania. This along with the finding that most early American crania are different from recent American Indians means that the history of American populations is much more complex than has generally been supposed."

A well expressed perspective is summarized by Steele and Powell (1994:158) "...the late Pleistocene and early Holocene populations of northern Asia and the Americas differed morphologically, but we are unsure of the cause of these differences. One view is that these differences substantiate that the earliest colonizing populations entering Beringia had a different genetic structure than later northern Asians and their North and South American descendants. The second view is that these differences reflect an adaptation of later populations to a different environment or lifestyle, possibly associated with the origins of agriculture, and that these adaptations were accomplished by the general plasticity of a common genome."

Spirit Cave Man Craniometric and Non-metric Studies

In the Jantz and Owsley craniometric study of Spirit Cave Man (Jantz & Owsley 1997), Spirit Cave Man's cranial dimensions were compared to 39 groups around the world (including eight North American Indian groups) with the number of comparison sample individuals ranging from 22 to 111. Multivariate analysis of individual components included vault profile, vault and face breadth, facial forwardness and prognathism, and face height, breadth and projection.

The Jantz and Owsley analysis identified the Spirit Cave Man cranium closest to "Norse" and "Ainu." It should be noted that the probability for Norse was 0.00084, with Ainu an even lower probability. Table 11 (Jantz & Owsley 1997:80) shows the distances of Spirit Cave Man from all of the comparative samples sorted from the smallest to the largest, showing Zalavar, Blackfeet, Numic, Atayal, and "Egypt" as the next five with a much lower probability. Jantz and Owsley note that the "...major conclusion is that the skull falls outside the range of variation of any modern population represented by currently available samples" (1997:79). That is not to say the measurements fall outside of the range of variation for modern Homo sapiens; more likely the currently available samples are insufficient to cover the range of variation in modern Homo sapiens.