

**AFFINITY OF TWO SOUTH FLORIDA POPULATIONS THROUGH  
NONMETRIC DENTAL ANALYSIS**

by

Daniel Benitez

A Thesis Submitted to the Faculty of

Dorothy F. Schmidt College of Arts and Letters

In Partial Fulfillment of the Requirements for the Degree of

Master of Arts

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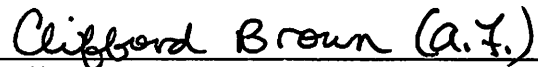
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This thesis was prepared under the direction of the candidate's thesis advisor, Dr. Meredith A.B Ellis, Department of Anthropology, and has been approved by all members of the supervisory committee. It was submitted to the faculty of the Dorothy F. Schmidt College of Arts and Letters and was accepted in partial fulfillment of the requirements for the degree of Master of Arts.


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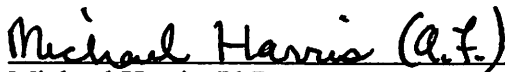
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## ABSTRACT

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This research examines the relationship of two archeological populations in Southeastern Florida from the Middle Woodland Period. The two sites chosen include the Belle Glade site in the Belle Glade Cultural Area and the Highland Beach Mound site in the East Okeechobee Cultural Area. The determination of relationships was done through an analysis of nonmetric dental traits. A series of traits were recorded in an ordinal scale and later dichotomized into present or absent, in order to conduct a biological distance analysis. The statistical method chosen for this analysis was the Smith's Mean Measure of Divergence. Results indicate that both populations have a minimal degree of divergence. These results corroborate the evidence gathered from past archeological investigations

**Statement on NAGPRA Status:**

**The Highland Beach collection discussed in this master's thesis and housed at Florida Atlantic University, is currently listed in the Native American Graves Protection and Repatriation Act (NAGPRA) Culturally Unaffiliated database. However, compliance is ongoing at Florida Atlantic University, and out of respect for interested tribal parties, the raw data from these analyses is not presented here. The data from the Belle Glade Mound, housed at the Smithsonian Institution, is not subject to NAGPRA regulations; however, out of respect for tribal interests, that information is also not included. Such data can be made available to other researchers if requested directly.**

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NONMETRIC DENTAL ANALYSIS**

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## CHAPTER 1: INTRODUCTION

The current understanding of the relationship between pre-Columbian human populations in Florida is limited. As a result, it is difficult to determine the degree of relatedness within and between these groups. Historically, genetic analysis has been the most effective method of analyzing population relationships; however, this procedure presents several obstacles that include budgetary costs, as well as legal, and ethical considerations. Previous analytical attempts at deciphering and determining relationships among South Florida populations has primarily been conducted through intensive archaeological investigations (Goggin, 1947; Furey, 1972; Carr and Beriault, 1984; Milanich, 1994; Sears et al., 1994; Pepe, 1999; Griffin, 2002; Davenport, C. D. et al., 2011).

Archaeological investigations, primarily conducted in the early 20<sup>th</sup> century, in tandem with historical accounts are responsible for much of the information that allows anthropologists to reconstruct pre-Columbian populations and their dynamics. As these original investigations were documented poorly, or what documentation existed was lost in the intervening decades. While it would be ideal to revisit these previous excavation sites most of these have been subsequently destroyed by intensive development in the late 20<sup>th</sup> century further restricting anthropologists' collective understanding of the social interactions among prehistoric South Florida populations (Weisman, 2003, p. 220). Therefore, it is clear while archaeological investigations can provide interpretations of

Pre-Columbian sociocultural interactions through material analysis, such work can and should be further supplemented with other fields of inquiry, such as biological analyses.

A biological analysis can help address the question of population interactions, not through the past material culture, but through the biological markers like morphological data that can be found in regional populations with similar genetic ancestry (Griffin et al., 2001; Kles, 2013, p. 14). More specifically, one can examine the degree of gene flow or genetic drift that populations could have experienced in the past (Stojanowski, 2004; Ullinger et al., 2005; McIlvaine et al., 2014, p. 246). Biological analysis can reveal not just group relationships, but also shows genetic variation within populations (Powell, 2005, p. 193).

Biological interpretations can aid in anthropological understanding concerning population interaction in the past. At the time of European contact, the majority of indigenous populations underwent immediate and extreme changes regarding their social, political, and economic frameworks within which they had interacted prior to this period. Because the genetic variation of descendants of these indigenous populations have been altered so dramatically, it would be fruitless to examine modern indigenous populations to formulate and apply ideas concerning social interaction to prehistoric groups (O'Fallon and Fehren-Schmitz, 2011). Therefore, bioarcheological analysis provides a viable, and empirically sound methodology with which to investigate biological trait frequencies within and between populations to determine degrees of social and cultural continuity or disparity.

### **Major Research Questions**

There were two major research goals for this project:

- The primary goal was to determine whether there are significant differences in dental trait frequencies between the coastal and interior populations of Southern Florida.
- The secondary purpose was to determine the degree of interaction between the two groups.

Answering these questions is of intellectual merit because the current understanding of population relationships is based on inferences from early colonial era firsthand accounts, as well as archeological interpretations based on material cultural remains. Past archeological investigations have provided diverse insights into the undocumented past, but do not demonstrate the biological evidence for interaction. Aside from answering these research questions the null hypothesis is that there is overlap in the frequency of traits and that the deviations will be insignificant.

### **Sites**

This investigation examines the question of cultural affiliation through a biological perspective, along with the current archeological interpretations. To accomplish this, the following methodology was employed: an examination of the frequency of dental traits to determine the degree of relatedness of the people buried at two sites known as Highland Beach (8PB11) and Belle Glade Mound (8PB41). The Belle Glade sample is currently housed at the Smithsonian Institution, and the Highland Beach sample was stored in Florida Atlantic University in the Department of Anthropology. A total of 88 individuals were examined, 50 individuals from the Belle Glade Mound site and 38 individuals from the Highland Beach Mound. Both sites share similar chronometric dates, which places them in the same cultural period.

Florida is a relatively unknown region for understanding biological relationships between groups in Middle Woodland time period. Poor ethnographic records contribute to the lack of a coherent framework of cultural and biological relationships, especially in South Florida. The problem is further complicated by poor archeological records from previous investigations and the destruction of archeological sites. Many skeletal remains have been removed from their primary context, making it difficult to determine their chronological, social, and potential cultural area affiliations. The environment can provide clues to what types of interactions the indigenous populations could have encountered with one another.

Florida's unique geography and environment create areas of interest for population interactions. Southeast Florida is characterized as having several different types of terrains, which include the Everglades, tree islands, coastal strands, Atlantic Coastal Ridge, coastal dunes, lagoons, estuaries and sloughs (Griffin, 2002). The aquatic features would have provided a means of transportation, and trade which can serve as a conduit for interaction between groups that were separated by considerable distance. Such environmental factors can have pronounced effects on genetic transfer and can leave indications of intercultural interactions via biological evidence. These interactions would have had long lasting effects on the biological profile of the two populations.

### **Importance of Nonmetric Dental Analysis**

The examination of past populations can reveal important information regarding past interactions between individual groups (Ullinger et al., 2005; Willermet et al., 2013; McIlvaine et al., 2014; Hubbard et al., 2015; Irish et al., 2017). Genetic analysis is a robust method for evaluating changes in populations but requires destruction of skeletal

material which can limit research in regions that have restrictive legislative cultural resource management frameworks, such as the United States and Canada. There are alternatives to analyzing past populations through non-destructive techniques such as nonmetric trait analysis. Nonmetric trait analysis is an effective qualitative methodology for examining population relationships through the documentation, comparison, and contrasting of physical variation among dental traits within and between individuals and populations (Irish, 2005; Turner, 2006; Scott et al., 2018). Previous studies have demonstrated that dental analysis is a viable form for analyzing and characterizing regional populations (Scott and Turner, 1997; Hanihara, 2008; Scott et al., 2018). Population dental characteristics have a strong genetic component and are physically expressed through the dental morphology of individuals within a population (Scott and Turner, 1997; Scott and Irish, 2013). The frequency of dental characteristics allows for the construction of a dental profile for a population, which can be compared to other populations which have previously undergone documentation and had dental profiles already established (Taylor and Creel, 2012; Khudaverdyan, 2013; McIlvaine et al., 2014). Comparing the dental analysis between populations through statistical analysis can demonstrate the degree of divergence between groups that are included in dental research (Harris and Sjøvold, 2004; Ullinger et al., 2005).

The following analysis focuses on the biological evidence of relatedness through dental analysis of non-metric dental traits which included the examination of morphological variations of the roots and crowns, the differences of which are known to be controlled for by genes (Scott and Irish, 2013, p. 38; Scott et al., 2018, p. 164). This method is important because it allows for replication of data collection and is useful for



exploring trends in population migration which can aid in examining and identifying relationships between disparate, regional populations (Turner et al., 1991).

## **Results**

Results of this analysis provide an interesting insight on the examination of population relationships between the two sites. After analyzing a total of 88 individuals and examining traits on the incisors, canines, premolars and molars. A correlation analysis was conducted. After the correlation analysis was conducted many traits had to be cut out due to sharing a strong interrelation. Out of 36 traits, only 28 were able to be used for statistical analysis. The remaining traits were inputted into the program R to determine the MMD values. The results indicate that both sites show little variation difference in population in regard to distance values.

## **CHAPTER 2: BACKGROUND OF ARCHEOLOGICAL SITES**

Two sites were examined for this research, the Highland Beach site (8PB11) and The Belle Glade Mound site (8PB41). These sites were chosen because they are in two different cultural areas in Southeastern Florida and also occupy different environments. The Highland Beach site is located in the East Okeechobee Cultural Area, and the Belle Glade Mound site is located in the Belle Glade cultural area (Winland 2002; Smith 2015). The two sites were also occupied during the same time period as demonstrated through ceramic analysis and carbon dates of the two sites (Winland, 2002; Stojanowski and Johnson, 2011). Each site shares similar artifacts and similar cultural practices in regards to mortuary internment patterns (Willey, 1949; Bullen, 1957). Additionally, large numbers of human remains have been uncovered from each site which allowed for a detailed examination of the two sites through dental investigations of each individual buried at these two locations.

### **Florida Chronology**

The chronology that is used when discussing the two archeological sites of Belle Glade Mound and Highland Beach Mound will be based on the Belle Glade Chronology, developed by William Sears from his examination of the prehistoric ceramic series from the Fort Center Site in Glades County, Florida (Milanich, 1994; Sears et al., 1994).

### **Highland Beach (8PB11)**

The Highland Beach Site (8PB11), is also part of the Spanish River Complex, as defined by Furey (1972), and Wheeler et.al (2002). This site was chosen because it is

located in the East Okeechobee Archeological Area. This archeological area was first proposed by Carr and Beriault (1984), in their contribution to a volume on the geology of south Florida and is considered a cultural transitional zone. Griffin also recognized the East-Okeechobee archeological Area as a transitional zone, due to the mixture of common archeological assemblages found from the Belle Glade and Glades cultural areas (Griffin, 2002, p. 130; Wheeler et al., 2002, p. 121). Carr and Beriault (1984) also point out that many of the sites in the East Okeechobee cultural area are made up of shell middens along the coast as well as black dirt middens in the interior, which could be a result of influences from the Belle Glade region (1984). The East Okeechobee area is defined by its southern boundary at approximately the modern-day Broward/Palm Beach county line (Carr and Beriault, 1984, p. 7; Griffin, 2002, p. 130; Wheeler et al., 2002, p. 121). The northern boundary is located at the St. Lucie Inlet (Carr and Beriault, 1984; Griffin, 2002; Green, 2016). This region also includes the eastern portion of the Allapattah Flats, which is also associated with the Belle Glade archeological area.

### **East Okeechobee Archeological Area physiography**

There are several physiographic regions that compromise the East Okeechobee region. These include the Eastern Flatlands, cypress sloughs, the Allapattah Slough, Allapattah Flats and the Atlantic coastal ridge. The East Okeechobee Archeological Area occupies a large region that is referred to as the Eastern Flatlands (Griffin, 2002, p. 9). This physiographic region is characterized by the presence of low sandy soil with poor drainage, along with the presence of the Atlantic coastal ridge (Griffin 2002). The vegetation is predominantly compromised of pineland, but also incorporates prairies and cypress sloughs (Griffin 2002). The Allapattah Marsh and the Allapattah Slough are part

of the same drainage system of the St. Lucie River (Griffin, 2002, p. 9; Park et al., 2002, p. 11). With the slough flowing south towards the northern everglades and west into Lake Okeechobee (Park et al., 2002). The Allapattah Marsh flows from northwest to southeast into the eastern portion of Martin and St. Lucie counties (Griffin 2002). The Loxahatchee slough is found farther south on the eastern edge of the East Okeechobee cultural area and drains into the Atlantic Ocean (Griffin 2002).

