Chapter 13

A Cladistic Evaluation of Ancient Thai Bronze Buddha Images: Six Tests for a Phylogenetic Signal in the Griswold Collection

Ben Marwick

Abstract

Fine art objects are often described as representative of certain craft or artistic traditions. In the case of Thai bronze Buddha images, art historical scholarship suggests that new styles often emerged from combinations of older styles transmitted between craft specialists. This process of transmission with modification is a key attribute of Darwinian evolutionary processes and suggests that lineages of artistic traditions such as Buddha images may be fruitfully investigated using quantitative evolutionary methods. The dominant method for reconstructing evolutionary lineages is cladistics. A cladistic analysis of 42 well-provenanced images in the Griswold collection is presented here to evaluate the usefulness of this approach. Six statistical tests are employed to determine if historical lineages can be reliably reconstructed using cladistic methods. All tests support the robustness of the results of the cladistic analysis. Quantitative evolutionary methods are concluded to be suitable and useful for understanding the evolution of craft traditions such as Thai bronze Buddha images.

Introduction

This chapter addresses the problem of whether or not concepts and methods borrowed from Darwinian evolution may produce reliable and useful results to advance our understanding of the history of Buddha images in Thailand. The key requirements of classical Darwinian evolution are that historical change in organisms occurs when variation and competition is present, and successful variants are inherited accumulated over time (Mesoudi *et al*. 2004). Adaptation, convergence and the loss or changes of function are also part of Darwinian evolution. All of these processes have also been shown to be at work in human culture (Mesoudi *et al*. 2004, 2006). As a result, archaeologists have been increasingly benefiting from the adoption of Darwinian evolutionary concepts in attempting to understand lineages of prehistoric and historic cultures and artifacts (O'Brien *et al*. 2001; Tehrani and Collard 2002; Collard and Tehrani 2005; Buchanan and Collard 2007; Lycett 2007, 2009). The most widely accepted and powerful method for investigating evolutionary lineages is cladistics, a quantitative method of analyzing comparative data to produce tree diagrams representing historical relationships between different groups as sequences of branching lineages (Kitching *et al*. 1998).

Darwinian evolutionary concepts are not entirely foreign to fine arts scholarship, but most efforts to date have focused on understanding the origins of the first human art and the adaptive functions that help explain its persistence (e.g., Dissanayake 1995; Bedaux and Cooke 1999; Dutton 2003; Steadman 2008). Here I explore the claim that Darwinian evolutionary methods have relevance beyond questions of origins and persistence by contributing to questions about the history of specific lineages in established artistic traditions. The aim of this chapter is to determine if the evolutionary history (or phylogeny) of Thai Buddha images can be reliably hypothesized using cladistic methods.

Bronze Buddha statues in Southeast Asia are typical of much religious art in having complex religious functions as objects of worship, admiration, inspiration, demonstrations of donor wealth and signals of membership of certain traditions and doctrinal schools (Reynolds 1978; Stratton and Scott 2004). Although fine art scholarship has a long and fruitful tradition of describing and analyzing the formal qualities, stylistic and iconographic details of fine art objects such as Buddha images, it lacks a coherent method for quantitatively comparing variation between objects and systematically representing this variation over time. For example, Buddha images are often described in aesthetic and emotional terms such as "carrying tendencies" of certain styles, and having "relaxed" features or showing "tension" with "severe expressions", "electrically charged curves" and so on (Woodward 1997; Stratton and Scott 2004). In this analytical tradition, quantitative details typically include basic geometric and morphological attributes and relative comparisons of size. This approach to describing objects is widely employed by fine arts scholars and has made substantial contributions to our understanding of many key areas of art history. For example, the Khmer style of Buddha images is frequently characterized as having a wide face with straight sides, a square jaw and undulant lips, distinct from the Sukhothai style with the vibrancy and energy that its curved facial features evoke.

However, a complement to this prevailing art historical approach may be found in quantitative comparison of the morphological details of facial features that convey these aesthetic impressions. This kind of quantitative comparison provides a statistical framework for exploring the degrees of relatedness between different styles in a craft tradition. In this chapter I demonstrate how cladistic methods can provide tools for this comparison. I present the results of a statistical investigation of the goodness-of-fit between the results of a cladistic analysis and a dataset derived from the Griswold collection at the Walters Art Museum in Baltimore. The results show that the evolutionary histories generated by cladistic analysis are reliable and that they present valid hypothetical phylogenetic relationships between groups of Buddha images.

Archaeological Cladistics

The starting point in pursuing a quantitative evolutionary analysis of Buddha images is investigating the likelihood that the key Darwinian process of descent with modification has occurred. If I can establish that craft traditions were transmitted between different generations of workers in lineages related to their geographic location and cultural affiliation then I can attempt to understand the forces that shaped these lineages. If styles were freely and simultaneously transmitted across geographic regions and between different cultural groups then I am unlikely to be able to reconstruct lineages.

Previous work on Buddha images suggests that transmission of stylistic information between craftspeople was an important source of new styles and largely constrained by geography and cultural affiliation. The basic art historical framework of Thai Buddha images suggests a system of transmission with modification of styles between generations, with its chronological succession of styles emerging in different parts of the country (Dvararati, Khmer, Sukhothai, Lanna, etc.). These styles are well-documented as inheriting elements of older styles as well as introducing novel details (Woodward 1997). Specific historical accounts also support a transmission with modification process. For example, King Sri Dharmatraipitaka is described as ordering craftspeople in his city (Pitsanulok) to visit established centers of Buddha image production at Si Satchanalai to combine those styles with that of the king's home town (Chaeng Saen, whose craftspeople were thought by the king to be insufficiently prestigious) to develop new styles to characterize the king's reign (Chulalongkorn 1961). While the historicity of events surrounding King Sri Dharmatraipitaka is questionable because of supernatural elements contained in the account, historian Damrong Rajanubhab similarly described how the Sukhothai style emerged out of craftsmen from Chiang Mai and Sukhothai taking the most beautiful characteristics from each school of sculpture and combining them to create a new style (Huan Phinthuphan 1971). This suggests that a model of transmission with modification, in which new styles arise from existing ones, is a good fit for the history of Buddha images.

Given that the process of transmission with modification seems to be a reasonable model for the production of Buddha images, I now turn to methods of classifying and analyzing the results of this process. Cladistics is a method of classifying organisms, artifacts, languages and cultures to show probable relationships between ancestors and descendants. This method is widely used by biologists, and to an increasing degree, by archaeologists (e.g., O'Brien *et al*. 2001; Collard and Tehrani 2005; Buchanan and Collard 2007; Lycett 2007; Riede 2009), anthropologists (Mace and Holden 2005; Nunn *et al*. 2010), linguists (e.g., Rexová *et al*. 2003; Gray *et al*. 2009), philologists (e.g., Spencer *et al*. 2004; Eagleton and Spencer 2006) and business administrators (Leseure 2002; McCarthy 2005).

