Archaeology and aDNA in Oceania

- Debates on migration patterns the past 50 years

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Abstract

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The aim of this thesis is to investigate how discussions in archaeology and genetics influence the consensus on human origins and migrations in the South Pacific. By analyzing the genetic research on chicken- and sweet potato-DNA, I present a general overview of how genetics and archaeology shape the understanding of how humans have colonized the Pacific. By deconstructing a review on how the Pacific was settled based on aDNA, I analyze a geneticist’s perspective on archaeological problems. Through this analysis I suggest how archaeology should be approached on a theoretical level in order to be relevant in understanding human migrations in the Pacific. I propose that archaeology’s strength lie in interpreting material culture through an agency perspective in order to reach a dimension not obtainable by biological perspectives.


**Keywords:** Ancient DNA, migrations, sweet potato, chickens, Polynesia, Oceania, South America, mitochondrial DNA, nuclear DNA, human DNA, archaeological theory, deconstruction, cultural evolution, paradigm shift, agency


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Part I, prerequisites

1. Introduction

1.1 Current debates and the future of archaeology

Genetics have been on the rise in archaeology for quite a while now. From sampling ancient remains to analyzing modern DNA in order to determine origins of populations and migration movements in pre-history. Genetics can be a versatile tool for archaeology in that it provides answers that have previously been unattainable. As genetic methodology become more advanced, working with ancient samples becomes more and more worthwhile and reliable (Knapp & Hofreiter 2010). Since the implementation of authenticity criteria (Cooper & Poinar 2000; Gilbert et al. 2005), contamination is no longer the great hurdle for geneticists working with ancient DNA as it once were. While multidisciplinary projects make great research there still seems to be a bit of a discrepancy between the fields when it comes to scientists understanding one another (Lidén & Eriksson 2013). This discrepancy is not exclusive for archaeology and genetics (see Meiron Jones 2013 and Larsson 2013) but is both an important part and an inquiring aspect in understanding the archaeology-genetic dialectic.

In a previous study, I examined the interplay of archaeology and genetics in terms of Neolithic Europe (see Johansson 2014). I found that in order for both fields to fully complement each other there needs to be a greater understanding for both fields from the same researcher. In this study, I hope to further investigate and evolve an archaeologists view on genetics by researching the discussions of migration from both archaeological and genetic perspectives. The setting chosen for this endeavor is the South Pacific, as it is an apt case study for human migration. Many islands and island groups are separated by vast amounts of ocean which limits migration capabilities by technological factors (Bell et al. 2015) like creating and using boats and carrying capacity on these boats, restricting how many colonizers could manage to move out across the water at the same time. This makes these islands excellent cases for studying bottleneck effects, founder effects and migration strategy for both biology (genes) and material culture. Polynesia is also homogenous in language and culture so applying genetic analysis could provide a new angle in figuring out how humans have settled these islands.

In Swedish and Scandinavian archaeology there has been discussions regarding archaeology’s future over the past few years (Olsen 2012a; Lidén & Eriksson 2013; Kristiansen 2014 see also Olsen 2012b). This discussion highlights some of the fundamental difficulties of archaeology and genetics. However, this discussion in Pacific archaeology has been, to my knowledge, conspicuous by its absence. Instead, genetic methodology and discourse is swallowed hook, line and sinker as a key to the cipher that is Pacific pre-historic migrations.

In Current Swedish Archaeology the discussion went from Olsen (2012a: 20-21) predicting a return to things and a focus on the artifacts based on trends he observed in archaeological research. Even though he was met with some harsh criticism from Holtorf (2012:57-59) and Källén (2012: 63) for arguing about the overuse of theory in archaeology and that theoretical interpretations of things are often more enticing than things just being things (Olsen 2012a: 22-23).

The following year, Lidén and Eriksson (2013) discussed how natural scientific methods used in archaeology were supposed to revolutionize archaeology but had some inherent problems (Lidén & Eriksson 2013: 11-12). They were of the opinion that the information and discussion across disciplines always occurred through a “filter” due to differences in ontologies and theory of the various disciplines. This leads to important aspects of the
discussion being misunderstood due to the other part not really comprehending the complexities of the other (Lidén & Eriksson 2013: 12). This hasn’t really stopped anyone from employing methods from another science than their own if the scientist feel it reinforce the results of their research. According to Lidén and Eriksson (2013) this is why scientists themselves are the culprits for worsening the problem even further. Archaeologists, for example, can rather freely make use of natural science without any real background and without much thought of source criticism (Lidén & Eriksson 2013: 16). This can also be true the other way around where interpreting archaeological contexts can be based on natural scientific methods by a scientist who is not an archaeologist/anthropologist (Lidén & Eriksson 2013: 13). The implications of this being oblivious applications of modern cultural phenomena on archaeological contexts (Lidén & Eriksson 2013: 14-15) and the dismissing of results not in favor of what was hypothesized (Lidén & Eriksson 2013: 17).

So where is archaeology headed? There clearly seems to be something going on, the rise of genetic studies based on big data sets has started confirming or disproving theories that has been discussed for a long time. The processual versus post-processual schools of archaeological thought is not really counterpoints any more as they are being re-shaped (Kristiansen 2014: 17). Kristiansen (2014) argues if the new paradigm for archaeology is really a post-paradigm era coming into play where archaeological theory and methods are being experimented with (Kristiansen 2014: 12, 14). The move towards big data analysis and the engaging in questions of population movements, warfare and evolution clearly shows the shifting trend in European archaeology (Kristiansen 2014: 14).

So with a new methodology, how will an archaeologist of the future act? Do you have to be an expert in both materiality studies and agency-based micro models, meanwhile also understanding the impact of genetic macro scale studies? The role of the archaeologist may shift towards understanding multiple fields simultaneously and collaborating across fields without any “filter”. In other words, future archaeologists acting as mediators between archaeological discourse and genetics might be a future way to move forward and here I agree with Kirch (2007: 9) when he states that “archaeologists, in other words, are well situated to act as interlocutors between the concepts and languages of social and natural sciences”. This seems especially true in Pacific archaeology where this meta-discussion appears completely overlooked but truly is an important part of figuring out how to engage in multidisciplinary studies and it why I as a student of archaeology want to explore the field of genetics and how it has been used in the discussions of migrations in the South and, to some extent also, the East Pacific.

1.2 Purpose and research topics
Following the suggestion of Kristiansen (2014) that a new paradigm in archaeology is at hand where the interaction between archaeology and genetics is the epicentre for this new paradigm or “post-paradigm”, then the purpose of this thesis is threefold. Firstly, I aim to understand how genetics influence the existing debates on archaeological topics in the South Pacific. This in light of the current debates, highlighted in the introduction, on a new paradigm in archaeology as well as the rapid advancement of genetic studies on ancient DNA where non-archaeologists can engage in archaeological discussions from a different scientific perspective.

Secondly, I aim to review, summarize and provide a comprehensive comparison of the archaeological and genetic debates on human migrations in the South Pacific to present the current, general consensus in the debates of domestic animals, domestic plants and human migration movements.

The third purpose in this thesis I aim for is to exemplify the scientific perspectives of these debates in order to evaluate the state of “meta-discussion” in Pacific archaeology. The agenda of the third aim is also to find what an appropriate perspective might be for
archaeology in Pacific contexts. To accomplish this, the research topics are formulated as follows:

- Where does the current genetic and archaeological research stand on human migration patterns in the South Pacific?
- How is the current research, based on animal DNA (as represented by the discussions on chickens), discussed to investigate human migrations in the South Pacific?
- What does genetic and archaeological research conclude on sweet potato dispersal patterns in the South Pacific?
- How is the current research of genetics and material culture discussed in Pacific contexts?