### *Atlantic Coastal Ridge*

Another major physiographic region is the Atlantic Coastal Ridge, which covers the eastern coast of the southern portion of the state and ends at the Everglades National Park (Griffin 2002). The northern portion of the ridge is broad, and it is usually less than 1.8 meters in elevation (Griffin 2002). The Atlantic Coastal Ridge is cut by a few rivers, which allow water to drain into the Atlantic Ocean (Griffin 2002). This physiographic feature also acted as a dam that held water from the Everglades up to 2.4 to 3 meters (Parker 1981 in Griffin 2002). The vegetation that covered the Atlantic Coastal Ridge prior to development included a continuous strand of pine forest, along with tropical hardwood hammocks that dotted the region (Griffin 2002). The environment that makes up this coastal region of includes barrier islands, such as Hutchinson Island (Carr and Beriault 1984). The coastal environment is also characterized as having major inlets that are located in St. Lucie, Jupiter and Boca Raton along with mangrove and salt marshes, and shallow estuaries (Carr and Beriault 1984 Griffin 2002).

This region is again characterized as having estuaries such as the Loxahatchee River and the St. Lucie River (Carr and Beriault 1984). Another important note is that the environment has changed due to modern development, and this has resulted in changes in

the way river systems and estuaries flow throughout Florida. This has limited the field's collective understanding of population movements throughout Southern Florida prior to European contact. This included river systems which flowed into estuaries and the coast, which were destroyed due to changes of the environment for agricultural purposes, as well as the development and dredging of the intracoastal system. For example, Furey indicates that the coastal region also was characterized by extensive river systems which flowed from the north and south (Furey 1972). These river systems would have facilitated travel using boats, which would have resulted in increased interaction between settlements. This would have provided a means for which various settlements could have traded with one another. The interior environment of this subarea changes to pine flatlands, ponds, cypress domes, oak hammocks, and sloughs that drain westward towards Lake Okeechobee (Carr and Breault 1984).

#### *Climate of the East Okeechobee Archeological Area*

The climate of the interior regions or portions of East Okeechobee archeological area near the border of the Belle Glade Cultural area is characterized as being part of the tropical savanna climate zone (Griffin, 2002, p. 2). The Atlantic coastal region is characterized as being part of the transitional tropical climate zone (Griffin, 2002, p. 2). Furey notes that the climate for the region is associated as having relatively warm winters with warm moist summers (Furey, 1972, p. 3). The average annual precipitation for South Florida ranges from 113 cm to 138 cm, with the area near or on the Atlantic coast to have the highest amount of precipitation compared to Charlotte Harbor on the gulf coast, having the lowest (Griffin, 2002, p. 2). The wet season occurs between April and

October, with the majority of rainfall occurring between June and October. On the other hand the dry season occurs from November through March (Griffin, 2002, p. 4).

*Cultural association and history of the Highland Beach Site*

The association of the Highland Beach site with the Belle Glade cultural area was determined due to the high frequency of Belle Glade pottery recovered during excavations completed in the early 1970s (Furey 1972). In the following decade, it was inferred the Highland Beach site not only lay within the Belle Glade archeological area, but more specifically within the East Okeechobee archeological area. The Highland Beach site is associated with a network of earth and oyster shell middens along the coastal hammock (Winland, 1993, p. 29). The estimated occupation range is between 600 and 1200 AD based on the serration of the pottery, which would place it in the Belle Glade II/III time period (Winland, 1993, p. 29; Sears et al., 1994). This is further corroborated with carbon dates from two deer bone samples from the top and bottom layers of the Highland Beach Mound. The first sample was from the second level of the mound and placed at  $1070 \pm 30$  BP (Beta-439877, deer bone collagen;  $\delta^{13}C = -16.1\text{‰}$ ). The second sample was from the 10<sup>th</sup> level of the mound and placed at  $1480 \pm 30$  BP (Beta-439878, deer bone collagen;  $\delta^{13}C = -20.2\text{‰}$ ).

This site has been examined by many researchers, the first being John Goggin, who gave a brief description of the site in the 1940s (Goggin, n.d). Bullen was the first archeologist to conduct excavations of the Spanish River Complex, with a focus on Barnhill Mound (Bullen, 1957). John Furey was the first archeologist to conduct detailed excavations on the Highland Beach Mound during the 1970's, these two sites are part of the Spanish River Complex (Furey, 1972; Wheeler et al., 2002). The analysis included a

detailed study of the ceramics recovered from the excavation(s), with the results leading him to conclude that the overarching Spanish River Complex belonged within the Belle Glade cultural area. The analysis indicates that Glades Plain accounted for 47.30% and Belle Glade Plain accounted for 39.88% of the total amount of pottery recovered at the site (Furey, 1972). This demonstrates that there is an association at least culturally with the Belle Glade culture based on the ceramic assemblage.

In 1980, construction of an apartment building began, and part of an existing mound was destroyed, and the construction crew found human remains. Mehmet Yasar Iscan conducted an excavation and recovered an estimated 128 individuals (Winland 1993, 2002). Kenneth Winland (1993) conducted a skeletal analysis of the individuals recovered and from that data estimated that a living population of 100 to 200 individuals occupied the site at a given time. In addition, Winland conducted an analysis of the skeletal collection's paleopathologies. Further analysis was conducted by Christopher Hennessey (2015), who estimated that there are 216 individuals present at the site. His analysis suggests a higher number of individuals than the 128 reported by Winland. He explains the differences are due to a high degree of taphonomic damage found within the collection.

#### *Skeletal analysis of the Highland Beach site*

As mentioned above there have been two researchers who have published skeletal analyses of the Highland Beach remains. In Winland's 1993 skeletal analysis, he discusses the paleodemography of the site. population, concluding the population of Highland Beach was relatively healthy with a high life expectancy, with a low incidence of trauma, and a low frequency of nutritional disorders (Winland, 1993, p 114). The

exception to the relative health of the individuals was the high incidence of treponematosi s or infections that are associated with syphilis, found within this population, with an incidence of 15 percent (Winland, 1993, p. 108). Christopher Hennessey (2015) also conducted a paleodemographic profile of the population and found different results compared to those by Winland (1993). These differences are likely due to the fact that Hennessey's paleodemographic study examined the collection using a different method compared to Winland's analysis by applying the methods outlined by the Rostock Manifesto (Chamberlain, 2003), in which he finds higher frequency of male to female ratio, more individuals in the fetal development stage, and age at death estimations exceeding 70 years of age (Hennessey, 2015, pp. 24–26).

Miranda Kles (2013) also examined the cranial morphology of 30 individuals from the Highland Beach Site. She included these results with others from various prehistoric populations throughout Florida to determine biological variation (Kles 2013). The results of her analysis will be discussed in further detail later in this investigation.

### **Belle Glade Mound (8PB41)**

Belle Glade Mound (8PB41) is the archaeological type site of the Belle Glade Ceramic Series, which is one of, if not the, defining cultural attribute of the larger Belle Glade archeological area. This site is also subsumed under the Democratic River Complex (Davenport in prep). The Democrat River Complex is comprised of numerous sites that occupy the area around lake Okeechobee and were interconnected by the now extinct Democrat River (Davenport in prep). The upper portions of the mound are estimated to have been occupied around 920 BP (Stojanowski and Johnson, 2011; Smith, 2015). This would place the occupation range contemporaneous to that of Highland



Beach in the similar Belle Glade II/III periods (Sears et al., 1994). The environment of the Belle Glade archeological area is compromised by the presence of the Kississimnee River Valley, Lake Okeechobee Basin and Northern Everglades (KOE). The southern boundary of the Belle Glade archeological area overlaps with the Everglades and the eastern boundary adjoins or abuts with the East Okeechobee cultural area (Carr and Beriault 1984).

#### *Belle Glade Archeological Area's Physiographic Environment*

The Belle Glade regional environment is characterized by the presence of Lake Okeechobee as well as the mosaic environmental characteristics of the everglades and various drainage systems. These drainage systems include Kissimmee River, the Caloosahatchee River, Taylor Creek, and Fisheating Creek along with several unnamed sloughs (Carr and Beriault 1984). One major environmental feature is the Everglades. This feature covers a large area from Lake Okeechobee to the Gulf of Mexico and ends just north of Cape Sable (Griffin 2002). This feature is referred to as the “river of grass” by Griffin and is one of the largest freshwater marshes in North America (2002). The soils here are predominantly wet and low lying, making them prone to being inundated (Griffin 2002). Sloughs and tree islands also encompass the Everglades which are flanked by the eastern and western flatwoods (Griffin 2002 and Mount 2009).

Another major feature aside from the Everglades is Lake Okeechobee. It is estimated that Lake Okeechobee appeared around 6,000 years ago (H. Brooks 1984 in Griffin 2002). This body of water is the second largest lake in the United States (South Florida Water Management District [SFWM] 2007 in Mount 2009). Evidence suggest that the area around Lake Okeechobee was heavily populated. Prior to 2007 there were

10 archeological sites in the area around Lake Okeechobee (Mount 2009). After 2007, when a major drought struck the area decreasing water levels to a historic low, much of the lakebed was exposed (Mount 2009). The Boyer survey conducted during this drought found an additional 33 new sites (Davenport et al. 2011).

#### *Climate of the Belle Glade Archeological Area*

The climate of the Belle Glade Cultural area is similar to that of the East Okeechobee Cultural area. Both regions share the same climatic environment as they both occupy South Florida's tropical savannah climate (Hela 1952 in Griffin 2002). The wet season for this archeological area is part of the Everglades wet season in which the highest amount of precipitation occurs April through October (Griffin 2002).

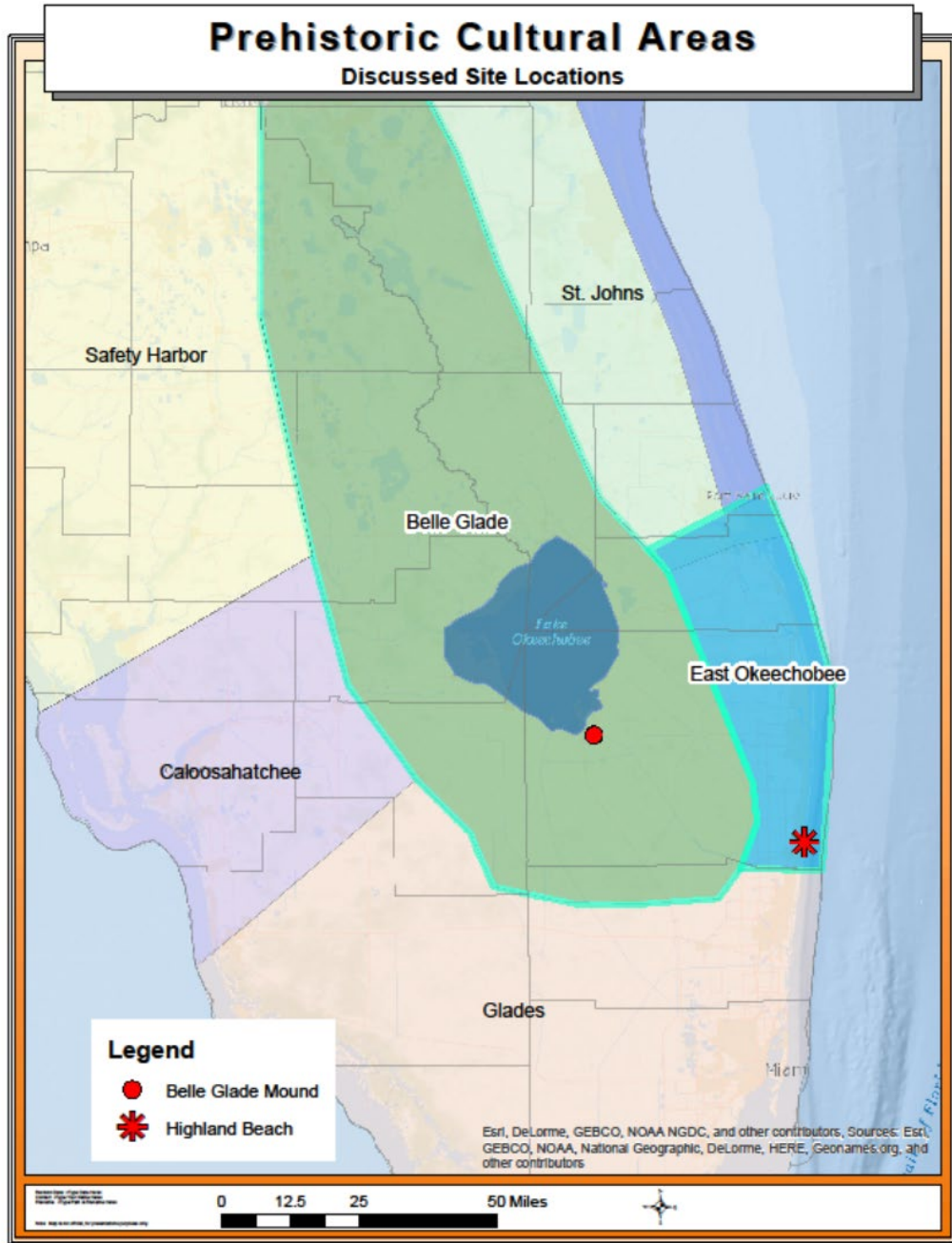
#### *Belle Glade Archeological Area Previous Investigations*