Cladistic methods result in hypothetical or possible reconstructions of historical relationships depicted by tree diagrams showing the relatedness of different taxa or artifact classes according to their shared derived (or new) attributes, rather than their shared ancestral attributes (O'Brien *et al*. 2002). For example, two taxa or artifact groups are considered to be more closely related to one another than either is to a third if the two share a common ancestor that is not also shared by the third taxon or artifact group. In other words, two taxa are considered to share a common ancestor to the exclusion of a third if they exhibit novel attributes that are not also exhibited by the third taxon. The basic steps of a cladistic analysis are, briefly, (1) choosing the taxa (or artifact groups) whose evolutionary relationships are of interest, (2) determining the attributes (known as characters) that will be used to provide evidence for relationships and preparing a character state data matrix showing the state of each character for each taxon, (3) analyzing the attributes to reconstruct relationships between the taxa. This step typically results in a cladogram, which is a tree diagram depicting a hypothetical branching sequence of lineages leading to the taxa chosen in step one (Buchanan and Collard 2007).

Amongst the many challenges in the adaptation of this biological evolutionary method for archaeological purposes is the selection of characters or attributes that are considered relevant to the evolutionary history of the taxa or object under study. The ideal characters for reconstructing lineages are those are identical in different lineages because they have been transmitted between generations, in particular from a time when a single lineage split into two. This is described by cladists as a homologous character; one that is hypothesized to have been inherited from a common ancestor by vertical transmission. The alternative type of attribute is one that is identical in different lineages because it appeared (or evolved) in those lineages after they diverged from their common ancestor. These types of attributes are known as analogous characters and are of no use in cladistics because they do not reveal any heritable continuity; instead they are a result of independent adaptation, convergence or horizontal transmission between lineages.

In an archaeological cladistic study, the units of transmission are not the proteins encoding genetic information that molecular biologists rely on, but nebulous and intangible information socially transmitted between individuals over generations. As Stephen Lycett notes (2009), these entities are not directly empirically measurable in archaeological data; instead we must rely on proxies such as the morphology and morphometry of artifacts. Alex Mesoudi *et al*. (2006: 335) and Mike O'Brien *et al*. (2001) argue that archaeology and palaeobiology share this dependence on proxies but it has not hindered the efforts of palaeobiologists to explain evolutionary histories of extinct animals such as dinosaurs for which DNA is unavailable or rare. The assumption here is that just as genes manifest themselves in the skeletal morphology (as well as trace fossils such as casts and burrows) of extinct animals, socially transmitted ideas likewise manifest themselves as subtle quantifiable differences in the morphology of artifacts.

The problem of identifying a generalizable approach for determining which morphological features of artifacts are homologous and thus best suited to cladistic analysis has received only limited attention (see O'Brien and Lyman 2003). In previous archaeological cladistic studies, researchers typically selected characters relating to artifact shape, especially in the case of flaked stone artifacts (O'Brien *et al*. 2001; Buchanan and Collard 2007; Lycett 2009). Jamie Tehrani and Mark Collard's study of Turkmen textiles (2002) is probably the most relevant to a study of Buddha images because it uses decorative ornaments and border motifs on the textiles as characters for the cladistics analysis and excludes any technological or manufacturing attributes. The common theme in character selection of all of these studies is that they try to choose characters that are relatively isolated from the effect of technological, economic and performance-related variables which might dilute the signal of stylistic traits acquired by vertical transmission.

Another important detail from these previous studies is that even when the specific mechanisms of transmission of the characters chosen for analysis are unknown or poorly understood, they are still found to contribute information about continuity and change that is useful for testing hypotheses about the evolutionary history of culture (see O'Brien *et al*. 2003). These studies suggest that it is likely that cladistic analysis can be useful for detecting phylogenetic signals in many kinds of artifacts. In this paper I test the hypothesis that phylogenetic signals can be detected in assemblages of Thai bronze Buddha images. If a phylogenetic signal is present, then I can use the output from these cladistics methods to represent and describe the history of Buddhist imagery and gain insights into the sources of stylistic variations.

Materials and Methods

The sample employed for this analysis consisted of a selection of 42 cast metal Buddha images in Griswold collection of sacred sculpture of Thailand held in the Walters Art Museum in Baltimore, U.S. [Fig. 13.1]. This collection was assembled by Alex Griswold in Thailand during 1945–56 and is exceptional because of the detailed provenance information that he recorded with each item. It is also exceptional because of the detailed catalogue of selections from the collection was published by the museum in 1997 that included photographs, and for many of the images, thermoluminescence dates (TL) of the clay cores, petrographic data indicating the origins of the clays in the cores of the images and elemental analysis of

Fig. 13.1: Example of a bronze Buddha image (h. 92cm) from the Griswold collection (accession number 54.2775). This image is a classic example of the Sukhothai style (Reproduced with permission of The Walters Art Museum).

the metals (Woodward 1997). This collection was chosen as the source of data for this study because the detailed catalogue provides data to evaluate the outcomes of the cladistic analysis.

The catalogue presents the images in seven chronologically ordered but overlapping groups, corresponding to widely recognized major culture-historical units (see Wyatt 2003) which are briefly summarized here. The Dvaravati group relates to a poorly understood early Mon political entity or entities in central Thailand centered on Nakhon Pathom and U Thong (Lyons 1979; Mudar 1999). There are very few relevant inscriptions or texts despite nearly 400 years of artistic and architectural output (Brown 1996). In general, Dvaravati Buddha images are thought to derive from a combination of Sri Lankan and Indian Amaravati and Gupta styles integrated with local Thai innovations (Sirisena 1978: 153–5; Promsak Jermsawatdi 1979: 63). Hans De Casparis and Ian Mabbett (1992) note that the distinctive features of Dvaravati Buddha images are the broad face and the eyebrows continuing above the nose, as well as other details about hair decorations, hand postures and frequently depicted attendant deities.

The Khmer group corresponds to the period of the maximum extent of the Angkorian Empire, which included the important Buddha image production centers of Phimai and Lopburi in Thailand and Angkor itself in Cambodia. Hiram Woodward (1997) describes the typical facial features of Khmer Buddha images as a square to round face often with straight sides, broad and straight mouth and square jaws.

The Thirteenth Century group represents a diminution of Khmer influence as the Angkorian empire receded and there was a revival of a form of Buddhism with links to Burma (as the Pagan empire expands into modern Thailand) and iconography from Sri Lanka and northern India. During this time, Lopburi remained an important centre of production where Khmer artistic traditions continued and Haripunjaya emerged as a new centre combining Burmese styles from Pagan with local Mon styles. Carol Stratton and Miriam Scott (2004: 95) claim that Haripunjaya was the direct artistic predecessor to the Lanna group of northern Thailand. Most of the stylistic unity of the Thirteenth Century group comes from hand gestures and locations relative to the body. The main facial feature noted by Woodward (1997: 123) as common to the Thirteenth Century group are eyebrows joined across the bridge of the nose and an intersection of the brow bar with the nose.