1.3 Presenting the cases

To explore the purposes of this thesis, three cases has been selected to represent the symbiotic relationship of genetic and archaeological discussions while simultaneously examining the complexities of Pacific migrations. The first case is an analytic summary of the debate on a South American-Polynesian connection based on chicken bones excavated in Chile (Storey et al. 2007). In this case genetics have provided a controversial, challenging perspective on the presence of chickens in South America and is representative of genetics changing the current consensus in archaeological discourse. Meanwhile it also functions as an example of investigating human migrations by proxy as chickens have been brought, by humans, to new islands throughout the Pacific.

The second case is an investigation of what genetics have concluded on sweet potato dispersals in the Pacific. While also acting as a proxy for human migrations, this case explores a genetic confirmation of established hypotheses and how this influences the general consensus in archaeological contexts. The sweet potato introductions are considered effects of human agency and also a representative of a South American-Polynesian connection.

The third case explores Pacific human DNA through a review conducted by Elizabeth Matisoo-Smith (2015). This case represents a geneticist’s view on what genetic research has been made in Pacific, archaeological contexts and how archaeology is treated as a science. It also provides a summary of what the current state of research in South Pacific, human migration movements are. In order to examine this case, the review will be deconstructed to provide an archaeological perspective on a genetic perspective.

1.4 Methods, materials and theory

The subject in this thesis will be explored through case studies where each case represents a topic in South Pacific archaeology in which archaeology and genetics meet. Each case is also representative of different approaches in which genetics provide a different perspective on archaeological discussions. As the major theme of this thesis is human migrations in the South Pacific, each case is coupled with human migrations. Either by proxy, like chickens and sweet potato or directly through a review of the current state of human ancient DNA research.

This means that each case is analyzed through qualitative literary studies of current genetic research. Thus, the materials for this thesis consist of literary sources, in the scope of this thesis there is no room for conducting any experiments of own volition. The literary sources are composed of published articles, books and doctoral theses concerning the South Pacific that will be subject to analytical review of what research has been done and what
conclusions have been made. These reviews will then be deconstructed in discussions to compare perspectives of scale and ontologies of different approaches.

A set of theoretical perspectives outlines the foundation for this thesis, theoretical concepts of migration is relevant as a part of the discussion of how and why people have set out to colonize the Pacific area. Rather than only discussing origins and patterns the theoretical outlook on why migration occurs can provide a helpful platform to understand these migration movement and interactions influences. This also brings in concepts of human agency and structuration as humans makes decisions in social contexts.

A different perspective on the archaeological record is that of evolutionary archaeology or neo-Darwinism, where material culture is explained as evolution. How this shapes what archaeology can accomplish and how this fits in with the current paradigm of genetics and macro scale, big data studies are an important aspect of working with Pacific archaeology. This perspective is also important to consider to explore the “meta-discussion” of archaeology as a science alongside genetics and other natural sciences.

In order to deconstruct Matisoo-Smith’s review (2015), Jacques Derrida’s use of deconstruction (1995; 2005) is explored as it is significant in this thesis for the reason of interpreting perspectives from a different perspective. It is explained, here, under methods despite Jacques Derrida’s notion that it is not a method but an ongoing process (Derrida 1981; 1995; 2001). Deconstruction in this thesis means to outline a perspective and examine the source through this perspective, it is not to criticize the source but to highlight thoughts and arguments that are problematic from a different perspective. However, “[a] thinker with a method has already decided how to proceed…” (Beardsworth 1996: 4). This highlights the flaws with viewing deconstruction as a method. How deconstruction will be used in this thesis is further discussed in chapter 4.4.

1.5 Delimitation and source criticism

There have been many discussions on different aspects of human migration in the South Pacific. This thesis will not explore the entirety of South Pacific research in depth but will instead focus on current debates were archaeology and genetics meet. The overarching purpose of this thesis is to review and deconstruct how archaeological research on material culture and genetic research corresponds or diverge concerning human migration theories.

As genetic studies improve methodology (e.g. Knapp & Hofreiter 2010; Pinhasi et al. 2015) and negates risk of contamination more effectively (see Cooper & Poinar 2000; Gilbert et al. 2005), recent studies will be selected to represent the field of genetics. This makes it less relevant to review a history of genetic studies as these are reviewed within the recent research (e.g. Wilmshurst et al. 2008; Matisoo-Smith 2015). This admittedly leads to three specific cases of debate being representatives of the entirety of the current general consensus. Resulting in certain complexities of South Pacific migrations being overlooked as they are only visible by considering all sources simultaneously or only apparent in certain cases which will not be accounted for.

In terms of plants used for this thesis, an emphasis has been placed on the sweet potato because of its cultural impact on societies, which is arguably best approached by studying material culture, as well as its role in suggesting a South American-Polynesian connection in pre-history. As for domestic animals, the chicken has been selected as it has been highly debated during the past decade due to the controversial results of chickens arriving in South America before Europeans as well as methodological criticisms. Both the sweet potato and the chicken represent a possible connection between Polynesia and South America which is also a reason for them being selected over other proxies like the Bottle Gourd or Pacific rats. Another reason is the latest research on sweet potato and chickens being fairly recent and extensively researched.
As for human ancient DNA a review has been selected to be deconstructed as it represents a genetic perspective on the current consensus. This means that the selected representatives of what the genetic consensus of human Pacific research is, may not be selected to best represent archaeology and genetics, albeit the review in itself represents a geneticist’s perspective on what the current state is and will have to suffice within the scope of this thesis. Through this review however, issues with genetic studies is considered by the reviewer, as someone who is actively working in the scientific field of genetics.

Dealing with genetic studies in Pacific environments is to be cautiously approached as the warm and humid climate make for extremely poor preservation conditions for DNA yielding samples (Matisoo-Smith & Horsburgh 2012: 63). Implied through this is that most genetic studies conducted in Pacific environments are based on modern DNA (Hagelberg 2014: 132) which is not ideal for archaeological contexts.

1.6 Understanding genetics and ancient DNA

Genetics is a complex subject, understanding the biology and chemistry of genes and how they replicate, mutate, recombine, how they are constituted of base pairs of nucleotides and held together by hydrogen bonds, how the double helix is constituted by base pairs etc. requires more than a short chapter in this thesis. There are, however, other places to learn this (e.g. Sadava et al. 2011) and it is not required for grasping the contents of this thesis. But some aspects of genetics need to be explained as the analysis in this thesis is heavily reliant on genetic research.

DNA carry a lot of information and it can be found in different parts of any living organism. Most of the DNA is found in the cell nucleus, and contains the inherited biological information from both parents. In every cell there is mitochondria which also contains DNA, but much less than in the cell nucleus. While mitochondria are found in multiple copies in every human cell it is different than nucleus DNA. The mitochondria are inherited entirely and completely from the mother, meaning mitochondrial DNA (mtDNA) can be used to explore female lineage (Birky 1995; 2008). In a similar manner DNA from the Y-chromosome (yDNA), which is one of two sex chromosomes determining the sex of the organism. The Y-chromosome is only present in males and is inherited entirely from the father, meaning yDNA can be used to explore male lineage (Bachtrog 2013).

In archaeological contexts DNA can be extracted from dead organisms and be used to study prehistoric relationships of these dead organisms (Hofreiter et al. 2001). The DNA will however, be severely degraded and damaged (Geigl 2002; Matisoo-Smith & Horsburgh 2012: 60). This means that only fragments of DNA still remains in ancient DNA (aDNA) and in order to work with these fragments of DNA they need to be amplified and sequenced. The methods and technology for sequencing aDNA has advanced through the years, from only using mtDNA because of its high frequency of copies (Hofreiter 2012) to having hopes of mapping entire ancient genomes with the use of Next Generation Sequencing technologies, to actually sequencing full ancient genomes (Pääbo et al. 2004; Millar et al. 2008; Hofreiter 2012) like the Neanderthal genome (Green et al. 2010).