The Belle Glade site was initially excavated in 1933 under the control of the Civil Works Administration (Setzler and Strong, 1936; Willey, 1949). The significance of the site was first identified due to it being a true refuse heap instead of a shell heap above muck deposits (Setzler and Strong 1936). Gordon Willey gave a more detailed description of the site, noting the presence of a shell midden and a burial mound, with the burial mound consisting of three superimposed mounds (1949). He mentions that the mound is compromised as having an old muck burial mound at the bottom and first and final sand burial mounds at the top (Willey, 1949 p. 21). He also mentions the presence of marine artifacts such as shark teeth and Busycon shells, both of which originate from coastal environments (Willey, 1949).

### *Excavations of human remains*

An estimated 100 burials were discovered with associated artifacts that were similar to the ones discovered in Key Marco (Setzler and Strong 1936). Many of the remains are curated at the Smithsonian Institution National Museum of Natural History (Smith 2015). Subsequent excavations during 1975 were undertaken prior to the construction of a house on top of the mound. At least seven burials were discovered and are curated at the Department of Anthropology at Florida Atlantic University, and three other individuals are held at the Florida Museum of Natural History (Smith 2015). The remains from the 1975 excavation were later reinterred. Prior to this investigation Catherine Smith (2015) was the last known researcher to conduct an investigation of the biological profile of individuals from the Belle Glade Mound.

Figure 1: Cultural areas of Southern Florida, with the red circle indicating the location of the Belle Glade site and the red star asterisk indicating the location of the Highland Beach site. Map provided by Davenport (N.D)



## **Burial Practices**

The majority of information on the Belle Glade Culture comes from archeological investigations (Willey, 1949; Griffin, 1989, 2002; Sears et al., 1994; Johnson, 1996). Indications are that they inhabited the area around Lake Okeechobee and possibly extending eastward to Boynton Mound and possible influence on the coast based on ceramic frequencies (Furey, 1972; İşcan and Kessel, 1988; Ryan J. Wheeler et al., 2002). The Belle Glade culture is characterized by the construction large earthworks associated with linear A and B shaped mounds with embankments as well as large middens (Johnson, 1991, 1996; Milanich, 1994; Sears et al., 1994; Smith, 2015). There is also the presence of canals that extend for several miles that are also associated with the Belle Glade sites (Milanich 1994, p. 283).

The aboriginal groups that inhabited the Belle Glade and East Okeechobee regions are known to have practiced a wide variety of burial treatments and positions, since many of the mounds throughout the region have a mixture of prone and bundle burials as well as fragmentary human remain (İşcan and Kessel, 1988; Sears et al., 1994; Smith, 2015). Prone and bundle burials could be indicative of social organization within a society and to a degree a representation of similar social symbolic norms (Binford, 1971, p. 16; Felmley, 1991). The two important burial types include charnel pond burials as well as mound burials. This is seen in many Belle Glade sites, most notably in Fort Center, in which he notes a large number of individuals interred in both the pond and mound (Sears et al., 1994, p. 196). For this analysis only mound burials were examined.

Fort Center is an archeological site located west of Lake Okeechobee, which was occupied from 450 B.C to the Contact Period (Sears 1982). This site is also an example

of charnel ponds used for burials (Milanich 1994 and Sears 1982). These burials are associated with the Period II occupation, which began in 200 A.D and ended between 600 to 800 A.D (Sears 1982). Though often overlooked, the Highland Beach site shares this similarity with Fort Center.

#### *Highland Beach Burial Patterns*

Construction of the A1A highway during the 1940s produced evidence of a possible pond burial based on the recovery of several human remains, which potentially indicates similar burial practices among Spanish River Complex and Belle Glade cultures (Bliss, 1940). This is another possible indicator that the Spanish River Complex having similar practices to that of the Belle Glade culture. The Highland Beach mound and Belle Glade mound sites are contemporaneous with each other as indicated by their respective ceramic chronologies (Sears 1982, Winland 1993, 2002). Excavations conducted by Bullen on the Barnhill Mound site, which is part of the Spanish River Complex, demonstrate a variation in burial patterns and interment practices (Bullen, 1957). Burial patterns from the site include a mixture of prone, bundle and single elements (Bullen, 1957). As defined by Wheeler (2002) Barnhill Mound is associated with the Highland Beach mound, in which similar burial patterns that have been practiced, but the stratigraphic difference is unknown.

#### *Belle Glade Mound Burial Patterns*

The Belle Glade Mound site has a similar burial pattern to Highland Beach Mound which Willey described in his 1949 report of the site. As mentioned previously (in the past excavations of Belle Glade cultural area section it is comprised of three occupation layers, with the oldest burials occupying a muck deposit (Willey, 1949). The

majority of burials were uncovered in the muck deposit, within which the undisturbed burials demonstrated a prone position (Willey, 1949, p. 22). The majority of the disturbed burials indicate that they were disturbed by subsequent internments and resulted in the comingling of remains (Willey, 1949). At least seven individuals examined in this analysis were identified to be from the muck layer and are assumed to be the oldest individuals from the site based on the staining on the skeletal elements and muck adhering to the skeletal and dental material.

### **CHAPTER 3: DENTAL TRAITS**

Past research has been conducted on dental traits with a focus on estimating population migrations and ancestry (McIlvaine et al, 2014, Willermet et al. 2013, and LeBlanc et al. 2008). The results indicate a general agreement on the usefulness of dental traits for examining biological relatedness. The majority of research on dental traits relies on the Arizona State University Dental Anthropological System (ASUDAS) (Turner et al., 1991; Sutter and Verano, 2007; Irish, 2016; Stojanowski and Hubbard, 2017; Scott et al., 2018). The primary focus of ASUDAS research was to explore how the analysis of dental characteristics could aid in determining whether individuals from Belle Glade mound and Highland Beach mound share any biological similarities. ASUDAS studies suggest that dental characteristics analysis is an adequate approach in determining similarity among groups.

#### **Dental anatomy**

In order to examine the relatedness of Belle Glade and Highland Beach populations, this research examined dentition, focusing on morphological trait frequencies and variation. It is important to have a clear understanding of tooth morphology and development to conduct an analysis of dental traits. All human teeth are composed of one soft tissue and three calcified tissues (Alt et al., 1998). The soft tissue that is found at the center is known as the pulp, and the calcified tissues include the dentine, cementum and enamel (Alt et al., 1998). The layer surrounding the pulp cavity is known as the dentine (Hillson 1996).



A fundamental aspect in understanding tooth morphology is how individual teeth are sub-divided. Teeth are divided into two primary components, known as the crown and the root (Hillson 1996, Scott and Turner 1997). The crown is the portion that projects into the mouth and is exposed to the environment (Hillson 1996, Scott and Turner 1997). The root, on the other hand, is embedded in the maxilla and mandible (Hillson 1996). The crown is primarily composed of four macroscopic units, which include the lobes, marginal ridges, cingulum derivatives, and super numerary coronal structures (Scott and Turner 1997: 20). The crown is coated with an outer layer known as the enamel (Hillson 1996). The point in which the crown and the root meet is known as the cervix (Hillson 1996).

#### *Crown and root anatomy*

It is important to cover key traits of crown and root morphology for all the dental classes in both the maxilla and mandible. What follows are brief descriptions of the crown and root traits that are characteristic for each tooth. The nonmetric variations will be covered in greater detail in the section that gives a brief background of the traits examined for this analysis.

As mentioned above crowns are composed of macroscopic units. These units served as a basis of examining variation of nonmetric dental traits. Maxillary and mandibular molar cusps vary from one another. Upper molars typically have four cusps; paracone, protocone, metacone, and hypocone (Hillson, 1996; Scott and Turner, 1997; Scott and Irish, 2017). Although upper molars have on average four cusps there can also be reduction as well as additions in cusp numbers. For the lower molars there are on average five cusps, which is a characteristic in the apes and modern humans (Scott and

Turner, 1997). The cusps of the lower molars include protoconid, metaconid, hypoconid, entoconid, and hypoconulid (Hillson, 1996; Scott and Turner, 1997; Scott and Irish, 2017). Similar to upper molars cusp pattern there can be the reduction or addition of cusp number (Hillson, 1996).

Upper molars on average have three roots, with the lingual being the largest and two buccal roots (Hillson 1996 p. 49). The number of roots can vary depending on whether it's the first upper molar, second upper molar, and third upper molar (Hillson, 1996). The pulp chamber resides at the base of the crown and root trunk (Hillson 1996 p. 49). Lower molars exhibit a lower number of roots ranging from two to one (Hillson, 1996). This depends on the tooth in question, with the number of roots normally decreasing from the first molar to the third, and roots fusing towards the last molars (Hillson 1996 p. 58).

Similar to molars, premolars exhibit variation of upper and lower cusp number and size (Hillson, 1996). The upper molars typically have larger cusps and have a lingual and buccal cusp (Hillson, 1996). Accessory ridges can be observed on the occlusal surface of the premolars as well as marginal tubercles, which are additional features observed in the upper premolars. Other observations include the rotation of the buccal cusp and addition of premolar odontoma. Lower premolars vary in cusp number with a dominant buccal cusp and smaller lingual cusp that varies from two to three (Hillson 1996 p. 39).

Premolar root numbers vary between the upper and lower premolars. On average the first upper premolars have two roots and the second premolar normally has one root (Hillson, 1996). A premolar with complete root separation will normally have a larger

buccal root and a smaller lingual root (Hillson, 1996). Single rooted premolars have grooves on the mesial and distal sides, on the other hand lower premolars exhibit a single root (Hillson, 1996).

Canines have central cusp on the incisial edge, which extends down to the tuberculum (Hillson 1996 p. 29). There are variations for the canine when focusing on the crown surface. One notable variation is the distal canine accessory ridge which varies in size. There are also marginal ridges on the mesial and distal, with the distal ridge being larger (Hillson 1996 p. 23). The key difference between the lower and upper canines is their size. Maxillary canines tend to be larger compared to mandibular canines.

The root characteristic of canines is straightforward, with the dentition exhibiting a single long root with shallow grooves on the mesial and distal portions (Hillson, 1996). The apical portion of the root curves distally, which can be used for siding (Hillson, 1996). There is certain variation of the canine root number which can be observed on the lower canines.

Incisors also have an incisial edge, but with three mamelons or low cusplets (Hillson 1996 p. 17). The lingual surface has a distal and marginal ridge that vary in the degree expression, this will be discussed in further detail in the traits list (Hillson 1996 p. 17). There are two types of incisors central and lateral incisor, with lateral incisors being more variable (Hillson 1996 p. 21). The labial surface of incisors is more convex, compared to the lingual surface being more concave with a tuberculum at the base of the lingual surface of the crown (Hillson 1996). There are several differences between upper and lower incisors, in which the upper incisors are larger and broader compared to the

lower incisors (Hillson 1996 p. 20). Another difference is that lower incisors are more chisel-shaped, and a flatter lingual surface (Hillson 1996 p. 20).