The Sukhothai group is defined by a period of radical news styles of sculpture and direct influence from Sri Lanka following the Thai overthrow of Khmer control of the town of Sukhothai. Woodward (1997) describes a v-shaped mouth, bulging eyes as characteristic of the face, but most of the distinctive attributes for the Sukhothai group relate to the body, such as the free-standing walking posture and the curves of the limbs and robes.

The Early Ayutthaya group refers to the time of the founding of the Ayutthaya dynasty at U Thong, which is an important centre of bronze Buddha image production during this period. Ayutthaya is also notable as a period of increased engagement of Thais with international cultures including East and West Asian groups. The Ayutthaya style is thought to have emerged from a combination of influences from Sukhothai and the Khmer styles at Lopburi (Volunteers 1987: 47). Distinctive facial features noted by Woodward (1997) include arched and joined brows, a straight hairline, an incised chin and an outline or trace incised around the lips.

The Lanna group corresponds to images produced in northern Thai towns such as Chiang Mai and Chiang Saen as the influence of these towns rose under powerful leaders. The Lanna style has a very diverse range of influences including stylistic connections with the Sukhothai and Early Ayutthaya groups, Khmer styles of central Thailand (such as Lopburi), Burmese styles from Haripunjaya, northern India and Sri Lanka (Woodward 1997; Stratton and Scott 2004). The Lanna group is described by Woodward (1997: 210) as a “stylistic potpourri” and characteristic facial features are limited but include crowns, planar eyes, and v-shaped mouths.

The Late Ayutthaya group is marked by the beginning of the rein of King Ramathibodi II and a time of an expansion of cultural and commercial contact with European and Asian nations. Distinctive features of images in this group are mostly found in the decorations such as the depiction of jewels in the Buddha’s crown and the Buddha’s clothing, especially the regal attire that reflects the rise of absolutism of the Ayutthaya kings during this period (Woodward 1997).

The division of the images into these seven groups is based on stylistic and aesthetic criteria described by Woodward (1997). These groupings are supported by mineralogical and textural analysis of the clay cores (Reedy 1997) and elemental analysis of the metal alloys (Drayman-Weisser *et al*. 1997) for many of the images. The clay analysis shows especially clear differences between Sukhothai, Ayutthaya and Lanna images. The metal analysis was effective at distinguishing between all seven groups though the different proportions of lead, tin, lead, copper and arsenic. Although the seven groups used here compress some chronological and stylistic variation, they receive good support from the clay and metallurgical data and are a useful starting point for testing hypotheses about lineages of craft transmission.

Taxa and Characters

These seven groups described above were employed as taxa for the cladistic analysis. Within each group all cast metal heads were analyzed to create a character state matrix, excluding a few highly corroded or very small images that where the full suite of characters could not be unambiguously observed. The total number of images analyzed was 42, with a minimum of three in the Dvaravati group and a maximum of nine in the Early Ayutthaya group

Initially 30 morphological characters were proposed, but replicate analyses of the images by multiple people revealed that only 17 of these characters could be reliably measured. These 17 morphological characters were analyzed on each image by inspecting the photos in the published catalogue and reviewing the accompanying descriptive text. Because none of the photographs contained measurement scales it was not possible to take measurements of continuous variables from the photos to use with morphometric characters [as O'Brien *et al*. (2001) and Buchanan and Collard (2007) did]. Thus the selection of characters for this study was limited to discrete and non-overlapping variables. A few shape-related characters used here, such as whether the brows are flat or arched or whether the lips are straight or undulant, might be more accurately resolved with continuous measurement data, but this remains a task for future work.

All of the characters used here focused on the face of the Buddha image. There were two reasons for this, first that it allowed for the largest possible sample of comparable characters because some images consist only of a head. The second reason is that facial features are almost completely uninfluenced

Table 13.1: Details of morphological characters used in this analysis

Character	Description
1	Eyebrows separated (0) or connected (1).
2	Eyebrows detached from nose (0) or connected vertically (1).
3	Eyebrows detached from nose (0) or connected horizontally (1).
4	Eyebrow ridge raised (0) or incised (1).
5	Eyebrows flat (0) or arched (1) over the eyes.
6	Mouth wider than the maximum with of the nose (0) or equal to or narrower than the nose (1).
7	Lips straight (0) or undulant (1), i.e. the line between the left cheilion, stomion and right cheilion is straight or undulating.
8	Upper lip straight (0) or undulant (1) i.e. the line between left cheilion, labial superius and right cheilion is straight or undulating.
9	Lips thick (0) or thin (1).
10	Mouth ridges absent (0) or present (1) i.e. there is / is not a recessed rim or trace running around the outside of the lips, sometimes interpreted as a moustache.
11	Curl at corner of mouth (1) or none (0) i.e. the cheilions come to a linear termination or a spiral termination.
12	Chin absent (0) or present (1) i.e. there is/is not an incised line to indicate the presence of a chin.
13	Hairline obscured under crown (0) or present and level across the forehead (1).
14	Hairline obscured under crown or flat (0) or peaked above the eyes on the forehead (1).
15	No crown (0) or crown present (1).
16	Eyes planar (0) or swooping (1) i.e. the line between the endocanthion and the exocanthion is horizontal or angled upwards.
17	Eye socket not divided from brow (0) or divided by an incised line (1).

by design conventions relating to the specific posture (i.e., seated, standing, walking or reclining) and the different activities and stages in the life of the Buddha (Stratton and Scott 2004). This means that facial features are more likely to encode subtle design features that can vary freely relative to the rest of the image. They are likely to be less correlated with overall body posture than details such as the hand posture. Because of this lack of correlation I expected to capture a greater degree of variation through analysis of these features. Although this focus on the facial features results in the exclusion of some details of the body and limbs used by art historians to identify styles (and that are also not correlated with posture), I consider this a necessary compromise to limit the complexity of this pilot study. Table 13.1 provides the details of the characters employed in this study [see Leslie Farkas (1981) for explanations of the anthropometric landmarks]. For each image, all characters were coded as present or absent. Table 13.2 shows the character state matrix for the individual images.