Human dispersals can be examined as certain historic events create bottleneck effects for genetic variation (Figure 2). A lot of studies on human dispersals is not based on aDNA, however, but on modern DNA. A famous example is that of Cann et al. (1987) where human mitochondrial DNA variation was surveyed worldwide and resulted in tracing human mitochondrial lineages to a single lineage in Africa 200 000 years ago, which was called “mitochondrial Eve” (Cann et al. 1987). This study confirmed previous “out of Africa” hypotheses and showed that modern DNA can be used to infer major population movements through time by phylogenetics. In phylogenies for human mtDNA and yDNA common ancestors is identified through a set of genetic markers inherited as a unit, which is referred to as a haplotype. A group of haplotypes is referred to as a haplogroup (Matisoo-Smith &
Horsburgh 2012: 178). Modern mtDNA haplogroups have been utilized in European Neolithic contexts, showing discontinuity between populations via mutation rates and general population structures (Brandt et al. 2013; Brotherton et al. 2013). Modern DNA in Europe have shown a strong correlation with geography (Pinhasi et al. 2012: 4) however, to fully understand prehistoric events from genetics, successful ancient sequences is required (as in Bramanti et al. 2009; Malmström et al. 2009; Skoglund et al. 2012).

Figure 2 Visual representation of a genetic bottleneck. Genetic variation is reduced as a population moves through a bottleneck event.
2. A South Pacific setting

2.1 Initial settlement in Near Oceania
The South Pacific is rather young in terms of archaeology and archaeological discussions (Kirch 2000, 2010), and as in many other parts of the world genetics is making a breakthrough applying phylogenetic and aDNA studies to explore how the island landscape have been settled by humans. This turns it into an ample case to study how a possible new paradigm, as suggested by Kristiansen (2014), might affect the research. What impact will the genetic results have on currently proposed hypothesis based on archaeological research of material culture?

In large scale migration terms the island landscape of the South Pacific is the last place on earth that has seen major human migrations. The first modern humans reached the Pacific coast of Asia 60 000 years ago (Anderson et al. 2012: 16), colonizing Australia, New Guinea and the western Pacific, that made up the greater continent Sahul at that time, at 42 000 – 45 000 years ago (O’Connell & Allen 2004). This makes it the last point reached in early ‘Out of Africa’ models. However, the continent of Sahul was separated by large stretches of water which would require some kind of watercraft to cross (Figure 1) (Kirch 2000: 68; 2010: 135; Matisoo-Smith 2015: 1-2). As the southernmost parts of, what is today, Australia was colonized, so was the Bismarck archipelago and the Solomon Islands at roughly 28 000 years ago (Figure 3) (Wickler & Spriggs 1988). This was as far as the initial settlement went and today this is the region referred to as Near Oceania (Kirch 2000).

2.2 The Austronesian expansion and the Lapita Cultural Complex
With the discovery of sailing and the horticulturalist lifestyle with domestic animals like pigs, dogs and chickens, fishing techniques and ceramics, some 5000 years ago, migrations picked up pace again as people from Island Southeast Asia expanded into Near Oceania in what is referred to as the Austronesian expansion (Kirch 2000: 91-93; Anderson et al. 2012: 16-17).
Following the Austronesian expansion was the discovery of red-slipped pottery expanding human material remains into remote Oceania. This is known as the Lapita expansion and began around 3200–2900 years ago (Kirch 2010: 137). Its origin and expansion history is somewhat complicated and disagreed upon however. According to Bellwood (1997) and Kirch (2000: 91; 2010: 137), Lapita people originate from Southeast Asia with the earliest evidence of pottery making on the island of Taiwan (Figure 3) roughly 5000 years ago and expanded in an “Express Train”, demic diffusion model (see Diamond & Bellwood 2003). This “express train” or “out of Taiwan” model suggest that Polynesian culture originates in the Austronesian expansion and that material culture diffused alongside languages and genes (Oppenheimer & Richards 2001: 160). In research papers by Winter et al. (2012) and Clark et al. (2010) there are discussions for a broader Island Southeast Asian origin for material culture of these peoples, which later developed into Lapita culture in the Bismarck archipelago. Oppenheimer & Richards (2001) and Oppenheimer (2004) has also argued against the “Express Train from Taiwan to Polynesia” model.

The Lapita Cultural Complex is, as mentioned, identified by handmade earthenware pottery, crafted without a wheel and tempered with beach or river sand (Kirch 2000: 101-102). The ceramic style of the Lapita started gaining attention in the archaeological record during the 1960s (Kirch and Green 2001: 121) and has since been a key focus in figuring out Polynesian migrations. However, viewing the Lapita expansion as the sole migration phenomenon shaping Polynesians today has been questioned (see Addison and Matisoo-Smith 2010). As Anderson et al. (2012) states it, “[r]ather than thinking of Polynesian origins in Taiwan, it is more realistic to regard them as the result of a conjunction of Asian and Pacific genetic contributions, material culture assemblages, and economic commodities and strategies that

Figure 1 Map of Oceania with points of interest marked.
coalesced in or around the Bismarck Islands about 3,500 years ago” (Anderson et al. 2012: 22).

About 3000 years ago, the Lapita expansion halted its expansion further east as people reached Samoa/Tonga (Clark et al. 2010: 21; Anderson et al. 2012: 24). The southern and eastern parts of Polynesia was not settled until roughly 2000 years later (Kirch 2010: 138). Lapita pottery turned into Polynesian plainware and the Lapita phase is considered ended at 2500 years ago (Anderson et al. 2012: 25).

2.3 The Polynesian triangle and South American connections

Eastern and southern Polynesia was the last part to be settled by humans. An expansion beginning some 1000 years ago, spread humans across these islands with the expansion reaching the most remote islands of Rapa Nui, Hawaii and New Zealand at 600–700 years ago (Figure 3) (Martinsson-Wallin & Crockford 2002; Wilmshurst et al. 2011; Martinsson-Wallin et al. 2013). Exact dates on when people reached these islands have been debated as well as from where. There is also a large difference in climate that needs to be considered from eastern Polynesia to that of southern, where the latter is more temperate than the former (Anderson et al. 2012: 34).

In 1947 Thor Heyerdahl set out to prove sailing from South America to Polynesia was actually possible without any particular navigation skills (Martinsson-Wallin 2014). This left an impact on the pre-history discussions as he showed there was a possibility Polynesia had been settled from the east. This hypothesis has been rather controversial throughout Pacific archaeology (Kirch 2010), however some components show that at least contact between Polynesia and South America has been established. The greatest advocate for this connection is the sweet potato, which is a plant of South American origin, present in Polynesia (see Ballard et al. 2005). Recently, mtDNA has been procured from chicken bones in Chile that also advocate a connection between South America and Polynesia (Storey et al. 2007; 2010).
Part II, outlining theoretical prerequisites

3. Theory of migration

3.1 Who migrates

To understand migration as a phenomenon it is important to begin with the question, who migrates? Who is the individual, group or collective that for some reason decides to relocate and start anew in a different place? Hodder (1992) discuss the reasoning for hunter/gatherer societies in Europe to completely ravish their life style and begin a life as farmers (Hodder 1992: 243). What makes them believe that a sedentary, farming life style is worth changing to? How do they, hunter/gatherers, some 5000 years ago reason to settle down?