Incisor roots are similar to canine root, in which they only exhibit one root. The roots of incisors exhibit shallow mesial and distal grooves. Similar to canines the root of the incisor curves distally, which allows for siding of both the lateral and central incisors.

Humans develop two sets of teeth throughout our lifetime which are referred to as the deciduous and permanent teeth. This indicates that humans have a diphyodont dentition (DiGangi and Moore, 2012). The first set of teeth are known as deciduous teeth and are present during the early development, between 14 and 16 weeks after fertilization and through pre-adolescence (Hillson 1996). For this investigation, the primary focus is adult dentition. Deciduous dentition was not considered for this analysis because of smaller sample size, and because deciduous teeth are more susceptible to taphonomic impacts there are also no set standards for collecting data on deciduous dentition (Scott and Turner 1997).

### **Variability of tooth number and morphology**

Human dental morphology can be highly variable and can deviate from the typical tooth crown and root morphology. Scott and Turner (1997) state that there are two types of dental blueprints that have been documented across human populations. The first variation is in the number of teeth that individual and or population has (Scott and Turner 1997). This implies that there are observed variations from the original dental blueprint or total number of teeth in a typical individual, that is  $(\frac{2-1-2-3}{2-1-2-3})$  which can include the fusion of teeth (reduction in the total number) and the presence of supernumerary teeth (Scott and Turner 1997, p. 4-5 for images). More or fewer teeth from the “ideal dental

blueprint” can demonstrate specific traits such as dental crowding. The second variation focuses on the individual teeth instead of the total number of teeth. For example, genetics affects tooth size as well as tooth morphology (Scott and Turner 1997). Such genetically controlled morphological traits include variations of secondary cusp morphology, occlusal fissure patterns and super numerary roots (Scott and Turner 1997). The later factors were the primary methodological focus of this project.

### **History of Nonmetric Dental Analysis**

Ales Hrdlicka was one of the first researchers to examine the importance of the tooth morphology of human dentition (1921). He provided the one of the earliest examples of detailed descriptions of the morphology of human dentition, as well as new observations on dental characteristics, such as identifying shovel shaped incisors along with comparing it to other primates (Hrdlička, 1921, 1924). This was followed by P.M Butler’s field theory, in which he proposed that pattern genes would determine the type of tooth to be developed (Butler, 1939; Scott et al., 2018). Much of the information on dental anthropology at the time was largely descriptive. There was not much work done until the 1940s when the field of dental anthropology began to expand its exploration of dental variation (Scott and Turner 1997). Albert Dahlberg later adopted Butler’s field theory, but instead of using three classes (incisor, canine, and molar), he proposed that there were four morphological classes by adding premolars (Dahlberg 1945 as cited in Scott and Turner 1997). Dahlberg also played an important contribution in standardizing the observation of dentition by providing reference plaques, which are dental casts that were gathered to provide examples of non-metric dental traits, along with a ranked scale for scoring these traits (Scott and Turner 1997).

With the increased interest in human variation, researchers began to look at the genetic component of dental morphology. Many researchers believed that dental morphology followed a Mendelian mode of inheritance (Scott and Turner 1997). This led to the examination of the heritability of these traits through pedigree charts as well as admixture estimates (Kraus, 1951; Turner, 1969). These were initial attempts to determine whether dental traits were associated with simple modes of inheritance (Scott and Turner 1997). Further analysis from the previous data indicated that dental traits are not controlled by a single gene (Goose and Lee, 1971; Lee and Goose, 1972; Scott and Turner, 1997). This led to a reevaluation of the degree to which genes control dental crown and root morphology (Scott and Turner 1997). Instead dental traits were quasicontinuous which are traits that have a continuous variable and have multiple modes of inheritance with a physiological threshold into ordinary and anomalous traits or that they are counted as present or absent, but have a continuous distribution from low level to high level of expression (Grüneberg, 1952; Sofaer, 1970, p. 1505; Scott and Turner, 1997). These modes of inheritance play a major role in non-metric dental trait frequencies within a population, because it allows the data to be dichotomized into present or absent. Dichotomization of data was also an initial step toward standardizing population movements through non-metric dental traits.

Non-metric dental trait frequencies have been used to determine the characteristics of a population and allows for the identification of individuals that derive from a specific geographic region (Scott and Turner 1997). This methodology later developed into distance analysis as a way to measure the degrees of differences and relatedness among different populations through methods such as pseudo-Mahalanobis

and Smith's mean measure of divergence (Mahalanobis, 1936; Sjøvold, 1977; Konigsberg, 1990; Scott and Turner, 1997). These methods have been applied to populations in Europe, the Americas, and Africa (Willermet et al., 2013; McIlvaine et al., 2014; Irish, 2016). This has allowed for researchers to test several models that could not be answered through archeological analysis alone. One example of this is in South America, in which researchers explored whether Moche sacrificial victims were from the site Huaca de la Luna 3C or from other polities (Sutter and Cortez, 2005; Sutter and Verano, 2007). The analysis of non-metric dental traits indicated that the sacrificial victims were from other regions and were not local warriors that partook in a sacrificial ceremony (Sutter and Verano 2007). Non-metric dental traits have also been used to determine migration patterns either through colonization or trade (McIlvaine 2014, Ullinger et al. 2005, and Willermet et al. 2013).

### **Dental Morphological Theory**

Several theories have been proposed to explain the development of individual teeth and what mechanisms are responsible for the development of dentition as well as variation in morphology.

#### *Field theory*

The first dental development theory, proposition of field theory, was suggested by P.M Butler. He proposed that pattern genes would determine the type of tooth to be developed (Butler 1937 as mentioned in Scott and Turner 1997). He also classified teeth into three subdivisions based on morphology and suggested that the location of the germ cells plays a larger role in the development of teeth and not timing, with tooth development starting with the anterior teeth, and the last teeth to develop being in the

posterior (Butler 1937 as mentioned in Scott and Turner 1997). The most important aspect of Butler's theory is that each individual tooth develops independently from one another (Butler, 1939). Dahlberg later modified Butler's theory through the addition of premolars as a separate subdivision, compared to Butler's inclusion of the premolars with the molars (Scott and Turner 1997).

#### *Clone theory*

Several decades after Butler's field theory, J.W Osborne proposed clone theory. His theory proposes that each tooth develops from a clone of mesenchymal cells deriving from cranial neural crests (Osborne 1978 as mentioned in Mitsaidis and Smith 2006). These mesenchymal cells develop into three primordia during the development of teeth, known as odontogenesis (Osborne 1978 as mentioned in Scott and Turner 1997). Unlike Butler's field theory the tooth germs do not have the same set of instructions during development. The development of the morphology is determined by the genes found within the tooth germ. The group of cells clone themselves from the original cell, with the similar pattern of development from anterior to posterior position (1978, 1997).

#### *Homeobox theory*

The final theory proposed for odontogenesis, the formation of teeth, is P.T Sharpe's 1995 homeobox theory (Scott and Irish 2013, p. 36). Instead of clones or regions affecting tooth morphology, there are homeobox genes which are responsible for multiple dental phenotypic traits, several of which have been identified and demonstrate trends in temporal and spatial patterns including Msx, Dlx, Barx, Lhx, and Pitx classes (Mitsiadis and Smith, 2006; Townsend et al., 2009; Scott and Irish, 2013, p. 36). These temporal and special patterns are based on mouse models, which affect the entire tooth



class, but in human it affects specific dentition (Mitsiadis and Smith, 2006). Tucker and Sharpe found that MSX1 and MSX2 affect the incisors and the DLX2 and BARX1 affect the molar region in mouse (2004).

### *CGI Theory*

Field theory, clone theory, and homeobox theory explain how dentition develops and why variation exists among the tooth classes. Many researchers have proposed a new model, known as the Co-operative Genetic Interaction model or CGI, that incorporates all three theories by contending that the formation of tooth cells begins as plastic but becomes more permanent throughout development (Mitsiadis and Smith, 2006; Townsend et al., 2009).

The theories mentioned above provide an explanation on the formation of dentition and how it can affect dental variability. All models propose a genetic component plays a major role in the formation and variability of dentition. The co-operative genetic interaction model attempts to incorporate the field, clone and homeobox theories. In the following section it is evident that nonmetric dental traits have a stronger genetic component. These theories help provide a framework for explaining the phenotypic variation in nonmetric dental traits.

### **Genetics of nonmetric dental traits**

As briefly mentioned previously, nonmetric dental traits have a strong genetic component. Much of the dentition is affected by genes that have a pleiotropic effect, when a single gene is responsible for multiple phenotypic expressions in an individual (Burian, 2004). Multiple research studies conducted on baboon dentition suggests that there are partial pleiotropic effects between premolars and molars, that there is a strong

genetic component responsible for the upper and lower molar cusp sizes respectively, and implies the same potential for such conditions in humans (Koh et al., 2010; Grieco et al., 2013). These studies demonstrate that certain genes are having partial effect on two tooth types and cusp size and are further evidence of genetic influence on morphological features.

Similar studies focusing on the effects of specific genes on dental morphology have evaluated the relationship between dental morphology and evolutionary advantages. One such study examined the relationship of shoveling of the incisors to increasing the delivery of vitamin D to infant through the increase of mammary ducts around 20,000 years ago. The researchers attributed this to a specific gene known as EDAR 370V (Hlusko et al., 2018).

Heritability estimates have also been conducted on nonmetric dental traits, in particular narrow-sense heritability. Narrow-sense heritability is the “proportion of phenotypic variance due to additive genetic variation” (Evans et al., 2018). Two studies examining narrow-sense heritability demonstrate low to high hereditary values for nonmetric dental traits, although these results demonstrate a range in hereditary values, the authors explain that small sample size can affect the data in their analysis (Stojanowski et al., 2018, 2019). The results bolster the evidence of a genetic pleiotropic effects on nonmetric dental traits (Stojanowski et al., 2019).

#### *Environmental effects*

There are several environmental factors that can affect the morphology of human dentition. Environmental factors include; trauma, pathologies and dental wear (Scott and Irish, 2013, p. 38). When examining dental traits, dental wear was the predominant factor

that affected observations of nonmetric dental traits. Wear obscured many traits as well as affected the scoring of traits, and certain traits were scored lower due to wear.

Pathological observations did not affect the scoring of traits, because the predominant pathology observed was Linear Enamel Hypoplasia and was predominantly found on the lower canines. Environmental components play a small role in dental morphology and had a minor impact on the data collection of both populations.

### **Native American Dental complex**

There are several key dental characteristics that are predominantly found in Native American populations. This type of dental complex is referred to as sinodont dentition. Turner described sinodonty as being present in East Asia as well as North and South America (Turner 1983). This led to many researchers to better define sinodont dentition in the New World with certain traits that are in higher frequencies (Scott and Turner, 1997; Hanihara, 2008; Scott and Irish, 2013). There were eight high frequency traits that were identified for indigenous populations in the New World (Scott and Turner, 1997). The traits that were in high frequency included winging, shoveling, double shoveling, interruption grooves, odontomes, enamel extensions, cusp 6, and the deflecting wrinkle for crown traits (Scott and Turner, 1997; Scott et al., 2018). The root traits that were found to be in high frequency for sinodont dentition include a 1- rooted lower premolar and low frequencies include 2-rooted first upper premolar and 3-rooted second upper molar (Scott and Turner 1997). Hannihara (2008) also found similar results, with the added observation that dental variation being the lowest in the new world as compared to the rest of the other regions of the globe.

There is a debate whether there is a sundadont dental complex present in North and South America along with a sinodont dental complex. The characteristics of the sundadont dental complex is that sundadont's have an average frequency of traits compared to sinodont dentition which is characterized as having more extreme frequencies due to the proposed idea that the dental pattern is more specialized (Turner, 2006; Scott et al., 2018). Although there is much debate whether the sundadont dental complex is present in the new world, current evidence indicates that the majority of the populations examined demonstrate a predominantly sinodont dentition with a few traits that would fall under the sundadont dental pattern. This analysis was not centered on the debate of whether sundadonty was present in Native American populations, but a cursory analysis indicates that few trait frequencies that were observed could fall under the sundadont complex, but majority of trait frequencies indicate the presence of a sinodont dental complex. These observations are limited and might not be the whole representation of the populations.