Table 13.2: Character state matrix for individual images

	Character																
Catalogue number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
9	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1
15	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
18	1	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0
22	1	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
32	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
41	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0
43	1	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0	0
44	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
46	1	0	1	0	0	1	0	1	0	1	0	0	1	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
48	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
50	0	1	0	0	1	1	1	1	0	1	0	1	1	0	0	0	0
53	0	1	0	0	1	0	1	1	0	1	0	0	0	1	0	0	1
54	0	1	0	0	1	1	1	1	0	1	1	1	0	1	0	1	0
55	0	1	0	0	1	1	1	1	1	1	0	1	1	0	0	1	0
56	0	1	0	0	1	1	0	0	1	1	0	0	0	1	0	0	0
57	0	1	0	0	1	1	1	1	0	1	1	0	1	0	0	0	0
58	0	1	0	0	1	1	1	1	0	1	0	1	0	1	0	0	1
59	1	0	1	0	1	1	1	1	1	0	0	0	0	1	0	0	0
61	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0
62	1	0	0	0	0	0	0	1	1	1	0	0	1	0	0	0	0
63	1	0	1	0	0	1	1	1	0	1	0	0	1	0	0	0	0
65	1	0	0	1	1	1	1	1	0	1	0	0	0	1	0	0	1
66	1	0	0	1	1	1	1	1	0	1	0	0	0	1	0	0	1
67	1	0	1	0	1	1	1	1	1	1	0	0	0	1	0	0	1
73	1	0	1	0	1	1	1	1	0	1	0	1	1	0	0	0	0
75	0	0	0	0	1	0	1	1	0	1	1	1	0	1	0	0	1
77	1	0	1	1	1	0	0	0	0	0	0	0	0	0	1	0	1
78	1	0	1	0	1	1	0	1	1	1	0	0	1	0	0	0	0
79	0	0	0	1	1	0	1	1	0	1	0	0	1	0	0	0	1
81	0	0	0	1	1	1	0	1	0	1	0	1	1	0	0	0	1
83	0	0	0	1	0	0	0	1	1	0	0	0	0	1	0	1	1
84	1	0	1	0	1	1	0	1	1	1	0	1	1	0	0	0	1
90	1	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0	1
91	0	0	0	0	1	1	0	1	1	1	0	0	1	0	0	1	1
92	1	0	1	0	1	1	1	1	1	1	1	1	0	0	1	0	1
93	1	0	1	0	1	0	1	1	0	1	0	1	0	0	1	1	1
94	1	0	1	0	1	1	0	1	1	1	1	0	0	0	1	1	1
97	1	0	1	0	1	1	1	1	1	1	1	0	0	0	1	1	1
98	0	0	0	0	1	0	0	0	1	1	0	0	0	0	1	0	1

This method of creating a character state matrix for the 42 images was successful in capturing the diversity of the images, with only two pairs of images with identical character states (catalogue numbers 44 and 48 in the Thirteenth Century group and 65 and 66 in the Ayutthaya group). That each set of clones occurs within a single group informally suggests that characters selected for cladistics analysis support the use of the seven culture-history groups as taxa.

In describing the seven taxa, it was necessary to choose a method to summarize the variation in the images that comprise each taxa. Cladists describe the presence of this kind of variation amongst character states in a single taxon as polymorphism and they have developed a variety of approaches to handle these. John Wiens (1995) reviewed eight different methods for coding polymorphism and tested their performance on seven data sets, ranking the performance of each method against five criteria. He found that the frequency method performed best in all criteria, so this method was adopted here also. For each of the 17 characters, the average character state for all images in a taxon was calculated. These average values were then rescaled so that an average of zero for a character was equivalent to "absent" (0), an average of 0.1–0.49 was equivalent to "rare" (1) and 0.5–1.0 was equivalent to "common" (2). There were no average values between 0 and 0.1. Three states of abundance was the maximum number of states possible to ensure comparability between the different taxa because the smallest taxon has three images. Table 13.3 shows the resulting character state matrix for the taxa.

Parsimony Analysis

The character state matrix for the groups was then subjected to parsimony analysis to identify the cladogram or set of cladograms with the most parsimonious fit to the data. Parsimony analysis refers to the principle that the simplest explanation that can explain the data is the best. In this case, parsimony means that the best hypothesis of relationships between the groups is the one requires the smallest number of character changes (Kitching *et al*. 1998: 5). It results in a hypothetical evolutionary history with the fewest evolutionary changes. I treated the 17 characters in the simplest possible way with the least assumptions by using Walter Fitch's (1971) parsimony algorithms. This means that all characters were considered to be unordered (the lineages are not restricted to having characters change in order from absent to rare to common, they can change from zero to abundant or any state to any other state in a single step), freely reversing (characters in lineages are allowed to go from zero to abundant or abundant to zero with equal probability), and all character states were considered equally likely to occur (Swofford *et al*. 1990; Forey *et al*. 1993).

To help identify the order of character state changes, for example which character states are ancestral and which are new throughout the evolutionary history of the groups, it is necessary to include an outgroup amongst the taxa analyses. There are several competing methods for ordering character states and there is controversy about which is the most effective (O'Brien *et al*. 2003). I followed Tehrani and Collard (2009), Lycett (2009) and Buchanan and Collard (2007) in using the stratigraphic criterion to define an outgroup. In this case the outgroup is considered to represent the ancestral character from which the

Table 13.3: Character state matric for the seven groups (or taxa)

	Characters																
Groups (taxa)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Dvaravati	1	0	0	0	0	0	0	1	0	0	1	2	2	0	0	1	1
Khmer	2	0	0	0	0	0	1	1	0	1	1	2	0	0	2	0	0
Thirteenth Century	2	0	1	1	0	1	0	1	0	1	0	2	2	0	0	1	0
Sukhothai	1	2	1	0	2	2	2	2	1	2	1	2	1	2	0	1	1
Early Ayutthaya	2	0	1	1	2	2	2	2	1	2	0	2	2	1	0	0	1
Lanna	1	0	1	2	2	1	1	2	1	2	1	2	2	1	0	0	2
Late Ayutthaya	2	0	2	1	2	2	1	2	2	2	1	2	1	1	2	2	2

order of character state changes amongst the other groups can be determined. The stratigraphic criterion uses the oldest taxon in the dataset, in this case the Dvaravati, as the outgroup. Figure 13.2 shows the distribution of thermoluminescence dates available for the Buddha images used in this study, taken from Woodward (1997). Woodward gives TL ages as ranges only and notes there are some complications in TL dating the clay cores of Buddha images because repairs to the images can involve extensive recasting which can reset the TL signal. Nevertheless, there is a broad chronological trend evident in the TL dates for the seven groups. Although Woodward did not obtain TL dates for any of their Dvaravati images, they cite similarities between the Dvaravati images in their catalogue and to infer an age of AD 600–800 for their Dvaravati images, based on similarities to objects recovered from dated contexts at archaeological sites such as Chansen and U Thong (Lyons 1973). The use of the Dvaravati group as an outgroup does not imply that this site represents the initial source of variation for all subsequent Buddha images. It simply implies that, because of its early age, the Dvaravati group retains the most ancestral character states of the groups in this study.