This is a similar problem to finding out the reasoning why people in Oceania decided to leave their respective communities and sail out for new islands to settle on (Kirch 2000: 68). By drawing parallels to modern phenomena of migration, past migrations can be theoretically discussed as well. Similar reasons may be the cause of migration like economic gains, how much of an economic gain would be required for someone to migrate? This is highly subjective but could, in a general sense, be calculated through a human capital model as argued by Chiswick (2000: 62). Other economic motivations could also be considered, like supporting a family or a lack of labor / lower wages in the home country. In todays modern society, transnationalism with a freer market and economy makes migration a positive net gain in wealth for the whole world (Chang 2000: 207). Transferred to a Pacific, pre-historical setting, what is to say migration has not been favorable for the entire region, like Pacific trade routes, despite the absence of a modern capitalist system?

Despite all of this, however, it is not everyone who has the opportunity to leave his or her home for someplace new. A financial prerequisite at a convenient time, somewhere to go and a good enough reason to do so is required. If, again, transferred to the Pacific it might not be appropriate for the head of a family to migrate. Hypothetically, the man’s second or third son however may have more reason to do so if the first son would inherit his father’s land and status while younger siblings would stand nothing to gain.

3.2 Building identity in a new social environment

Something happens when people come to a new place. Things are no longer what they once were. The building of new social identities begins. As a migrant to a new country or state with an existing social structure and government, a place must be found and an identity must be made that fits into the existing culture. A new social class that co-exists with society, a class that maintains its original cultural heritage while at the same time takes on and becomes part of new traditions and beliefs. It becomes something new, something more than what it originally was. A hybrid culture of the old and new.

I believe something similar would occur, if part of a social class would migrate and settle on new land and build an entirely new community. It would not become a hybrid as there is no new culture to become part of, but as practice of culture takes place outside of its origin it will begin to change, little by little. Eventually it will evolve into something new, vastly different from what it once was. In the Pacific there have been discussions about “transported landscapes” when Austronesian groups move into islands that has not been colonized before. This means that people structure themselves in the landscape in the same way that they used to in their old setting. For example, they give certain places that appear in a certain way the same names (see Kirch 1984). This can be true to some extent but there is also very much a
difference if you live on a low atoll island or a high volcanic island where there are various resources to be found.

Strictly biological this can also be viewed through genetics as a small founding population, moving away from its source population, takes only a subset of genetic diversity with them. This is called founders effects (Figure 5) in population genetics and is a bottle neck of genetic variation. The subset of genes will mutate and form new variants within the subset population, meanwhile the original population with a larger genetic variation will evolve differently. This is traceable in genetics as the frequency of gene variants in the subset population will be greater than in the original population. However, the gene variants will still be existent but at lower frequency in the original population, suggesting these genes originate in the original population (Beebe & Rowe 2008: 153-154).

It becomes interesting when looking at material culture however, as a similar founder effect could be argued for. The subset population would bring with them cultural mannerisms and ideas reflected in shape and decoration of pots, adzes, houses and rituals etc. (see discussion on memes in chapter 5) in the “transported landscapes”. Over time the subset culture would change in a different way than that of which they originate from, but similarities to the original would still remain, giving a bottle neck effect on material culture.

Here we reach a divide amongst archaeologists, should material culture be used to argue the evolution of ideas and explain the material culture as a biological phenomenon? Or should material culture be viewed as a representative of human agency? These conflicting views on the archaeological record will be discussed further in chapters 4 and 5.

Figure 5 Visual representation of founder effect
3.3 Returning home, wherever that is?

Another aspect of migration is that of back migration. A migrated group established in a foreign land has, as argued earlier, created their own culture influenced by their current surrounding culture but with a basis in their home culture. If this group, or part of this group, would return to their original home, how would they define it? Are they still part of their old home? This might not be an issue until someone returns indefinitely as smaller visits might not be telling of larger cultural changes, but the original home has been kept as an imaginative place, a memory of what was once left behind. When returned to, however this place might have changed and the returnee might feel like an alien belonging somewhere else (Diner 2000: 33). In a way this home has become like a light version of what Pierre Nora (2001) describes as a les lieux de mémoire. A place of memory that is torn between what it once was and a realization that it has changed (Nora 2001: 365). The memory of this home or place could still be used as a tool for immigrants when imaginatively constructing a new home (Brettell 2000: 105) but would ultimately only differentiate the migrant group from the original further.

3.4 Cultural change

This change in culture that exists and happens continuously is a complex phenomenon. Bhabha (2003) describes this phenomenon with the term hybridization. However, hybridization does not result in a hybrid culture. Hybridization is concurrent, abstract and ambivalent, always in change and always present, different for every perspective (see Bhabha 2003).

Applying hybridization to migration provides a new dimension of complexity to what occurs when a group of people is trying to create their own social class in a new culture. Hybridization is the changes happening in the people adapting, the people surrounding the adapted and the entire community where this is taking place. It is important to understand that the view of a new social culture (let’s call this culture A) within an existing social culture (and this culture B) changes from both sides. In the meantime, the new social cultures home culture (this will be C) is changing its view of its migrated people (A). So if a group from A then would move back to C, they would not become C again, they would become AB inside C (Figure 6). This is hybridization in action, everything is in a state of constant change. This constant change can also be considered through agency and structure for migrations. The migrants have power to shape their social, cultural, economic and political contexts while also being shaped by them, (Brettell 2000: 119) making them actors in their own hybridization.

As Bhabha (2003) describes hybridization by example, he uses colonial missionaries in India, where a group of natives have copied the bible for their own use in their own way. Through this they have started questioning how God can send the English missionaries as they eat meat. Which is not pure and correct through their own beliefs (Bhabha 2003:102-104). This is hybridization as the power has shifted from the missionaries with their holy book to the native group through their interpretation of the same holy book. This ‘thing’ that gave missionaries power over the natives is now used to take power away from them.
3.5 Considering time

Another aspect to consider in pre-historic contexts is that of time, or rather the perception of time. For us living in a western society in present day and age, time is constantly measured and used as a form of currency. We spend time as we see fit throughout the day, every day. So if asked to illustrate time, most people would most likely start by drawing a line. Put a start and an end with an arrow depicting in which way time flows. Then, events can be filled in on this time line to show some kind of progression or flow through time in its direction. But how we experience time is highly subjective, it appears progressive to us because it begins with our birth and ends in our death. In between, only the current experience we have is the one that is real (Heidegger 2003: 409). This subjective temporality would mean, as argued by Lucas (2005), that time is not a universal independent thing. Which in turn means that the past is not static, the difference between past and the present is difficult to discern, i.e. the past can not be explained by chronology (Lucas 2005: 36). According to Latour (1993) there is a future and a past, the difference is that the future is in the form of a circle, expanding in every direction while past events are, not static, but revisited, reinterpreted, reshuffled and repeated. Latour further explains that we do not move forward or backwards in time, we merely sort out elements belonging to different times (Latour 1993: 75-76).

The relevancy of this discussion lie in interpreting migration history in the Pacific. As the past is divided into periods defined by cultures and the typologies of objects that associate with these cultures (see Jensen & Karlsson 2000 and Shanks & Tilly 1987; also see Lucas 2005 for discussion on a simplified representation of time in archaeology). What past are we interpreting? We recreate a past from what we know, but how people act and how these people reason for their actions is very much our own imagination of how the past was.

Lucas (2005) suggest that time is multi-layered, time is not a single linear dimension but rather multiple events happening over varying time periods and at different time scales (Lucas 2005: 43). This relate to how we perceive time, our subjective view of time is cultural and contemporary. So how should we define history, what is history? If it is only the current now that is real, and time is temporal and subjective, Heidegger (2013) explains that history is not primarily the past, but what emerges from the past. As a being related to human culture and as something separate from nature itself (Heidegger 2013: 415).