#### *Differences in New World populations*

New world populations exhibit the lowest degree of dental variation, which is in line with the genetic variation of new world populations (Powell, 2005; Hanihara, 2008). Although indigenous populations exhibit low genetic variation, this major overarching population category can be subdivided into three subgroups. Powell outlines three major population groups in the Americas proposed by Turner which include the Na-Dene, Eskimo-Aleut, and Amerindian populations (Powell, 2005, p. 206). The genetic variation within these groups differs between groups when evaluated through population comparisons. The groups with the lowest variation are the Eskimo and Na-Dene. On the

other hand, Amerindian groups have the highest genetic variation (Powell, 2005, p. 210). This suggest that Amerindian populations were the group that had a longer period of sedentary occupation on the North American continent, which allowed for an increased period of dental divergence (Powell, 2005, p. 210).

### **Trait List**

The following traits were chosen from the ASUDAS, as they have been documented to be present in Native American populations as well as East Asian populations. The traits list includes the teeth that exhibit this trait, key tooth and its break point.

### **List of Dental Traits:**

Table 1 The following table demonstrates the traits that were recorded along with the dentition that exhibits that particular trait, the key tooth and breakpoint. Traits marked as present or absent indicate that they only have two grades.

Trait	Observed Tooth/Teeth	Key Tooth	Breakpoint
Palatine Torus	Oral Torus	N/A	Grade 2
Winging	I <sup>1</sup> , I <sub>1</sub>	I <sup>1</sup>	Grade 1
Shoveling	I <sup>1</sup> , I <sup>2</sup> , C <sup>1</sup> , I <sub>1</sub> , I <sub>2</sub> , C <sub>1</sub>	I <sup>1</sup>	Grade 3
Double Shoveling	I <sup>1</sup> I <sup>2</sup>	I <sup>1</sup>	Grade 2
Interruption Grooves	I <sup>1</sup> , I <sup>2</sup>	I <sup>2</sup>	Presence of any groove
Tuberculum Dentale	I <sup>1</sup> , I <sup>2</sup>	I <sup>2</sup>	Grade 2
Canine Distal Accessory Ridge	C	C	Grade 2
Premolar Accessory Ridges	PM <sup>1</sup> , PM <sup>2</sup> , PM <sub>1</sub> , PM <sub>2</sub>	PM <sup>2</sup>	Grade 2
Marginal Tubercles	PM <sup>1</sup> , PM <sup>2</sup>	PM <sup>1</sup>	Grade 1
Uto-Aztecan Premolar	PM <sup>1</sup>	PM <sup>1</sup>	Grade 1 (Present or absent)
Metacone	M <sup>1</sup> , M <sup>2</sup> , M <sup>3</sup>	M <sup>3</sup>	Grades 0-3 (for trait absence)
Hypocone	M <sup>1</sup> , M <sup>2</sup> , M <sup>3</sup>	M <sup>2</sup>	2-6 (for trait presence)

Bifurcated Hypocone	M <sup>1</sup> ,M <sup>2</sup> ,M <sup>3</sup>	M <sup>2</sup>	Grade 1(Present or absent)
Cusp 5	M <sup>1</sup> ,M <sup>2</sup> ,M <sup>3</sup>	M <sup>1</sup> ,M <sup>2</sup> ,M <sup>3</sup>	Grade 1
Marginal Ridge	M <sup>1</sup>	M <sup>1</sup>	Grade 1(Presence or absent)
Tubercles			
Carabelli's Cusp	M <sup>1</sup> ,M <sup>2</sup> ,M <sup>3</sup>	M <sup>1</sup>	Grade 2
Parastyle	M <sup>1</sup> ,M <sup>2</sup> ,M <sup>3</sup>	M <sup>1</sup>	Grade 2
Enamel Extensions	Buccal Surface: M <sup>1</sup> ,M <sup>2</sup> ,M <sup>3</sup> M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	Buccal Surface: M <sup>1</sup> ,M <sub>1</sub>	Grade 2
Upper Premolar Root Number	PM <sup>1</sup> ,PM <sup>2</sup>	PM <sup>1</sup>	Grade 2
Upper Molar Root Number	M <sup>1</sup> ,M <sup>2</sup> ,M <sup>3</sup>	M <sup>2</sup>	Grade 3
Pegged/Reduced/Missing Third Molars	M <sup>3</sup> ,M <sub>3</sub>	M <sup>3</sup> ,M <sub>3</sub>	Grade 1
Premolar Odontomes	PM <sup>1</sup> ,PM <sup>2</sup> ,PM <sub>1</sub> ,PM <sub>2</sub>	PM <sup>1</sup> ,PM <sup>2</sup> ,PM <sub>1</sub> ,PM <sub>2</sub>	Grade 1(Present or absent)
Lower Premolar Cusp Number	PM <sub>1</sub> ,PM <sub>2</sub>	PM <sub>2</sub>	Grade 2
Anterior Fovea	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>1</sub> ,M <sub>2</sub>	Grade 3
Mandibular Torus	Oral Torus	Oral Torus	Grade 2
Lower Molar Cusp Number	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>1</sub> ,M <sub>2</sub>	Grade 1
Deflecting Wrinkle	M <sub>1</sub>	M <sub>1</sub>	Grade 2
Distal Trigonid Crest	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>1</sub> ,M <sub>2</sub>	Grade 1(Present or absent)
Mid-Trigonid Crest	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>1</sub> ,M <sub>2</sub>	Grade 1(Present or absent)
Protostylid	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>1</sub>	Grade 2
Cusp 6	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>1</sub>	Grade 1
Cusp 7	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>1</sub>	Grade 1
Lower First Premolar Root Number	PM <sub>1</sub>	PM <sub>1</sub>	Grade 4
Lower Canine Root Number	C	C	Grade 1(Present or absent)
Three Rooted Lower Molar	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>1</sub>	Grade 3

Lower Molar Root Number	M <sub>1</sub> ,M <sub>2</sub> ,M <sub>3</sub>	M <sub>2</sub>	Grade 1(Presence of one rooted molar)
Torsomolar Angle	M <sub>3</sub>	M <sub>3</sub>	Grade 1 (Present or absent)

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<sub>1</sub>=Mandibular, <sup>1</sup>=Maxillary, I=Incisor, C=Canine, PM=Premolar, M=molar  
1=1st tooth,2=2nd tooth, 3=3rd tooth

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## **CHAPTER 4: METHODOLOGY**

To address the research questions proposed in Chapter 1, the standards from Arizona State University Dental Anthropological System were employed (Turner et al., 1991). ASUDAS standards are designed to evaluate traits that withstand high dental wear and can be easily scored (Turner et al., 1991). The methods utilized by Scott, Turner and Irish were followed (1991,1997,2010, 2017). There were several advantages from using this system, which included procedural replicability and the ability to score the maximum expression of traits (Turner et al., 1991). Another advantage was that the traits outlined in this system are “most easily and reliably observed, most persist for many years in dentally harsh lifeways” (Turner et al., 1991). They also exhibit low to no sexual dimorphism and are powerful indicators of population affinity (Turner et al., 1991).

A disadvantage for this system is that not all traits are expressed in the same manner as described in the ASUDAS, which posed a challenge when analyzing dental traits of the two populations. Another disadvantage was that dental wear obscured many traits. In cases of wear where remnants of a trait were observed, that trait was scored at a lower grade to ensure a conservative, and more replicable, approach to the evaluation process.

### **Materials and methods**

As there were only two samples used for this analysis more individuals were analyzed than initially expected. This raised the question of what would be counted as an individual case. There are various methods utilized to count individuals. The first is the



total tooth count method, which treats each individual tooth as part of an individual. There is the advantage of an inflated sample size. The second method is the use of the side count method in which one antimer, or side of the maxilla or mandible, is chosen. For example, the examination of only the right side will be used. The last method is the individual count method which uses a single individual and traits that exhibit asymmetry, one trait that is more pronounced on one antimer over the other is scored. This results in choosing the side with the greatest expression. This is due to the assumption that the trait with the highest grade is associated with the strongest genetic expression (Turner et al., 1991; Scott and Turner, 1997).

The individual count methodology was chosen for this analysis. With the individual count method all antimeres of the maxilla and mandible were scored, but the side with the highest degree of expression was chosen to represent the individual for the reason mentioned above. If the individual was fragmentary and only had a partial maxilla or mandible, the side of the element observed would be assumed to have the strongest degree of expression.

Based on this count method a total of 88 individuals were examined, with 50 individuals from the Belle Glade Mound site and 38 from the Highland Beach site. The number of individuals from the Belle Glade Mound site that exhibited an intact maxillae and mandible were tallied to 25. There were 13 individuals that only had at least one pair of the maxilla and 12 individuals that only had the mandible.

The Highland Beach site also shared similar proportions on the number of individuals observed with having intact dental arcades. A total of 16 individuals had both

the maxillae and mandible present. Only 12 of the individuals had at least one portion of the maxilla and 10 of the individuals had at least the mandible present.

After choosing the method of how to count individuals, a spreadsheet was created in Excel and then printed in order to record the data. This sheet included all potential traits to be evaluated such as shoveling, protostylid, premolar odontomes etc. and allowed for additional space for any observation of anomalous traits. I followed the recording method of several authors in order to make proper observations (Turner et al., 1991; Scott and Turner, 1997; Hanihara, 2008; Jonnalagadda et al., 2011; McIlvaine et al., 2014; Scott and Irish, 2017). A magnifying lens was used to observe traits in a room with bright lighting. The dentition on the maxilla was recorded first and any additional observations of note were included on the back of the spreadsheet. The primary focus of this analysis is to examine adult dentition.

For determining the breakpoint, the ASUDAS system was used, but there were several instances in which the breakpoint could be determined at different grades. For example, shoveling of the incisor was determined by a grade two, but a higher grade of three could be used, and was up to the discretion of the researcher. For this analysis, I chose a grade three because populations from the Americas tend to have on average a high frequency of high grades of shoveling. This analysis examined the differences within two New World populations and a higher breakpoint for this trait would allow to adjust for a more precise analysis when comparing differences on nonmetric dental data from two populations that are in close proximity of one another. Other traits such as the upper premolar root number and lower molar root number, the frequency of one rooted molar was compared as outlined in the ASUDAS (Scott and Irish 2017). Certain traits put forth

more than one key tooth, in these cases the most pronounced expression of the trait was chosen on the whichever tooth had the highest frequency.

Traits were initially scored on an ordinal scale which varied depending on the trait under evaluation. As previously mentioned, there were several limitations in collecting data due to the nature of dentition being worn which obscured many traits on the occlusal surface. Traits which exhibited the loss of dentine were difficult to score and if the trait was partially observed they were scored at a lower grade. This was seen in traits such as Canine Distal Accessory Ridge (CDAR) in which the portion of the dentine that makes up the trait is easily worn away due to contact with the incisial surface of the other canines (Scott and Irish, 2017, p. 63). Other traits that are more sensitive of being obliterated such as premolar accessory ridges that exhibited high wear were not counted due to the trait being destroyed (Scott and Irish, 2017). I attempted to examine the root traits as well, but many were glued to the maxillae and mandible making it impossible to observe the trait without damaging the skeletal material. Although many dental elements were glued there were also many that were not.

Although this analysis is based on the observation of nonmetric dental traits, there was one trait that required the use of spreading calipers. This was the enamel extensions of the upper and lower molars. Another trait, the Uto-Aztec Premolar, required the use of a protractor in order to determine the degree of rotation of the buccal cusp (Scott and Irish, 2017).

Traits were observed on multiple teeth on the same individual as well as the same antimeres. This increased the number of observations for a specific trait. For example, shoveling was observed on the central upper incisor as well as upper lateral incisors. In

order to determine which dentition to use, a key tooth was chosen in order to be representative for the trait. This is done because it allows for the trait to be represented by the most conservative tooth that displays that trait, and is the most stable tooth in regards to development and evolution (Scott et al., 2018). In the case of shoveling of upper incisors the central upper incisor was chosen as key tooth. A total of 36 traits were observed between populations. These traits were chosen because they are predominantly found in sinodont dental patterns and are useful when comparing populations.