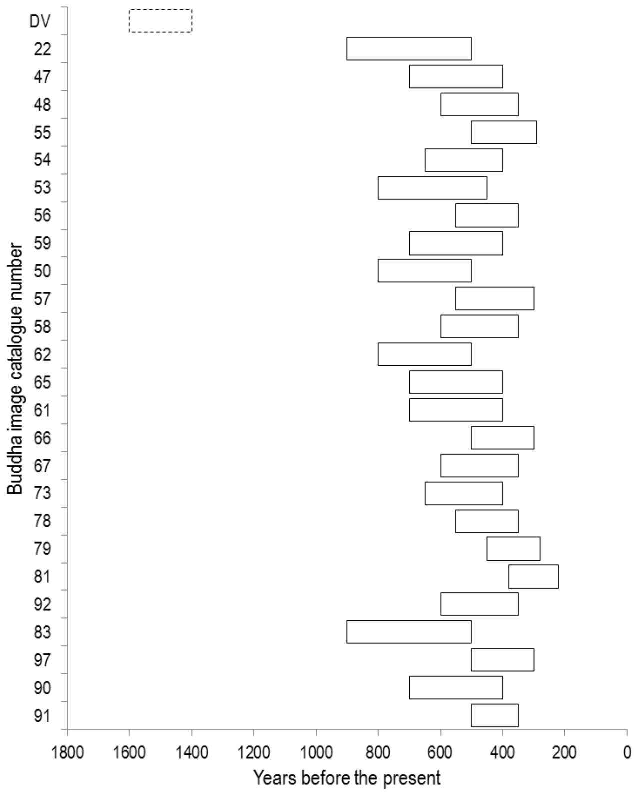

Fig. 13.2: Distribution of thermoluminescence dates for the Buddha images analyzed in this study (from Woodward 1997).

To find the most parsimonious trees for these data I used the PAUP* 4.0 software (Swofford 2002) to use parsimony criteria to exhaustively search through all possible trees that match the data. For each possible tree PAUP* finds the length (i.e., the number of character state changes required to explain the data set). The most parsimonious tree is the one with the smallest number of character state changes. Although branch-and-bound is a popular algorithm (O'Brien *et al*. 2001; Tehrani and Collard 2002; Buchanan and Collard 2007; Lycett 2009), I preferred the exhaustive search as it returns a frequency distribution of the lengths of all the possible trees. This distribution can then be used for one of the goodness of fit tests, the skewness test, discussed below.

Goodness of Fit Tests

I used six tests, none of which are reliable as exhaustive statistical tests by themselves, but taken together give a general indication of the goodness of fit between the resulting trees and the Buddha image data. PAUP* 4.0 was used to conduct all of these tests.

First I examined the skewness of the distribution of tree lengths, where a more normal distribution of tree lengths is thought to result from phylogenetically uninformative data and distributions with a strong negative skew (i.e., only a small number of very short trees and larger numbers of very long trees) result from phylogenetically informative data (Huelsenbeck 1991; Hillis and Huelsenbeck 1992). However, Mari Källersjö *et al*. (1992) have demonstrated that measures of skewness have been shown to be correlated with the frequencies of states within characters and claim that it is not reliable as a statistical test. Here I interpret the results of this skewness test as a general low-power indication of how phylogenetically informative the data are.

Second, I used the permutation tail probability test (PTP, Faith and Cranston 1992). This tests to see how likely the tree length of the shortest trees are to occur in random permutations of the original data. The permuted data are constructed by randomly reshuffling the character states separately for each character in the matrix. If the shortest trees found by the exhaustive search are significantly shorter than the trees generated by permuted data, then is usually taken to mean that a data set possesses a hierarchical signal. Since the discriminatory power of the PTP test is controversial (Peres-Neto and Marques 2000), I simply consider that if a dataset fails, the PTP test then is should not be used in a phylogenetic analysis rather than concluding a hierarchical signal is present from this test alone (Slowinski and Crother 1998).

Third, I used a more conservative test of the robustness of the shortest trees compared to a random sample, the bootstrap (Felsenstein 1985). The bootstrap procedure randomly samples the original characters together with replacement from the original dataset to form a pseudoreplicate data matrix with the same number of taxa, characters and character states as the original. The idea of "replacement" means that each taxon is "replaced" after it is randomly sampled and may thus appear more than once in a single pseudoreplicate data matrix. A large number of random pseudoreplicates are generated in this way, and each one is subjected to parsimony analysis. Then all the resulting trees are summarized in a single majority-rule consensus tree. Each branch of the consensus tree is annotated with the proportion of randomly sampled trees that contained that specific branch. This provides an assessment of how well supported the individual clades or branches are within a cladogram. Data that fit the archetypal bifurcating model will return consensus trees with higher proportions of support from the bootstrap samples. Like the PTP test, bootstrapping has been criticized as a method of testing the statistical significance of a cladogram (Kitching *et al*. 1998; Page and Holmes 1998: 222–3), so I use it here in parallel with the other tests as a general indicator of goodness of fit between the data and the trees. Although there is no agreed threshold value of the bootstrap proportions to accept or reject a clade (DeSalle *et al*. 2002: 82), David Hillis and James Bull (1993) suggest that bootstrap proportions of ≥70% usually correspond to a probability of ≥95% that the corresponding clade is real.

Fourth, I calculated decay index values as an alternative method to determine the reliability of the clades contained in the maximum parsimony trees. Decay index values, also known as branch support values, are a measure of the number of steps that the maximum parsimonious tree has to be increased in length before a particular clade disappears (Bremer 1988, 1994). The larger the index value for a given clade, the stronger the support is for that clade as a historical hypothesis. Simulation studies suggest that decay index values between three and 15 are indicators of clade reliability (Zander 2004). Interpretation of the decay index is not straightforward, especially for large datasets (Brower 2006), and it has been criticized as a poor estimate of clade reliability because of its correlation with the number of characters in proportion to the number of taxa in a dataset (Lee 2000). However, it is a widely used index amongst cladists, especially in palaeontology, so I employ it here in parallel with the other goodness-of-fit tests.

Fifth, I calculated the ensemble consistency index (CI) for the maximum parsimony trees as a measure of homoplasy in those trees. The CI is a simple ratio: the minimum number of character state changes expected given in the dataset divided by minimum number actually observed on the tree (Kluge and Farris 1969). The CI is a widely used measure in cladistics studies because of its simplicity and intuitive appeal (Klassen *et al*. 1991, Nunn *et al*. 2010). However, it also known to be problematic because of its high negative correlation with the number of taxa included in an analysis and with the percentage of characters that change per node of the tree (Sanderson and Donoghue 1989; Hauser and Boyajian 1997; Kitching, Forey *et al*. 1998). Consistency index values are also exaggerated by autapomorphies (unique character states that are found only in the terminal taxa of the tree and not part of an ancestor-descendant relationship), which are not informative in cladistics analyses (Bryant 1995). Despite these problems, the CI remains in use as a general low-power indicator of the amount of homoplasy in a tree. Sanderson and Donoghue have attempted to improve the CI by adjusting it to compensate for different numbers of taxa through use of a regression equation to evaluate CI values at a given number of taxa. Using this regression equation I compared the CIs of the maximum parsimony trees with the expected CI for a tree with seven taxa (see Buchanan and Collard 2007).