At the same time, if we are to trace change and evolution, a progressive singular time is a necessity. It is simply important to understand that assigning a static condition to historical
events, is a reconstruction from a contemporary temporality. Levi-Strauss (1966) argues that time as a linear function is invented when a writing system is employed. He means that before writing, time is perceived as a cyclical loop. Time changes in seasons and moves in intervals. These are what he calls ‘cold societies’. ‘Hot societies’ on the other hand has invented time as a linear progression and can, thus, record history and previous events (Levi-Strauss 1966: 233-234).

This would mean that time is perceived differently by all and history is created by us, therefore placing an event in a chronology is a created system and no more real than a phenomenological approach to understanding said event. This leaves us with two valid approaches to understanding history. Two approaches that defines the researchers’ views and theoretical background more than the historic event itself. Thus, understanding Pacific migrations through material culture becomes an ontological positioning that can be derived from one’s perception of time. In creating an origin model of Pacific migrations, time would best be considered as a straight line. Investigating the motivations behind migrations in the Pacific on the other hand could utilize time as a phenomenological tool.
4. Agency in archaeology and deconstruction of the text

4.1 A brief history of archaeological theory

What drives the motivation of migration is a complex matter, what is also complex is how we view these motivations. There are different ways to handle these complexities which fundamentals lie in the, somewhat, conflicting ontologies of archaeological theory. Should the motivations and societal structures of humans be considered in propelling the idea of migration or should migration be observed as a biological system? These very different perspectives go back to the dawn of archaeological theory and represent two different ontologies in how archaeology should be approached as a science.

In the 1960s, archaeology shifted to become concerned with anthropological theory and interpreting human behavior in past societies. This was a response to - and a release from - the views in traditional archaeology which was solely concerned with objects and artefacts (Olsen 2001: 38). This ‘New Archaeology’ that sprung from Binford’s article “Archaeology as Anthropology” (1962), argued that anthropological theory was to be the sole theoretical framework for archaeology (Dobres & Robb 2000: 6). The theoretical framework embraced by New Archaeologists was, however, solely the perspective in which human culture was explained as an ecological system and through evolutionary models (Hodder 2012: 2).

In the 1980s the view of archaeology shifted again, this time as a critique of the processual archaeology with its positivist theoretical perspective and empirical methodology (Hodder 1992: 84; Olsen 2001: 50-52). The post-processual archaeology that rose from this critique was hermeneutic in its approach and many archaeologists labelled as ‘post-processualists’ were influenced by Marxism, structuralism, gender research and symbolism (Dobres & Robb 2000: 6). It was among these ‘post-processualists’ that agency manifested in archaeology despite it being a concept in anthropology well before post-processual archaeology (Hodder 2012: 2).

In what theoretical direction archaeology goes from here lie in the discussions highlighted in the introduction to this thesis. Kristiansen (2014) suggest a new paradigm where agency and natural science methodology becomes amalgam and this thesis can be seen as a case study that explores how archaeology should theorize material culture.

4.2 An introduction to agency: agent, practice and structure

Agency is most commonly approached through the writings of Pierre Bourdieu (1977, 1990) and Anthony Giddens (1979; 1984). The theoretical concept of agency is, in social science, a way to explain human action as something more than deterministic, reactive behavior due to changing circumstances around them. It explains human action as affecting the world around the actor by purpose or choice and thus, the actor shapes the world around them that, in turn, shapes them (Dornan 2002: 304).

Bourdieu (1977) explains the symbiotic relationship of practitioner and practice through habitus, where an agent is influenced by a previous state of oneself. The previous state of the agent is influenced by the societal structures and experiences within it (Bourdieu 1977: 78-79). In this way, habitus is unconscious or forgotten history that structures the actions of the agent, simultaneously the agent is structuring the system by acting within it. This makes the agent a force that intentionally affect social structures around them as the agent is influenced by the very same social structures (Dornan 2002: 305). However, Bourdieu’s (1977) habitus
is determined by the agent’s social class, making it deterministic. What is learnt at home during a young age determines what is learnt at school which determines what is learnt later in life (Bourdieu 1977: 87). The habitus also determines how a person may act in a given situation as a result of the accumulated experiences. Because each person’s experiences through life is unique, and each experience affect future experience, each person’s agency is unique in their circumstances as a result of habitus. This makes actions unconscious and a result of achievable experiences within the actor’s social class (Dornan 2002: 306).

In Giddens (1979) theory of structuration there is a greater emphasis on the individual’s potential to act. The greatest difference from Bourdieu being that humans are conscious in their practice and choices and that an emphasis is placed on time and spatiality as structuring of the social systems (Giddens 1979: 54-55). Giddens expands on Bourdieu’s ‘practice theory’ by giving more control to the actors within the systems. He moves the role of the unconscious to being motives for action instead of directly orchestrating actions. Motives are not exactly unconscious though as it is the agent’s inability to articulate them that makes them different from reasons and intentions (Giddens 1979: 56-57). Actions directly influenced by an agent’s motivation is commonly only applicable under unusual circumstance as day-to-day routines are indirectly motivated (Giddens 1984: 6). The day-to-day routines are considered routine behavior as they are acted on such a regular basis that they become automated by the agent. They become tacit knowledge which can be reflected upon but are not actively thought on as they are carried out (Dornan 2002: 307). This is what Giddens refers to as reflexive monitoring of an agent’s own conduct (Giddens 1984: 6).

The structures in Giddens theory can thus be under conscious consideration by agents acting within them. As the actions shaping the structures are reproductive, everyday conduct or day-to-day routine. The intention of this conduct can, however, be different from its consequences as Giddens (1984) puts it, “[a]gency refers not to the intentions people have in doing things but to their capability of doing those things in the first place…” (Giddens 1984: 9).

However, there is a lack of irrational behavior accounted for in Giddens theory as all agents appear to possess both skill and knowledge in acting within their social class (Dornan 2002: 308). Structuration theory emphasizes that acting within a system from a set of rules created by it, shapes the system back which will create new social rules for acting within the system (Giddens 1979; 1981; 1984).

### 4.3 Archaeology and agency, critiques and definitions

Applying agency theory to archaeology is not all that simple as there are many nuances and different approaches to agency (Dobres & Robb 2000; Dornan 2002). There is also the dilemma of moving agency from its arena in which it was created into the unknown realm of pre-history. This raises questions of applicability, can agency help explain agents in context only viewable through archaeological inquiry and if it can, how (Dobres & Robb 2000: 12)?

There are more issues with agency, the most fundamental one lie in its definition. Dobres & Robb (2000) reduces understanding what agency is to two basic approaches. A wide definition in which agency operates in multiple instances all at once and which focuses on the ambiguity and contradictions of these instances. The second approach is a narrower, clearer definition of agency where restricting the scale to be relevant for the point in question. There are flaws with both of these, for the latter there is issues in selecting and defining the restrictions as reducing the concept of agency to a select few qualities might make it lose what makes agency interesting and relevant. The former is subject over-generalizing the very concept of agency making it mean everything and nothing at the same time (Dobres & Robb 8-10).

Problematicizing agency in archaeology further, there is definitely an issue in the political concept of agency. Understanding action and intention in individuals of past societies become
a projection of people from our own society acting in these situations (Dobres & Robb 2000: 13). This is not only problematic for archaeologists working with questions of political competition but for all archaeology concerned with identifying agency in past societies (Brumfiel 2000: 253-254). This does not mean agency has no value in archaeological studies, it is simply important to thoroughly discuss and motivate the agency approach selected.

One strength of agency in archaeology comes from examining humans as cultural beings rather than just reproducers of biological life. This also means that material culture is expressing agents purpose and intention rather than just being inanimate objects to trace where humans have been. However, culture should not be considered entirely dualistic of nature, Barrett (2012) means that there is a symbiotic relationship in play. He suggests that “[t]he world is, instead, meaningful by the simple virtue of being able to sustain life: it is meaningful because it makes sense through use. And in making sense by living in the world, this agency comes to recognize others as itself.” (Barrett 2012: 162).