In order to have a more complete record of individuals, sex and age were also scored whenever possible. For the Belle Glade Mound site, the majority of individuals were scored as probable male at an estimated total of 22 individuals, with 14 individuals being classified as probable female, and 14 individuals the sex was undetermined or unknown. Age estimation was based on the development of dentition and dental eruption and the results indicate that 49 of the 50 individuals were at least 21 years or older and were classified as mature and one individual that had all the lower molars erupted with the exception of the lower third molars. For the Highland Beach site at least 17 individuals were identified as probable male, seven individuals were identified as probable female, and 14 individuals were identified as undetermined or unknown. At least 33 individuals were classified as mature and five were classified as Juveniles. As mentioned previously the focus is on adult dentition and the individuals that were classified as Juvenile were included due to having adult dentition present and did not have remnants of juvenile dentition. Although sex and age play an important part in constructing a biological profile it was difficult to accurately determine the age and sex due to the collections being comingled. An advantage of nonmetric dental traits is that

both sexes are pooled, because dental traits tend to display little sexual dimorphism (Irish and Konigsberg, 2007; Aubry, 2009, p. 116; Irish, 2010; Rathmann et al., 2017). For this analysis sexes were pooled together since they do not factor into the analysis of nonmetric dental traits.

### **Statistical analysis**

In order to examine the differences in populations, several statistical analyses were conducted. The first step prior to the data being dichotomized a correlation coefficient analysis was conducted in order to determine intertrait correlation. A nonparametric test was conducted, specifically Kendall's tau-b. In order to conduct this test, the SPSS program was used. This statistical method was chosen due to it being conservative with the data that is being analyzed (Irish 2010). The results from both tests indicate that they are exactly the same with the same traits showing similar levels of correlation. After the data was inputted traits that show a strong correlation greater than 0.5 were removed. Although (Irish, 2010) suggests that there should be pair wise removal of highly correlated traits, for this analysis only traits with greater missing values were removed because they are the less informative or that had greater missing values. This resulted in the removal of 8 traits out of the original 36 traits. More traits were edited out due to insufficient data, such as marginal ridge tubercles, which resulted in a total of three observations. Removal of these traits prevents the alteration of data (Irish, 2010).

#### *Correlation Coefficient Test*

As mentioned above a Kendall's Tau-b test was conducted. Any trait that exhibited a p value of greater than 0.5 was deleted, due to it having a strong correlation to

that trait. Initially there were a total of 36 variables observed and were reduced to a total of 28. These traits that remained are the traits that were chosen in order to conduct the next phase of the statistical analysis.

#### *Data Dichotomization*

As Mentioned previously breakpoints were chosen in order to allow for dichotomization of dental traits. Any trait that exhibited or scored at the breakpoint grade and above is counted as present and is changed to a one indicating that the trait is present, and any trait below that threshold is replaced with a zero denoting the trait as being absent (Irish, 2010). For example, incisors that were scored at a grade three and above were dichotomized as ones, and any incisors that were below the threshold of three were dichotomized into zeros. Other traits that examined reduction of that feature such as the metacone, grades zero to three were counted as absent, even though the trait could be present, and any observation of a metacone that exhibited a greater grade of three was counted as present (Scott and Irish, 2017). Other traits such as the upper molar root number, which states that the breakpoint is the total frequency of three rooted second upper molars, any molar that exhibited three roots would be counted as present (Scott and Irish, 2017). The dichotomization is an important step that would allow data to be read by the Smith's Mean Measure of Divergence formula.

#### *MMD*

The Smith's Mean Measure of Divergence has been applied in many studies and has shown positive results to population affinity (Irish 2010). Smith's Mean Measure of Divergence (MMD) was created to measure biological divergences that develop through

time (Sjovold, 1977; Harris and Sjøvold, 2004; Irish, 2010). This method was designed to be used with the percentages of dichotomous data (Harris and Sjøvold, 2004).

Figure 2 Smith's Mean Measure of Divergence formula as provided by Harris and Sjøvold (2004).

$$\text{MMD} = \frac{\sum_{k=1}^r (\theta_{ik} - \theta_{jk})^2}{r} - \left( \frac{1}{n_i} + \frac{1}{n_j} \right)$$

The MMD formula has been modified by Harris and Sjøvold, replacing Smith's arcsine transformation with Anscombe's transformation and allowing for multistate traits. Although it is recommended to conduct Anscombe's formula for MMD analysis, both Freeman-Tukey and Anscombe's formula were used, because both formulas provide similar results (Harris and Sjøvold, 2004; Santos, 2018).

Figure 3 Freeman-Tukey formula for MMD analysis (Harris and Sjøvold, 2004)

$$\theta = \frac{1}{2} \arcsin\left(1 - \frac{2m}{n+1}\right) + \frac{1}{2} \arcsin\left(1 - 2\left(\frac{m+1}{n+1}\right)\right)$$

Figure 4 Anscombe's formula for MMD analysis (Harris and Sjøvold, 2004)

$$\theta = \sin^{-1} \left( 1 - 2 \left( \frac{\frac{m+\frac{3}{8}}{8}}{\frac{n+\frac{3}{4}}{4}} \right) \right)$$

After conducting the correlation coefficient analysis, the remainder of the data was dichotomized into present or absent, in order to conduct the MMD analysis. In order to conduct the data analysis in the statistical program R, the data which was originally in an XLS file was changed to a CVS file for the program to be able to read it. The program

R provides a package for conducting Smith's Mean Measure of Divergence, known as AnthroMMD. After the data was uploaded as a raw binary data set, two statistical tests were used to test significance. The Anscombe's transformation and Freeman-Tukey transformation were used. Both tests are similar to one another with Anscombe's transformation allowing for a larger sample size, and it can be written in simple arcsine and can extend to multistate traits (Harris and Sjøvold 2004).

In order to remove non-discriminatory traits, there were several options. The first option included the exclusion of nonpolymorphic traits, which allows for the removal of traits of the same value of zero and one (Santos, 2018). The second option was the exclusion of quasi-nonpolymorphic traits, which removes traits with variability that appear from a single individual (Santos, 2018). The third option was the Fisher's exact test and the last option was removal of traits based on the Measure of Divergence or MD values (Santos, 2018). Although both statistical measures were conducted, for these results the Freeman-Tukey formula exhibited the best fit for this analysis because it stabilizes variance for small sample sizes especially in archeological data, such as the case for this analysis (Freeman and Tukey, 1950; Irish, 2010)



## CHAPTER 5: RESULTS

The use of nonmetric dental traits for distance analysis is a valuable asset when examining the relationship between populations. Data of dental trait frequencies from both sites are represented in the appendix. All nonmetric data was subjected to several statistical analysis in order to determine whether the Belle Glade site and Highland Beach site share any similarities. The results of the Kendall's Tau-b correlation analysis indicate that several traits are intercorrelated and were excluded from the analysis. A total of 8 traits were removed from the analysis, with many also having a strong correlation with other traits. For example, canine distal accessory ridge was strongly correlated with two other traits, due to having a correlation greater than 0.5. Kendall's Tau-b allows for the removal of traits that could have affected MMD values due to them having strong correlations with one another.

Table 2 List of traits and their proportions from both sites, after Kendal's tau-b was performed.

Traits used for MMD analysis				
Traits	N_Belle Glade	N_Highlan d Beach	Freq_Bell e Glade	Freq_Highlan d Beach
Palatine Torus	30	25	0.0333	0.0400
Winging UI1	25	24	0.6400	0.7083
Shoveling UI1	22	24	0.5454	0.5833
Double Shoveling UI1	22	24	0.6819	0.6667
Interruption Grooves UI2	31	24	0.3226	0.2917
Tuberculum Dentale UI2	30	21	0.4334	0.2857
Marginal Tubercles UP1	17	19	0.4117	0.4211
Uto-Aztecan premolar UP1	32	23	0.0313	0.0435
Metacone UM3	18	19	0.3889	0.6316
Hypocone UM2	21	21	1.0000	0.9048

Bifurcated Hypocone UM2	11	16	0.0000	0.0625
Cusp 5 UM1	15	18	0.2000	0.2778
Carabelli's Cusp UM1	27	25	0.2221	0.2000
Parastyle UM1	22	26	0.0455	0.0000
Enamel Extensions UM1	24	24	0.4584	0.3750
Upper Molar Root Number LM2	12	22	0.3333	0.2727
Pegged Reduced Missing Third Molars UM3, LM3	31	29	0.1936	0.0690
Premolar Odontomes UP1, UP2, LP1, LP2	45	36	0.0444	0.0833
Anterior Fovea LM1,LM2	22	18	0.2727	0.4444
Mandibular Torus	36	23	0.0000	0.0000
Lower Premolar Cusp Number LP2	28	19	0.1429	0.0526
Lower Molar Cusp Number LM1	24	14	1.0000	1.0000
Lower Molar Cusp Number LM2	21	17	0.8095	0.5882
Mid Trigonid Crest LM1,LM2	28	18	0.0000	0.0000
Protostylid LM1	29	23	0.0000	0.0435
Cusp 6 LM1	18	13	0.3333	0.3846
Cusp 7 LM1	27	17	0.0714	0.0000
Three Rooted Lower Molar LM1	14	13	0.0000	0.0000
Torsomolar Angle LM3	22	19	0.1364	0.3158

### Freeman-Tukey results

MMD results indicate that both populations are closely related and display little divergence. Data that was ran with Freeman-Tukey's analysis with three strategies: No exclusionary strategy, exclusion of nonpolymorphic traits, exclusion of quasi-nonpolymorphic traits, and overall measure of divergence values greater than zero. Freeman-Tukey's formula provides smaller values of overall measure of divergence compared to the Anscombe's formula. The MMD organized them from high to low values. The traits with higher values indicate that these traits were more discriminatory to traits that provide little discrimination (Santos, 2018). The following table provides the

list of traits from highest discriminatory value to the least, with the metacone having a high discriminatory value and Cusp 6 having the least (Table 3).

Table 3 The overall measure of divergence as displayed under the Freeman-Tukey formula. Sorted from highest values on top to lowest values towards the bottom.

Overall MD Values for Freeman-Tukey Formula	
Trait List	Overall MD
Metacone UM3	0.1778
Pegged/Reduced/Missing/Third Molars UM3, LM3	0.0933
Lower Molar Cusp Number LM2	0.0892
Torsomolar Angle LM3	0.0574
Cusp 7 LM1	0.0405
Protostylid LM1	0.0195
Parastyle UM1	0.0175
Anterior Fovea LM1,LM2	-0.0005
Lower Premolar Cusp Number LP2	-0.0111
Tuberculum Dentale UI2	-0.0157
Enamel Extensions UM1	-0.0430
Premolar Odontomes UP1,UP2,LP1,LP2	-0.0474
Mandibular Torus	-0.0693
Uto-Aztecian PM UP1	-0.0697
Palatine Torus	-0.0720
Bifurcated Hypocone UM2	-0.0724
Hypocone UM2	-0.0726
Interruption Grooves UI2	-0.0734
Shoveling UI1	-0.0740
Winging UI1	-0.0743
Carabelli's Cusp UM1	-0.0766
Double Shoveling UI1	-0.0844
Mid Trigonid crest LM1, LM2	-0.0887
Upper Molar Root Number LM2	-0.0927
Cusp 5 UM1	-0.1063
Lower Molar Cusp Number LM1	-0.1084
Marginal Tubercles UP1	-0.1108
Three rooted Lower Molar LM1	-0.1190
Cusp 6 LM1	-0.1269

When no exclusionary strategy was applied the results indicate that MMD values are negative, indicating no divergence (Table 4). The symmetrical matrix of MMD replaces negative values with zeroes (Santos, 2018). As seen with the table with no exclusionary strategy, the overall MMD value is -0.0384 with a standard deviation of 0.0254, which indicates that the MMD value is zero. The non-exclusionary strategy demonstrates that the differences in the results are not significant.

Table 4 MMD values from non-exclusionary strategy with descriptors provided by the program R.

No Exclusionary strategy Freeman-Tukey formula		
Symmetrical matrix of MMD values		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0000
Highland Beach	0.0000	0.0000
MMD values (upper triangular part) and associated SD values (lower triangular part)		
	Belle Glade	Highland Beach
Belle Glade	0.0000	-0.0384
Highland Beach	0.0254	0.0000
MMD values (upper triangular part) and their significance (indicated by a * in the lower part; 'NS'='non significant')		
	Belle Glade	Highland Beach
Belle Glade	NA	-0.0380
Highland Beach	NS	NA

The exclusion of nonpolymorphic traits resulted in the increase of distance value by 0.0093 points, and the standard deviation of 0.0272 (Table 5). Similar observations regarding the symmetrical matrix which converts negative values into zeroes. Similar result came in regards of the significance, which indicates that the difference values between the two sites are not significant.