Finally, I calculated the ensemble retention index (RI) for the cladograms produced by the parsimony analysis. Like the CI, this index is a measure of homoplasy in a tree, or the amount of similarity in taxa of different ancestry that results from convergent evolution (Farris 1989). The RI is often used as an alternative to the CI because it is insensitive to the number of characters or taxa used in the analysis, and therefore RIs can be directly compared between different datasets. In a perfect cladogram, where a binary character changes from one state to the other only once and only at one branch of the tree, the RI would equal 1.0. In the real world, a given character state tends to change more than once at different nodes, resulting in a less than perfect fit with the topology of the shortest cladogram. To calculate the ensemble retention index I determined the ratio between the amount of synapomorphy (the number of characters shared by two or more taxa and their most recent common ancestor) expected from the data set and the amount that is retained as synapomorphy on the cladograms produced by parsimony analysis. I compared our RIs with RIs from 41 cladograms produced from anthropological and biological datasets published by Collard *et al*. (2006). If the cladograms resulting from the Buddha image analysis contain large amounts of homoplasy (perhaps due to parallel or convergent evolution) then I would expect RIs on the lower end or outside of the range of RIs in the Collard *et al*. (2006) dataset.

Due to the relatively small number of taxa in this sample I did not attempt sensitivity testing such as repeating the above tests after removing taxa with small sample sizes (see Buchanan and Collard 2007).

Results

The parsimony analysis found 945 possible cladograms for the data and three cladograms that have the same minimum tree length and are thus the most parsimonious cladograms. The cladograms were drawn using the TREEVIEW software (Roderic 1996) and are shown in Figure 13.3. The three trees are similar in the location of the Sukhothai, Early Ayutthaya, Lanna and Late Ayutthaya as in a single clade. Trees A and C are similar in having Sukhothai as a sister taxon to a clade containing Early Ayutthaya, Lanna

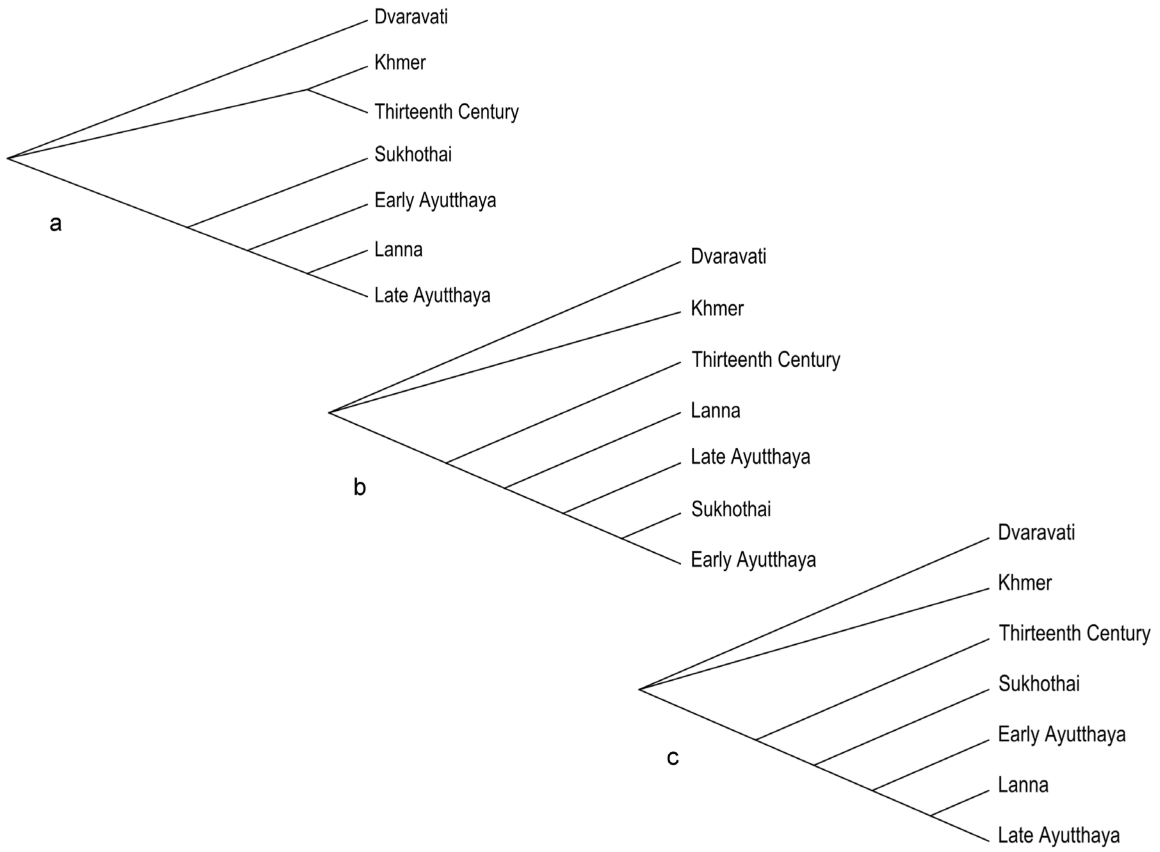

Fig. 13.3: Three maximum-parsimony cladograms for the Buddha image data inferred using the exhaustive search algorithm in PAUL* 4.0.