I believe that the point of incorporating agency into archaeological discourse is not to measure what humans do, but to promote a discussion of why humans act. Without it, there would be nothing human about archaeology.

4.4 Deconstruction and reconstruction

In the introduction I set forward my intention to deconstruct an article on human genetic research in the analysis section of this thesis. The reason for deconstructing is to examine the perspective of the author and to reconstruct the written with inserted ‘new’ ideas from my perspective. It would be simple to be satisfied with this explanation and only pick out what I find interesting and say “here’s what the author didn’t think of”. But there is a reason as to why deconstruction has a meaning and why deconstructing a text is valuable. First I will attempt to outline an understanding of deconstruction.

According to Derrida, the deconstruction of the text is closely related to the logic of language, writing and speech, the signifier and signified (as in Saussure 1986) as well as the undecided in binary oppositions. There is also the de-centering of the subject (see Giddens 1979). Derrida states that “the center is not the center” (Derrida 2001: 352) as in, what a system is based upon need not be part of the system. Take the Christian God as an example, God created the world but God is not part of the world, he is outside the world thus, the center can be outside of the system as an observer or signifier.

By a hardly perceptible necessity, it seems as though the concept of writing […] is beginning to go beyond the extension of language. In all sense of the word, writing thus comprehends language. Not that the word “writing” has ceased to designate the signifier of the signifier, but it appears, strange as it may seem, that “signifier of the signifier” no longer defines accidental doubling and fallen secondarity. “Signifier of the signifier” describes on the contrary the movement of language: in its origin, to be sure, but one can already suspect that an origin whose structure can be expressed as “signifier of the signifier” conceals and erases itself in its own production. There the signified always already functions as a signifier. The secondarity that it seemed possible to ascribe to writing alone affects all signifieds in general, affects them always already, the moment they enter the game. (Derrida 1995: 6-7)

It can be interpreted then, that a text is a signifier of itself and has meaning in its own context. Deconstruction is not understanding this meaning from one’s own perspective and reading, but as a text is written, it leaves the author’s thought and deconstructs itself within the structure in which it was conceived, this process is always ongoing, forever changing. When another person reads this text, it has been deconstructed and the reader places it in a new context.
It would seem to me then, that one does not “deconstruct”, one only partakes in the deconstruction process. Deconstructing would then mean to present one’s perspective from taking part in the deconstruction. This means that deconstruction is not a destructive process, a different understanding emerges from the deconstruction. For producing something new from the same ideas and framework of what one has gained from taking part in the deconstruction of a text I would suggest using the term reconstruction. As this new text, becomes an entity by inserting new ideas or perspectives it will begin its own deconstruction.

The text in itself and the importance of deconstruction exists in the written, as the writer uses a language to write, through this language exists logic, laws and systems that dictate what the writer can write. This also means that the text itself is not a representative of anything other than itself. The written may reference “real” events but they are only attainable through the logic of the language in its form as it was written (Derrida 1995: 157-164).
5. Evolutionary archaeology, neo-Darwinism and cultural memes

5.1 Archaeology as a natural science
The theoretical views in processual archaeology have grown into what today is evolutionary archaeology and behavioral archaeology. These archaeological perspectives are something that has to be brought up as a counterpoint, both as a strict counterpoint to agency-based archaeology and as acknowledgement of its presence in South Pacific archaeology (e.g. Cochrane et al. 2013). The argument behind an evolutionary approach to archaeology begins in defining the appropriate ontology for archaeology. As O’Brien and Lyman (2000) explains, essentialism is based on discoverable units or types while materialism is based on creating artificial units or types to explain variation (O’Brien and Lyman 2000: 34-36). Further explained, this means that essentialist ontology is concerned with identifying the various “real” traits. The traits being “real” means that once discovered they are unchangeable. In contrast the units artificially created in a materialist ontology is defined to specific cases and used to explain the problem at hand, like change or frequency. This, in turn, means that tracking evolution would optimally operate under materialist ontology as it, in contrast to essentialist ontology, tracks change over time, just like evolution (O’Brien and Lyman 2000).

So if the basis for evolutionary archaeology falls within a materialist ontology, an argument for the evolutionary approach in archaeology is to create a common ground for archaeology and biology in operating on a macro scale framework (Mesoudi and O’Brien 2009). Seeing if both sciences operate under similar manners this would facilitate discussion between the fields to a greater extent. This means classifying archaeology as natural science rather than humanities subject. The implications of placing archaeology in a natural scientific ontology is that human behavior is explained in a similar matter to all other living things, by the same principals. As Darwinian evolutionary theory has been established in biology over the past 150 years or so, these principles are considered a sound framework for archaeology as well. Thus promoting an empirical based result oriented science (Shennan 2012: 15). Humans, under these principals, are part of a biological system that strives for stability governed by general behavioral laws where survival of the fittest applies as well. In contrast to agency where human actions are conscious and choices can be predicted through constructed scenarios.

5.2 Cultural inheritance
As part of an evolutionary approach to archaeology, human culture or ideas can be seen as “memes”. Memes are a type of replicators just like genes. Unlike genes however, they are not identifiable outside of themselves. Dawkins presented the idea of memes as replicators in ‘the selfish gene’ (1979). By explaining how genes “program” every living organism to act in a certain way in order to ensure the survival of the genes through the organisms offspring, Dawkins placed behavior in the hands of genes. It can be thought of as a computer, a set of parameters or algorithms are set for a computer program to tackle every thinkable scenario or task. When the program is running it is utilizing these algorithms to act in the best possible option, the programmer is no longer part of what the program does. Dawkins suggest that
genes work in a similar manner where each gene “program” the organism it is part of for successfully acting within the world it exists (Dawkins 1979: 51-53). Basically this leads to a deterministic argument of biological life being “survival machines” for genes and that these “survival machines” behavior is reflected in the ultimate goal of furthering the genes that “programmed” them, making them successful.

The idea Dawkins continued from with this was that a new form of replicator had emerged, using human culture as “survival machines”. This type of replicator was ideas or cultural actions which Dawkins referred to as “memes”. He meant that memes replicated in the same selfish manner as genes but at a much higher mutation rate. These memes are also under the same selection pressures as genes and successful memes can spread and manifest as human culture. What happens to culture in this sense is that it evolves in a similar manner to biological life and that certain ideas or traces in material culture can be seen as snapshots in human cultural evolution (Dawkins 1979: 189-201).

Cultural inheritance in this manner can be explained by adopting a better idea one has seen in action. Adopting this better idea makes it manifest in the cultural population and can so be explained by “natural selection”. In the archaeological record natural selection on memes are what makes certain types of, for example, pottery, adzes or canoes successfully persistent. This is the “memes perspective” as suggested by Shennan (2012: 22) and means that every choice is affected by natural selection rather than human agency.

5.3 Dual inheritance theory and human behavioral ecology
Dual inheritance refers to a system of evolution by descent for both genes and memes. For genes this system of inheritance stems from Darwin’s theory of evolution where phenotypic variation exists in a population, this variation is selected upon and as environments change, so does selective pressures which may subsequently lead to another variant becoming dominant. As selective pressures on a new phenotypic variant increase, the fitness of that individual increase. Increased fitness means higher reproduction rate that mean higher frequency of the phenotypic variation expressed in offspring.

This system is then directly applied to human culture where ideas are thought of to manifest and survive in a similar manner. The main differences are that (1) as biological evolution reproduce, cultural evolution replicates. Reproduction is physical, resulting in offspring with phenotypic variation and recombined genotypic variation from both parents (O’Brien & Holland 1990: 41). Cultural replication, on the other hand, is copied from the source. Variation and mutation is created through copying errors rather than recombination and genetic mutations. This also means that (2) cultural replication is much faster as the ideas copied does not require any physical interaction, as the famous saying goes, “monkey see, monkey do”. Of course some skills need to be actively taught in order to replicate but seeing a more successful approach to a problem can be copied almost instantaneously.