Table 5 Exclusion of nonpolymorphic traits and resulting MMD values from the Freeman-Tukey formula, descriptions provided by program R.

Exclude nonpolymorphic traits Freeman-Tukey formula		
Symmetrical matrix of MMD values		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0000
Highland Beach	0.0000	0.0000
MMD values (upper triangular part) and associated SD values (lower triangular part)		
	Belle Glade	Highland Beach
Belle Glade	0.0000	-0.0291
Highland Beach	0.0272	0.0000
MMD values (upper triangular part) and their significance (indicated by a * in the lower part; 'NS'='non significant')		
	Belle Glade	Highland Beach
Belle Glade	NA	-0.0290
Highland Beach	NS	NA

Exclusion of quasi polymorphic traits resulted in similar MMD values (Table 6).

The symmetrical matrix again demonstrates that there is no difference between sites. The negative MMD values of -0.0315 with a standard deviation of 0.0284. these results indicate that there are no significant differences between sites.

Table 6 Exclusion of quasi-nonpolymorphic traits and resulting MMD values from the Freeman-Tukey formula, descriptions provided by program R

Exclude quasi-nonpolymorphic traits Freeman-Tukey formula		
Symmetrical matrix of MMD values		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0000
Highland Beach	0.0000	0.0000
MMD values (upper triangular part) and associated SD values (lower triangular part)		
	Belle Glade	Highland Beach
Belle Glade	0.0000	-0.0315
Highland Beach	0.0284	0.0000
MMD values (upper triangular part) and their significance (indicated by a * in the lower part; 'NS'='non significant')		
	Belle Glade	Highland Beach
Belle Glade	NA	-0.0320
Highland Beach	NS	NA

A fisher's exact test was not conducted because less than two traits were suitable for this analysis, therefore it was not conducted. The final exclusionary strategy was the exclusion of MD values less than 0, which excludes traits that have negative overall measure of divergence. These traits share similar trait frequencies between two sites, this can result in the removal of more traits that can affect MMD values. The results of the final exclusionary strategy demonstrate a low level of divergence (Table 7). This method also provides positive MMD values, but it results in the removal of majority of traits with only seven traits being analyzed (see table 2). The symmetrical matrix demonstrates an MMD value of 0.0707, which shows little divergence between the Belle Glade and Highland Beach sites. The standard deviation for the exclusion of overall MD values less than zero are 0.0490. Although there are differences between the two sites, the divergence is still not significant enough to demonstrate variation.

Table 7 Exclusion of traits with overall Measure of Divergence values greater than 0 and resulting MMD values from the Freeman-Tukey formula, descriptions provided by program R.

Exclude traits with overall MD Values less than 0 Freeman-Tukey formula		
Symmetrical matrix of MMD values		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0707
Highland Beach	0.0707	0.0000
MMD values (upper triangular part) and associated SD values (lower triangular part)		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0707
Highland Beach	0.0490	0.0000
MMD values (upper triangular part) and their significance (indicated by a * in the lower part; 'NS'='non significant')		
	Belle Glade	Highland Beach
Belle Glade	NA	0.0710
Highland Beach	NS	NA

## Anscombe's results

Anscombe's formula gave similar results to the Freeman-Tukey formula, with slightly larger overall MD values (Table 8).

Table 8 The overall measure of divergence as displayed under Anscombe's formula. Sorted from highest values on top to lowest values towards the bottom.

Overall MD Values for Anscombe's Formula	
Traits	Overall MD
Metacone UM3	0.1848
Pegged/Reduced/Missing Third Molars UM3/LM3	0.0972
Lower Molar Cusp Number LM2	0.0937
Torsomolar Angle LM3	0.0612
Anterior Fovea LM1, LM2	0.0017
Cusp 7 LM1	-0.0023
Lower Premolar Cusp Number LP2	-0.0078
Protostylid LM1	-0.0116
Tuberculum Dentale UI2	-0.0140
Parastyle UM1	-0.0149
Enamel Extensions UM1	-0.0423
Premolar Odontomes UP1,UP2,LP1,LP2	-0.0475
Mandibular Torus	-0.0685
Uto-Aztecian PM UP1	-0.0698
Hypocone UM2	-0.0719
Palatine Torus	-0.0720
Interruption Grooves UI2	-0.0734
Shoveling UI1	-0.0738
Winging UI1	-0.0741
Carabelli's Cusp UM1	-0.0766
Double Shoveling UI1	-0.0843
Mid Trigonid crest LM1, LM2	-0.0878
Upper Molar Root Number LM2	-0.0926
Cusp 5 UM1	-0.1055
Lower Molar Cusp Number LM1	-0.1069
Marginal Tubercles UP1	-0.1108
Bifurcated Hypocone UM2	-0.1136
Three rooted Lower Molar LM1	-0.1183
Cusp 6 LM1	-0.1269

Similar to the Freeman-Tukey samples same strategies were used when examining the overall MMD values. When no exclusionary strategy was included the resulting symmetrical MMD values were at zero. The non-symmetrical MMD values was -0.0424 a slight decrease compared to the other formula with a similar standard deviation of 0.0254 (Table 9). Similar to the previous formulas there was no major differences between the two sites with the resulting values indicating that they are not significantly different from one another.

Table 9 MMD values from non-exclusionary strategy with descriptors provided by the program R.

No Exclusionary strategy Anscombe's Formula		
Symmetrical matrix of MMD values		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0000
Highland Beach	0.0000	0.0000
MMD values (upper triangular part) and associated SD values (lower triangular part)		
	Belle Glade	Highland Beach
Belle Glade	0.0000	-0.0424
Highland Beach	0.0254	0.0000
MMD values (upper triangular part) and their significance (indicated by a * in the lower part; 'NS'='non significant')		
	Belle Glade	Highland Beach
Belle Glade	NA	-0.0420
Highland Beach	NS	NA

When excluding nonpolymorphic traits the MMD value decreased to -0.0339 with a standard deviation of 0.0272 (Table 10). The symmetrical matrix of MMD values again indicate that there are no differences between the two traits. The results are similar in regards of significant differences between the two sites is that they are not significant.

Table 10 MMD values from exclusion of nonpolymorphic traits strategy with descriptors provided by the program R.

Exclusion of nonpolymorphic traits Anscombe's Formula		
Symmetrical matrix of MMD values		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0000
Highland Beach	0.0000	0.0000



Belle Glade	0.0000	0.0000
Highland Beach	0.0000	0.0000
MMD values (upper triangular part) and associated SD values (lower triangular part)		
	Belle Glade	Highland Beach
Belle Glade	0.0000	-0.0339
Highland Beach	0.0272	0.0000
MMD values (upper triangular part) and their significance (indicated by a * in the lower part; 'NS'='non significant')		
	Belle Glade	Highland Beach
Belle Glade	NA	-0.0340
Highland Beach	NS	NA

The exclusion of quasi-nonpolymorphic traits the MMD value increased slightly to -0.0321 with a standard deviation of 0.0284 (Table 11). The symmetrical matrix of MMD values indicate that there is no difference between the two sites. With the similar results as the two sites are not significantly different from one another.

Table 11 MMD values from exclusion of quasi-nonpolymorphic traits strategy with descriptors provided by the program R.

Exclude quasi-nonpolymorphic traits Anscombe's formula		
Symmetrical matrix of MMD values		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0000
Highland Beach	0.0000	0.0000
MMD values (upper triangular part) and associated SD values (lower triangular part)		
	Belle Glade	Highland Beach
Belle Glade	0.0000	-0.0321
Highland Beach	0.0284	0.0000
MMD values (upper triangular part) and their significance (indicated by a * in the lower part; 'NS'='non significant')		
	Belle Glade	Highland Beach
Belle Glade	NA	-0.0320
Highland Beach	NS	NA

Similar situation occurred when conducting Fisher's exact test and was not included in this analysis. When excluding traits with MD values less than 0, the symmetrical matrix of MMD values is 0.0877. This indicates that there is a minor

difference between the two sites. The non-symmetrical MMD values was 0.0877 with a standard deviation of 0.0616 (Table 12). Although the distance values increase to 0.0880 there is still no significant differences between the two sites.

Table 12 MMD values from the exclusion of traits with greater overall measure of divergence values of zero, strategy with descriptors provided by the program R.

Exclude traits with overall MD Values less than 0 Anscombe's formula		
Symmetrical matrix of MMD values		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0877
Highland Beach	0.0877	0.0000
MMD values (upper triangular part) and associated SD values (lower triangular part)		
	Belle Glade	Highland Beach
Belle Glade	0.0000	0.0877
Highland Beach	0.0616	0.0000
MMD values (upper triangular part) and their significance (indicated by a * in the lower part; 'NS'='non significant')		
	Belle Glade	Highland Beach
Belle Glade	NA	0.0880
Highland Beach	NS	NA

Both formulas gave slightly different results, but the overall results indicate that the distance values for both Highland Beach and Belle Glade sites as being non-significant. This indicates that the differences between the two populations are not significant. Unfortunately, the sample size of sites was too small to conduct an MDS plot or Hierarchical cluster, due to the program requiring more than two sites. This proves the null hypothesis to be correct due to the strong overlap of traits observed between these two populations along with non-significant MMD values

## CHAPTER 6: DISCUSSION AND CONCLUSION

The results indicate that there are marginal differences between the Belle Glade and Highland Beach sites from a biological standpoint. The low degree of divergence suggests that these two groups were closely interconnected and had a consistent degree of gene flow between populations. This trend of intercultural interaction through the perspective of archeological areas can be seen in the archeological material recovered from the two sites, such as shark teeth in Belle Glade Mound site and Belle Glade pottery in the Highland Beach site (Willey, 1949; Furey, 1972; Wheeler et al., 2002). Furey's analysis of the Highland Beach Site found a high frequency of Belle Glade pottery, leading archeologists to infer the site was associated with the Belle Glade Culture, being either a coastal expression of the culture or possibly an outpost of interior peoples (Furey, 1972; Wheeler et al., 2002). The dental evidence corroborates with the archeological findings from both sites in regards of population interaction between the interior and the coast.

In this analysis the nonmetric dental traits demonstrated that there were no differences between the two populations examined. It is important to remember that nonmetric dental traits tend to be more conservative compared to other forms of nonmetric analysis such as craniometric traits, therefore it will demonstrate lower degree of divergence. Craniometric analysis from populations from South Florida during the transition from the Archaic to the Woodland Period indicate that there was an increase in variability possibly due to cultural barriers (Kles, 2013, p. 203). Nonmetric dental traits

demonstrate that there is a non-significant degree of divergence between two sites that have been associated to be part of the Belle Glade culture (Furey, 1972). Do the results answer the primary question of whether there are significant differences between the coastal and interior populations? In short no, but there are several important aspects that should be accounted for. First, the sample size involved two sites is insufficient in providing an accurate picture of the phenetic and genetic variation between populations in South Florida. There was a total of 300 human remains exhumed in Belle glade mound and only 50 were able to be examined for nonmetric dental traits (Smith, 2015, p. 57). Of those 300 exhumed were from one fourth of the mound excavated, which could possibly have another 800 human remains still interred (Smith, 2015, p. 57) . Similar situation in Highland Beach in which 128 to 216 remains were exhumed, but only 38 individuals were examined (Winland, 1993, 2002; Hennessey, 2015). One fifth of the Highland Beach mound was excavated and there could be another 500 to 800 individuals still interred. Second, only sites on an East to West axis were considered. The inclusion of more sites outside of the Belle Glade and East Okeechobee cultural areas is necessary for a better understanding of population interactions in the South Florida region. Along with the inclusion of more sites outside the Belle Glade and East Okeechobee cultural areas, there should be an inclusion of more sites from these two cultural areas to have a more representative sample for the two regions as a whole.

This research also provided answers concerning the level of interaction between these two populations. The low MMD values indicate that there is a high degree of geneflow between the two sites. From a biological viewpoint, that is evidence for a high degree of intermixing, which is further supplemented by the archeological material

evidence such as the distribution of ceramic types and coastal-inland exchange. Sites such as Rita Island, which is found in the interior, demonstrate that there is presence of Busycon shell which is native from a marine environment (Mount, 2009, p. 45). Willey also points out the presence of coastal material in Belle Glade Mound, including shark's teeth and Busycon shell celts (Willey, 1949, pp. 45–47).