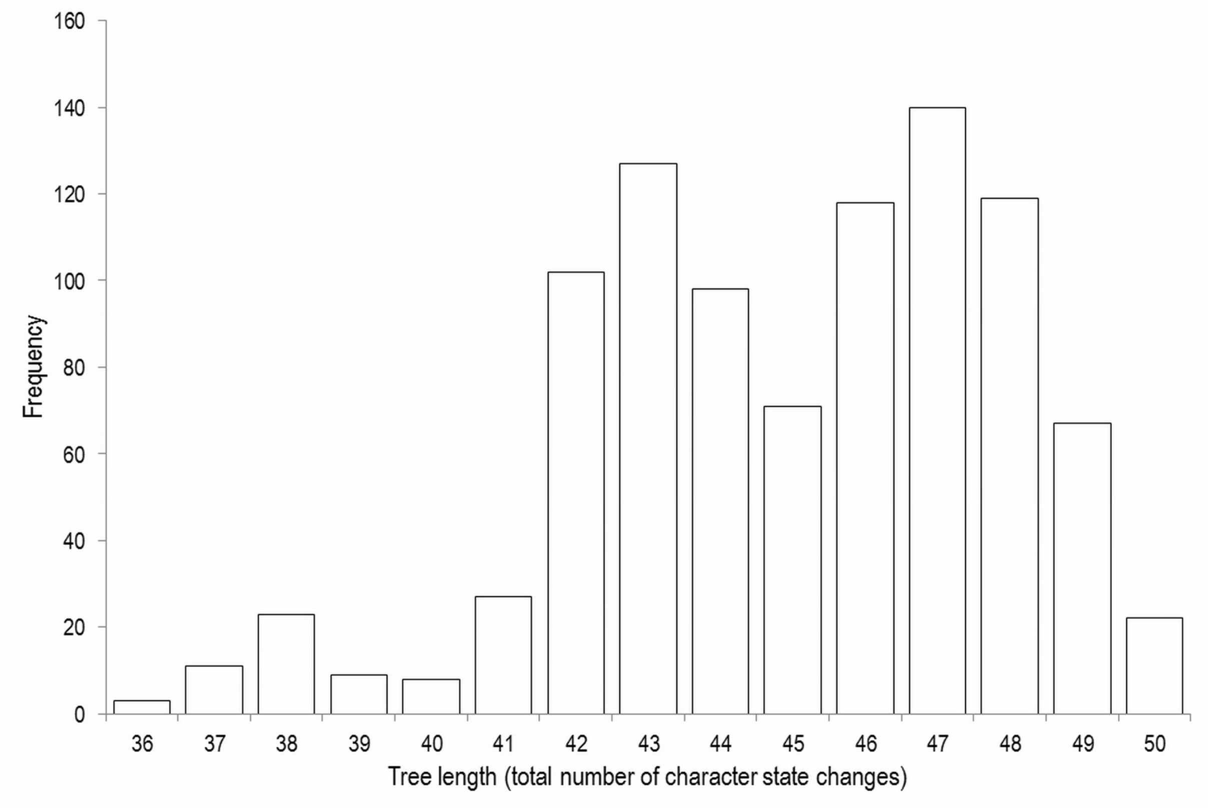

Fig. 13.4: Histogram showing the frequency distribution of the lengths of all possible trees.

and Late Ayutthaya, and Early Ayutthaya as a sister taxa to a clade containing Lanna and Late Ayutthaya. Dvaravati, Khmer and Thirteenth Century groups are consistently represented as part of a larger clade in all three trees and in tree A, they form a distinct clade by themselves.

The length of these three maximum parsimony trees was 36, indicating 36 character state changes across each tree. Figure 13.4 shows the frequency distribution of the lengths of all possible trees for these data. The distribution is bimodal and non-normal with the long tail on the left side, indicating a negative skew. The skewness statistic (g_1) is –0.552 which can be interpreted as moderately skewed (Bulmer 1979). These qualities of this distribution are suggestive of the presence of a phylogenetic signal in the data.

The second goodness-of-fit test, the PTP test, was undertaken with 100,000 cladograms generated from permutations of the original data. The shortest tree resulting from this process had a length of 32 and the longest had a length of 42 [Fig. 13.5]. Out of the 100,000 trees, 2002 were equal to or shorter in length that the three maximum parsimony trees, indicating a probability value of 0.02. This suggests that 98% of the cladograms resulting from the permuted data are longer than the shortest trees produced by the unpermuted data. These data pass the PTP test with a probability value of less than 0.05 that a random dataset would contain an equivalent phylogenetic signal to the original data. These results are equivalent to the 98% value observed by Tehrani and Collard (2002) for the Iranian textiles, supporting the above interpretation of the skewness data that these Buddha data contain a phylogenetic signal.

The third test, the phylogenetic bootstrap, used 100,000 resamples from the original data. Figure 13.6 shows the majority rule consensus tree which displays all clades that occur frequently in the 100,000 bootstrap samples, together with the percentage of bootstrap trees that contain that clade. The 86 value on the clade containing Sukhothai, Early Ayutthaya, Lanna and Late Ayutthaya indicates that 86% of the bootstrap trees contained this clade. This clade is present in all three of the maximum parsimony trees. The other clades in the maximum parsimony trees receive less support from the bootstrap data. The Sukhothai-Early Ayutthaya clade of tree B appears in 29% of the bootstrap trees and the Lanna-Late

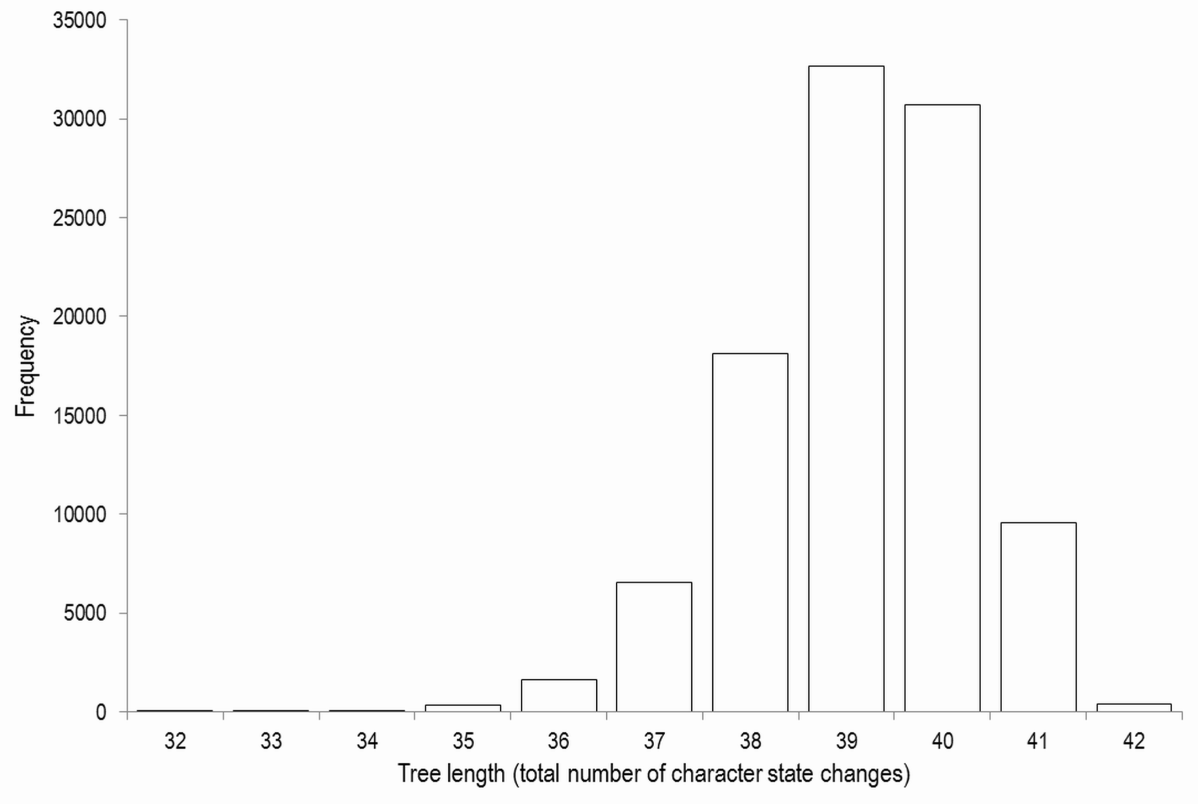

Fig. 13.5: Histogram showing the frequency distribution of lengths of 100,000 trees generated for the permutation tail probability test.