The DIT model is contrasted by human behavioral ecology where the variability in the archaeological record is accounted for by human behavior. It differs in the concept of cultural evolution in that HBE considers human behavior through complex strategies with human as the center but relying more on modeling these strategies than agency-based approaches (Bird & O’Connell 2012; LaMotta 2012).

5.4 The evolutionary approach to archaeology, critiques and definitions
Part of the evolutionary approach is that human desires and intentionality is the driving factor in generating idea variation. Human agency is discarded as it can not be empirically measured. This means contemplating individualistic intentionality can never be understood from this perspective and thus, studying the archaeological record should be objective and
generalizing. As Shennan (2012: 20) puts it, “[h]owever, even if cultural attributes are neutral and change simply as a result of drift, effectively random variation is what is copied, the fact that innovation and drift are dependent of the size of populations and the extent of their interaction means that demographic history remains central to any evolutionary perspective” (Shennan 2012: 20).
Part III, Analysis, the three cases: domestic animals, sweet potato and humans in the South Pacific

Figure 7 Thévet, A., (1557) Ipomoea batatas [drawing], accessed 2016-06-01 from https://commons.wikimedia.org/wiki/File:Hetich_Thévet_1557_53r.png
6. Domestic animals in the South Pacific

6.1 A history of domestic animals in the Pacific
As humans colonized the many islands of the South Pacific, they have brought animals with them to be able to sustain a living in new environments. Terraforming a new island into becoming habitable requires an array of domestic plants and animals. As recorded by the presence of animal bones at various Lapita sites, mainly there have been four species of animals to accompany humans, pigs, dogs, chickens and rats (Kirch and Green 2001: 129; Kirch 2000: 111; Matisoo-Smith 1994). This means investigating animals in the South Pacific is highly viable as a proxy for investigating human migrations, where humans go, some animals go. This is reflected in genetic research as tracing animal origins could also imply an origin for humans. In genetic variation, domestication events are apparent as they are bottlenecks similar to founder effects. A subset of a population is used to breed a new, domesticated population. There is also a question of agency involved as humans have actively brought these animals with them as many of them do not self disperse (Matisoo-Smith & Robins 2004: 9168; Storey et al. 2010: 2460).

Because of this traceability, and ethical issues with human DNA sampling in Pacific contexts (Matisoo-Smith 2015: 5), the presence of animals has been target for extensive genetic analysis over the past decades. Genetic studies of pig mtDNA has shown only one mtDNA lineage represented in Oceania, with origin in Vietnam (Larson et al. 2007). While the dog is one of the first animals with signs of domestication dating back to roughly 15 000 years ago and being spread out across multiple continents (Larson et al. 2012: 8882). In Pacific contexts, the oldest evidence of dogs is from the Australian dingo (Greig et al. 2015: 2; Oskarsson et al. 2012), originating from southern China and being brought as part of the Austronesian expansion around 6000 years ago (Savolainen et al. 2004: 12390). In New Zealand, only the dog was introduced from Polynesian domestic animals (Kirch 2000: 276). Dogs are, however, not as commonly represented in archaeological records as the other animals (Kirch & Green 2001: 129).

The Pacific rat has been investigated as a proxy for human migrations in the Pacific quite extensively compared to other animals (Matisoo-Smith 1994; 2002; Matisoo_Smith et al. 1998; Barnes et al. 2006; Thomson et al. 2014). The Pacific rat was likely introduced as a means of food and it is present where ever humans are (Matisoo-Smith & Robins 2004: 9168). Wilmshurst et al. (2008) set out to re-date bones from pacific rats (Rattus Exelans) on New Zealand that previously have led to discrepancies in the interpretations of when New Zealand was initially colonized (Wilmshurst et al. 2008). Based on archaeological records and recently carried out dating programs of rat bones, a later initial settlement at 1200 AD was suggested while datings carried out on earlier rat bones suggests an initial settlement at 500 AD (Kirch 2000: 277, 349; Wilmshurst et al. 2008: 7676). In light of this divide Wilmshurst et al. (2008) set out to re-date bones from the same sites that had yielded the earlier dates. 17 newly excavated bones from Rattus Exulans alongside 13 samples from the collection of previously dated bones was re-dated (Wilmshurst et al. 2008: 7677).

The results showed that the earlier dates are probably at the wrong. Most likely caused by laboratory methods at the time failing to remove old carbon from the samples. To complement this, they also dated 51 additional seeds gnawed by rats, since seeds are less complex in pretreatment methodology than bones (Wilmshurst et al. 2008: 7678). The conclusion of this study is convincing in that Rattus Exulans, which has been brought by
humans, have not been present on New Zealand before 1200 AD (Wilmshurst et al. 2008: 7679).

The last of the four animals is the chicken which introduction is a controversial issue in South Pacific research. Storey et al. (2007) provides data for the discussion on when, and from where, the chicken was introduced to the Americas (Storey et al. 2007) as well as on how it was dispersed during prehistory in the Pacific (Storey et al. 2010). The issue that acts as base for their study is two-fold: did chickens arrive in the Americas before the arrival of Europeans and is there any archaeological evidence of contact between South America and Polynesia? In Polynesian archaeological records the chicken is well represented (Kirch 2000: 216). The discussions on chicken origins in the Americas have seen three major arguments, the chicken is native to South America, Europeans introduced the chicken with their arrival in 1500 AD and that the chickens were introduced through Polynesian contacts (Storey et al. 2007: 10335). According to Storey et al. (2007) no evidence through archaeological or paleontological contexts has been reported for the chickens being native to South America. There is also contradictory evidence on a European introduction of the chicken as Francisco Pizarro discovered chicken was already well established in Incan economy when he arrived in Peru by 1532 AD. This indicates the chicken had already been existent in Incan culture for some time (Storey et al. 2007: 10335).

In order to examine the genetic–archaeological discourse on domestic animals in Pacific contexts, this chapter aims to review and summarize the discussions on a South American–Polynesian prehistoric connection based on the genetic research by Storey et al. (2007). This discussion serves as a case study for genetic and archaeological research on animals as a proxy for human migrations in the Pacific. This case has been selected as an example of genetics providing an alternative perspective while being a controversial issue in Pacific human migration hypotheses.

6.2 Chicken genetics

Through their study Storey et al. (2007) supports the argument of a chicken introduction to the Americas from Polynesia, before the Europeans reached South America. They support this with the first ancient DNA sequences for chickens in South America (Storey et al. 2007: 10335).

The earliest recovery of chicken remains in Polynesia coincide with Lapita sites on Vanuatu and Tonga that are 3000-2800 years old (Storey et al. 2007: 10335). Whether contact between South America and Polynesia has occurred in prehistoric times is debated through the presence of sweet potato, that is a South American plant, in Polynesia. Also there are suggestions of Polynesian linguistic and material influences in the south central part of Chile (Storey et al. 2007: 10335). This part of Chile is also the region where Storey et al. (2007) has recovered the chicken bone for their study, in the archaeological site of El Arsenal-1 (Storey et al. 2007:10335). The site is dated based on pottery and artifact analysis to 1000 – 1500 AD and belongs to the horticulturalist community complex of El Vergel, this makes the chicken bones from this site the earliest evidence of chicken in South America (Storey et al. 2007: 10335-10336).