Evidence of populations traveling from the interior to the coast has been observed through other forms of investigation, such as isotopic analysis from other sites from the St. Johns area located in Northern Florida, demonstrate migration from the interior to the coast. The thesis dissertation of Bryan Tucker demonstrates several aspects of human mobility, diet and mortuary treatment. This analysis concluded that a seasonal occupation pattern existed between the coastal and interior region of Florida, with populations occupying the coast during the summer and fall seasonal periods (Tucker, 2009, p. 145). This study was conducted on a population of the archaic period, which is not contemporary with this study's site chronology, but it demonstrates that populations were moving between the interior and the coast for some time. Although Tucker's analysis was conducted in a different region, this study demonstrates similar results in that there is contact from the interior to the coast and vice versa.

Inter-population interactions in the New World are still being inferred from archeological investigations. Evidence gathered from previous archeological investigations indicate intercultural interaction between the interior of the state to the coast. The incorporation of a biological line of inquiry greatly supplements these previous findings.

Nonmetric dental traits analyses provide more evidence that populations were not static and that they experienced a high degree of gene flow. These findings are significant because they corroborate the conclusions formed based on artifact assemblages from archeological investigations conducted at both sites, as well as other lines of inquiry derived from isotopic analysis.

This research sought to answer the question of the degree of biological affinity between two inferred archaeological cultural areas in South Florida, and the degree of gene flow between the Belle Glade and Highland Beach sites. The two sites were chosen because of their location in different environments, but similar occupational time ranges and similar cultural affiliations. In order to answer the proposed research questions, a nonmetric dental analysis was conducted. The nonmetric dental analysis employed followed the criteria set forth by the Arizona State University Dental Anthropological System. A total of 88 individuals were examined, with 50 individuals examined from Belle Glade Mound site and 38 individuals from Highland Beach site. After the data was collected, a Kendall's Tau-b a nonparametric correlation test was conducted to test for intertrait association. After the parametric test was run, the data was dichotomized into presence or absence in order to utilize the MMD statistic. The results from the analysis ranged from negative to slight deviation values, which strongly indicated that both populations were closely related.

The results indicate that both populations were very similar to one another, and this confirms the analysis of the archeological record which indicates evidence of material exchange between the coastal and the interior environments. These results provide a more complete insight into how populations interacted with one another. From

a dental nonmetric perspective, there is little genetic drift between the two populations. These results also demonstrate that these two groups were not isolated from one another. This shows that there was a high degree of both material and biological exchange between the two culture areas. This research supplements past archeological interpretations from South Florida by providing evidence of gene flow between the two sites. This research also supports results from nonmetric dental analysis conducted on the Gulf-coast of South Florida. In which Dr. Alison A. Elgart examined various sites to determine biological relationships (Elgart, 2019). The results indicate that there is no distinction between sites from different cultural areas (Elgart, 2019). Her results are in line from the two sites examined in this research, in which there are no major differences between populations.

There were several limitations for this research that affected the examination of the two collections. First, both sites exhibited comingled remains with taphonomic damage, which made it difficult to have a more complete analysis regarding dental data. Second, the manner in which the remains were exhumed was problematic. This removed context of burials and any cultural associations as well as chronological context. Another limitation was sample size, because both mounds were not entirely excavated the samples might still not be representative of one another. These limitations were not enough to affect the analysis but might have affected the results because of incomplete data.

### **Future research**

When conducting this analysis several other lines of inquiry regarding biological analysis of populations of these populations should be pursued for future research. Isotopic analysis is an alternative avenue of exploring migration and diet. Genetic

analysis can aid in the nonmetric dental trait interpretations as well as have more precise results regarding population affinity (Hubbard et al., 2015; Stojanowski and Hubbard, 2017). Additional to nonmetric analysis there is evidence that metric dental measurements have also been shown to have a strong genetic component (Stojanowski et al., 2017) . Lastly a dental pathological analysis should be incorporated for future analysis and compare between the two sites.

### **Concluding remarks**

To conclude the differences between the two populations examined is non-significant. This proves the null hypothesis that at least from the examination of two sites there is a lot of overlap regarding trait frequencies. Presence of Belle Glade ceramic in Highland Beach indicate that this population had strong contact with the Belle Glade population. This does not necessarily mean that the Highland Beach site was part of the Belle Glade culture, but it does indicate that they had a strong relationship with the interior. Future research on nonmetric dental traits should expand to other regions in Florida, especially more sites from the other cultural areas as well as regions such as the Glades, Caloosahatchee and other regions found in Northern Florida. This expansion to other regions will aid in the understanding of population relationships at a broader level.



## APPENDICES

**Appendix A Belle Glade Mound Total Trait Frequencies**

		<b>Belle Glade Mound (8PB41) Trait Frequencies</b>								
		<b>Grade</b>								
<b>Trait</b>	<b>N</b>	<b>0</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	
Palatine Torus	30	0.7333	0.2333	0.0333	0.0000	0.0000				
Winging UI1	25	0.3600	0.3200	0.2400	0.0800					
Shoveling UI1	22	0.0000	0.0909	0.3636	0.3636	0.0909	0.0000	0.0909	0.0000	
Double Shoveling UI1	22	0.1364	0.1818	0.0455	0.2273	0.3636	0.0455	0.0000		
Interruption Grooves UI2	31	0.6774	0.3226							
Tuberculum Dentale UI2	30	0.3667	0.2000	0.1667	0.1667	0.0667	0.0333	0.0000		
CDAR UC	14	0.0714	0.2857	0.2143	0.2857	0.1429	0.0000			
PxMAR UP2	8	0.0000	0.3750	0.2500	0.3750	0.0000				
Marginal Tubercles UP1	17	0.5882	0.2353	0.1176	0.0588					
Uto-Aztecan PM UP1	32	0.9688	0.0313							
Metacone UM3	18	0.0000	0.0556	0.1667	0.3889	0.2222	0.1667			
Hypocone UM2	21	0.0000	0.0000	0.0952	0.2857	0.4762	0.1429	0.0000		
Bifurcated Hypocone UM2	11	1.0000	0.0000							
Cusp 5 UM1	15	0.8000	0.1333	0.0667	0.0000	0.0000	0.0000			
Marginal Ridge Tubercles UM1	2	0.0000	1.0000							
Carabelli's Cusp UM1	27	0.4444	0.3333	0.1481	0.0370	0.0370	0.0000	0.0000	0.0000	
Parastyle UM1	22	0.8636	0.0909	0.0455	0.0000	0.0000	0.0000	0.0000		
Enamel Extensions UM1	24	0.3333	0.2083	0.4167	0.0417					
Upper Preomolar Root Number UP1	13	1.0000	0.0000	0.0000						
Upper Molar Root Number LM2	12	0.4167	0.2500	0.3333						
Pegged/Reduced Missing Third Molars UM3,LM3	31	0.8065	0.0968	0.0000	0.0968					
Premolar Odontomes UP1,UP2,LP1,LP2	45	0.9556	0.0444							
Anterior Fovea LM1,LM2	22	0.0455	0.3636	0.3182	0.2727	0.0000				
Mandibular Torus	36	0.8889	0.1111	0.0000	0.0000	0.0000				
CDAR LC	14	0.2857	0.3571	0.2143	0.1429	0.0000	0.0000			

MxPAR LP	14	0.5000	0.1429	0.2857	0.0714	0.0000			
Lower Premolar Cusp Number LP2	28	0.8214	0.0357	0.1429	0.0000				
Lower Molar Cusp Number LM1	24	0.0000	0.0417	0.0417	0.2083	0.2083	0.5000		
Lower Molar Cusp Number LM2	21	0.1905	0.0476	0.1905	0.0476	0.3333	0.1905		
Deflecting Wrinkle LM1	15	0.6667	0.0000	0.2667	0.0667				
Distal Trigonid crest LM1,LM2	24	0.7083	0.2917						
Mid Trigonid crest LM1,LM2	28	1.0000	0.0000						
Protostylid LM1	29	0.6897	0.3103	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Cusp 6 LM1	18	0.6667	0.1667	0.0000	0.1111	0.0556	0.0000		
Cusp 7 LM1	28	0.9286	0.0357	0.0357	0.0000	0.0000			
Lower First Premolar Root Number LP1	16	0.6875	0.2500	0.0625	0.0000	0.0000	0.0000		
Lower Canine root Number LC	14	1.0000	0.0000						
Three rooted Lower Molar LM1	13		0.0000	1.0000	0.0000				
Lower Molar Root Number LM2	11		0.0909	0.9091					
Torsomolar Angle LM3	22	0.8636	0.1364						

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**Appendix B Highland Beach Site Total Trait Frequencies.**

Trait	Highland Beach Mound (8PB11) Trait Frequencies								
	N	Grade							
	0	1	2	3	4	5	6	7	
Palatine Torus	25	0.8400	0.1200	0.0400	0.0000	0.0000			
Winging UI1	24	0.2917	0.2917	0.2500	0.1667				
Shoveling UI1	24	0.0000	0.0417	0.3750	0.3333	0.0833	0.0000	0.1667	0.0000
Double Shoveling UI1	24	0.1667	0.1667	0.0417	0.1667	0.3333	0.0417	0.0833	
Interruption Grooves UI2	24	0.7083	0.2917						
Tuberculum Dentale UI2	21	0.3810	0.3333	0.0476	0.1429	0.0000	0.0000	0.0952	
CDAR UC	7	0.0000	0.1429	0.1429	0.1429	0.5714	0.0000		
PxMAR UP2	12	0.7500	0.0000	0.0000	0.0000	0.2500			
Marginal Tubercles UP1	19	0.5789	0.3158	0.0526	0.0526				
Uto-Aztecans PM UP1	21	0.9565	0.0435						
Metacone UM3	19	0.0000	0.0000	0.0000	0.3684	0.4211	0.2105		
Hypocone UM2	21	0.0476	0.0000	0.0476	0.3810	0.2857	0.2381	0.0000	
Bifurcated Hypocone UM2	16	0.9375	0.0625						
Cusp 5 UM1	18	0.7222	0.0000	0.1111	0.1111	0.0556	0.0000		
Marginal Ridge Tubercles UM1	1	0.0	1.0						
Carabelli's Cusp UM1	25	0.5200	0.2800	0.2000	0.0000	0.0000	0.0000	0.0000	0.0000
Parastyle UM1	26	0.9615	0.0385	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Enamel Extensions UM1	24	0.5833	0.0417	0.1667	0.2083				
Upper Preomolar Root Number UP1	21		0.9524	0.0476	0.0000				
Upper Molar Root Number LM2	22		0.5000	0.2273	0.2727				
Pegged/Reduced Missing Third Molars UM3,LM3	29	0.9310	0.0000	0.0000	0.0690				
Premolar Odontomes UP1,UP2,LP1,LP2	36	0.9167	0.0833						
Anterior Fovea LM1,LM2	18	0.0556	0.2778	0.2222	0.3333	0.1111			
Mandibular Torus	23	0.9130	0.0870	0.0000	0.0000	0.0000			
CDAR LC	12	0.3333	0.3333	0.1667	0.0833	0.0833	0.0000		

MxPAR LP	13	0.3077	0.2308	0.0769	0.3077	0.0769			
Lower Premolar Cusp Number LP2	19	0.0000	0.9474	0.0000	0.0526				
Lower Molar Cusp Number LM1	14	0.0000	0.0000	0.0714	0.0714	0.5000	0.3571		
Lower Molar Cusp Number LM2	17	0.4118	0.0588	0.1176	0.1176	0.2353	0.0588		
Deflecting Wrinkle LM1	8	0.2500	0.3750	0.2500	0.1250				
Distal Trigonid crest LM1,LM2	18	0.9444	0.0556						
Mid Trigonid crest LM1,LM2	18	1.0000	0.0000						
Protostylid LM1	23	0.7391	0.2174	0.0000	0.0435	0.0000	0.0000	0.0000	0.0000
Cusp 6 LM1	13	0.6154	0.0769	0.1538	0.1538	0.0000	0.0000		
Cusp 7 LM1	17	1.0000	0.0000	0.0000	0.0000	0.0000			
Lower First Premolar Root Number LP1	15	0.6000	0.4000	0.0000	0.0000	0.0000	0.0000		
Lower Canine root Number LC	19		1.0000	0.0000					
Three rooted Lower Molar LM1	13		0.0000	1.0000	0.0000				
Lower Molar Root Number LM2	20		0.6500	0.3500					
Torsomolar Angle LM3	19	0.6842	0.3158						

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