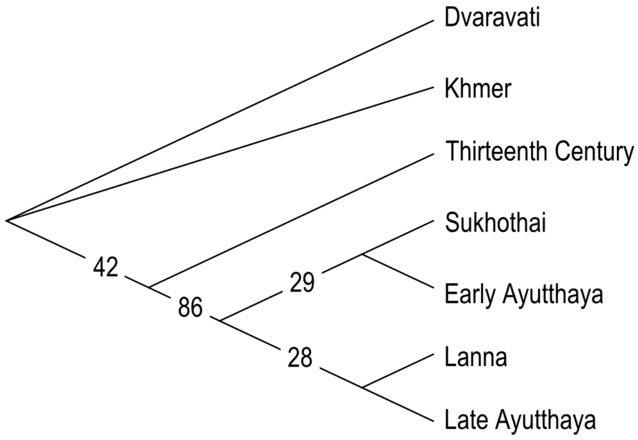

Fig. 13.6: Majority-rule consensus tree from 100,000 bootstrap samples.

Ayutthaya clade of tree C appears in 28% of the bootstrap trees. I interpret the results of the bootstrap procedure as suggesting that there is a reliable phylogenetic signal in the data. The bootstrap data suggest that of the three maximum parsimony trees, tree B is the most probable hypothetical reconstruction of lineages of the seven groups, but is only preferred by a small amount.

Complementary to the bootstrap test, I calculated the Decay Index according to the procedure proposed by Peter Forey *et al*. (1993). The strict consensus trees resulting from the iterations of parsimony analysis as tree length was increased included only a single clade for which decay values could be measured. This was the Sukhothai, Early Ayutthaya, Lanna and Late Ayutthaya clade with a Decay Index value of three. This is within the reliable range indicated by Richard Zander (2004), although it falls on the lower side of the range. I interpret this as a sign of support for the Sukhothai, Early Ayutthaya, Lanna and Late Ayutthaya clade which is present in each of the maximum parsimony cladograms. This decay index value represents a lack of evidence to reject the maximum parsimony cladograms.

Fifth, the ensemble consistency index values value for each of the three maximum parsimony trees was determined to be 0.72. This is not significantly different from the value of 0.75 predicted for seven taxa by Michael Sanderson and Michael Donoghue's (1989) regression equation. The CI obtained here is also a "high" value (i.e., >0.60) according to the simulations of Charles Nunn *et al*. (2010), which they interpret as indicating rates of low horizontal transmission and the distribution of observed cultural variation as a result of phylogenesis. I interpret this as indicating that there is no evidence for high levels of homoplasy in the maximum parsimony cladograms.

Finally, the ensemble retention index value for each of the three maximum parsimony trees was determined to be 0.60. This compares favorably with the mean RI of 0.59 (range 0.42–0.78) returned by Collard *et al*.'s (2006) 20 cultural datasets. It is slightly lower than the mean RI of 0.61 returned by their 21 biological datasets, but comfortably within the range of 0.35–0.94. This RI is also a "high" value according to the simulations performed by Nunn *et al*. (2010), indicating low rates of horizontal donation. I interpret this RI value as supporting the CI data regarding low homoplasy in the maximum parsimony cladograms and thus a further strand in the argument in favor of the presence of a phylogenetic signal in the Buddha data.

Discussion and Conclusion

The main goal of this study has been to test the hypotheses that the history of Thai Buddha images can be reliably hypothesized using cladistic methods. Although the six goodness-of-fit tests presented above are not formal tests of this hypothesis, they are all consistent in indicating that a phylogenetic signal is present in the Buddha image data. I interpret this consistency as support for both the original hypothesis and the reliability of cladistics methods for investigating fine art traditions in general. The implication of these results is that evolutionary processes acting on the vertical transmission of craft information has played a role in the historical changes documented in the seven groups of Buddha images investigated here.

The hypothetical relationships depicted in the cladograms resulting from this analysis are consistent with the relationships between the seven groups described by Woodward (1997). Although a detailed analysis is beyond the scope of this chapter, and the relatively small sample size limits the confidence of these relationships, we can see that the Lanna group shares many character states with the Thirteenth Century, Sukhothai, Early and Late Ayutthaya groups, reflecting the "stylistic potpourri" described by Woodward. Early Ayutthaya and Sukhothai are closely related on all trees and a very close relationship is depicted on tree B and the bootstrap majority consensus tree. The ambiguity of the Khmer influence on the Thirteenth Century group is expressed by the close relationship depicted in tree A, perhaps reflecting the influence of the Lobpuri images in the parsimony analysis, but trees B, C, and the bootstrap consensus tree show a more distant relationship between the Thirteenth Century and Khmer groups. These consistencies between the cladograms and Woodward's analysis are an important verification of the cladistic method with these data. It is significant to note that the cladistic results derive from an analysis of facial features, most of which were not used by Woodward in his classification system. Woodward's system is more wholistic and impressionistic. Undoubtedly the specific morphological details used in this cladistics study also contributed, perhaps subconsciously, to Woodward's classification, but we believe the cladistic method can make a significant contribution to fine art scholarship because of its advantages of repeatability, objectivity and amenability to statistical analysis.

Cladistic methods have the potential to improve our understanding of many kinds of fine art traditions and is gaining recognition as a key tool for phylomemetics, which is defined by Christopher Howe and Heather Windram (2011: 4) as "modeling the history of any system [of non-genetic data] in which (i) elements can be replicated with the incorporation of changes and (ii) any change between a progeny element and its parent is stably transmitted in subsequent generations". The success of this cladistics analysis of Buddha image data has opened up two specific and related lines of future work. First is that a cladistic analysis may have the potential to answer questions about the degree of influence of a prominent centre of sculpture production had on smaller centers in the region and the shifting importance of influential centers over time as craft specialists incorporated different influences into their work. By identifying sub-groups of the Buddha images according to the location of their manufacture, and analyzing these sub-groups as taxa, we will get higher resolution on the craft lineages that were most influential in the seven periods analyzed here. For example we may be able to measure the influence of the Lopburi style on 13th century and later period images.

Second, detailed histories of the morphological changes that contributed to each of the seven groups can be produced. In biological phylogenetics, this typically involves two analyses: ancestral character state reconstructions and estimation of speciation and extinction rates. Ancestral character state reconstructions are an attempt to infer the character states at ancestral nodes of a phylogeny from the distribution of traits in the analyzed sample of objects (Pagel *et al*. 2004). This is possible through the analysis of the character state changes at each node of the cladogram so that hypothetical ancestral states can be determined. It is a method of understanding evolutionary processes by revealing the pathways and pattern of character evolution (Qui-Yun Xiang and Thomas 2008). Using methods for estimating speciation and extinction rates, it will also be possible to determine the most stable and unstable characters in the lineages (Sanderson 1997; Ricklefs 2007), in terms of their frequency of change, and test hypotheses about the historical implications of these. The speciation rate data resulting from this can then be formally examined in light of cultural and population histories (e.g., of dispersals and fissioning of groups) to investigate associations between style change and major historical events (see Tehrani *et al*. 2010; Matthews *et al*. 2011).

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