The chicken bone from El Arsenal-1 yielded radiocarbon dates that fall within the appropriate time frame for the colonization of the more easterly-located islands in Polynesia at 1200 – 1400 AD (Storey et al. 2007: 10336). Even though this date was criticized by Gongora et al. (2008) for not taking into consideration the impact of marine carbon contribution on the sample (Gongora et al. 2008: 10309, 10311). Storey et al. (2007) investigated the origins of the El Arsenal-1 chicken bone through ancient DNA analysis of Polynesian chicken populations. To do this, a collection of 37 chicken bones was used from five different archaeological Polynesian sites within a time range of 2900 years ago to 500 years ago (Storey et al. 2007: 10336). Out of 37 samples, 12 yielded positive results from
PCR amplification, along with reference sequences from modern chicken populations and modern Araucana chicken feathers, a type of chicken with no tail that lays blue eggs and is suggested to be a pre-European breed from Chile (Figure 4) (Storey et al. 2007: 10339), Storey et al. (2007) was able to observe common SNPs in the most variable area of the D-loop of the mitochondrial DNA with the most common SNPs in the span of less than 150 base pairs (Storey et al. 2007: 10336). But this study was criticized by Gongora et al. (2008) for using a limited sample size saying that there is no genetic support for an introduction of European/Chinese chickens via Polynesia into Chile (Gongora et al. 2008: 10309).

The bone from El Arsenal-1 had an identical target DNA sequence as two prehistoric samples from archaeological sites in Tonga and American Samoa. The former dated 2000 – 1550 years old from upper plainware layers and the latter dated roughly contemporary with El Arsenal-1 at around 600 years old (Storey et al. 2007: 10336-10337). The El Arsenal-1 sequence shares a SNP mutation with all the ancient samples from West Polynesia as well as early Easter Island sample, Hawaiian sample and one of the modern Aracuana feather samples (Storey et al. 2007: 10337). The ancient West Polynesian samples, early Easter Island sample, Hawaiian and El Arsenal-1 samples also share three SNP mutations with modern chickens from China and Vietnam. However, later samples from Easter Island and Hawaii do not share this mutation but rather have more in common with modern samples from Lombok, Philippines and Thailand, which indicates two different lineages for chickens. However, Gongora et al. (2008) suggests that it is much more likely that modern chicken genetic diversity in the South America is derived from modern introgression of mtDNA genes from Asia. Further, they suggest, based on haplogroup affinity, that there is no support for South American and Polynesian contact since the ancient samples fall within the European/Indian subcontinentaal/Chinese haplogroup that is widespread (Gongora et al. 2008: 10311). This in turn was criticized by Storey et al. (2008) for being a hypothesis completely based on modern populations of chickens, thus missing the fact that both European and Pacific pre-historic chickens are from Asian decent (Storey et al. 2008: 1).

In a complement and response to Gongora et al. (2008), Storey et al. (2008) also sampled and dated an additional two chicken bones, both falling within the same date range and supporting a pre-Columbian introduction of chickens to Chile (Storey et al. 2008: 1). A later study from Storey et al. (2010) also showed results in support of their original claims. By sampling chicken mtDNA from the archaeological site Teouma on Vanuatu, they were able to identify haplogroup E in two successful samples which was also present in the El Arsenal-1 chicken. Suggesting a Lapita introduction for these chickens (Storey et al. 2010: 2465).

Interpreting the results Storey et al. (2007) draws support from earlier theories on Polynesian and South American contact, Thor Heyerdahl’s theories as well as the presence of the sweet potato in Polynesia in contrast to the genetic and linguistic evidence of Polynesian people originating from Southeast Asia (Storey et al. 2007: 10337). They bring up two hypotheses in South American chickens originating from the west, a hyperdiffusionist theory that suggests chickens were brought directly from the mainland of Southeast Asia to South America and the theory that seems most likely based on their own results of some chicken lineages originating from Polynesia (Storey et al. 2007: 10337-10338). The chicken dispersal to South America before any European contact has been challenged by Thomson et al. (2014), where they suggest modern DNA contamination was likely the source for these results (Thomson et al. 2014: 4830). This critique was rejected by Storey & Matisoo-Smith (2014) and Beavan (2014) by pointing out inconsistencies and flaws in Thomson et al.’s (2014) study as well as factual errors in their discussion.

The presence of an ancient haplotype in modern chickens mtDNA even after an introduction of European chickens may be an indication on selective breeding on special traits, no tail and blue eggs, in the Araucana chicken as well as it is an indication of overall low variability in chicken mtDNA that could mean problems conserving genetic diversity (Storey et al. 2007: 10338).
6.3 Concluding remarks

The discussion of authenticity of Storey et al.’s (2007; 2010) studies have been a very controversial subject. Perhaps more so than the South American – Polynesian prehistoric connection it promotes. Commensal animal DNA is however, a very strong option in studying human migrations. Using animal DNA from archaeological sites leans heavily on the sites integrity and contextual interpretation. Throughout the discussions, the questions of why the chicken is present is not explored in any depth. But as of now, the consensus seems to lean toward a West – East dispersal of chickens before Europeans arrived in South America suggesting Polynesian – South American contact. To what degree though stands to be explored further.
7. Sweet potato origins, dispersals and cultural impact in the South Pacific

7.1 The history of sweet potato in the Pacific

The sweet potato (Figure 7) is an important component when discussing human settlement in the South Pacific. Not only as a proxy for human migrations (Clarke 2009) but also as a cultural phenomenon that has influenced Oceanic peoples culture and economies since its introduction (e.g. Bayliss-Smith et al. 2005; Kirch 2010; Wallin et al. 2005). The sweet potato is often discussed alongside the Bottle Gourd (Clarke et al. 2006; Clarke 2009), taro and yams. The introduction of the sweet potato is, however, a debated topic (Ballard 2005; Wallin 2014). Since Thor Heyerdahl proved in 1947 through the Kon Tiki Expedition, sailing from America to Polynesia was fully possible, there has been little doubt that the sweet potato is of American origin based on biological data and later on genetic data (Yen 1974: 1, 245-246; Roullier et al. 2013a: 603). From there the discussions have mainly been concerning just how the sweet potato has reached the South Pacific islands, with a few exceptions of arguing on different origins (Ballard 2005: 3). Douglas Yen (1974) proposed a three-way introduction of sweet potatoes into Oceania, based on negative data from expected variation in plants had the sweet potato been introduced through a single line (Yen 1974: 251-252). The tripartide hypothesis proposed by Yen has become a well established hypothesis for how the sweet potato was introduced, even if Yen was not the first to propose such a hypothesis he molded the hypothesis into what is the commonly referred formulation of it today (Ballard 2005: 3), later it was further revised by Green (Green 2005).

With the three lineages of sweet potato, Kumara, Camote and Batatas, as the accepted hypothesis for sweet potato introduction, along with the wide acceptance that introduction occurred as a result of human agency rather than carried by birds or by free floating rafts (Green 2005: 2; Wallin 2014: 95-96). The discussion shifted to concern who, when and from where the sweet potato was introduced into Oceania (Ballard 2005: 3).

This chapter aims to understand the overlying theoretical approaches of the current discussions on sweet potato origins, dispersals and cultural impacts in the South Pacific. This while reviewing the history of research on the topic as well as more recent additions of research through DNA and genetics. Here, as a focus point emphasized in Oceania, New Guinea will play a role in the analysis of current debates for its role as a secondary centre of diversity for sweet potato genetic variety (Roullier et al. 2013b).

The purpose of this chapter is also to review the current debates on sweet potato dispersals as a proxy for human migration in the South Pacific. This while emphasizing the strengths and weaknesses of the research fields in relation to each other to complement the main thesis agenda of understanding how the current research on material culture and genetics is being discussed in regards of the South Pacific.

7.2 Background and analysis

7.2.1 Kumara and the pre-historic perspective

The lineages have different origins and were introduced at different sites in Oceania as well as during different time spans. The Kumara line originates in northern South America,
Peru/Ecuador, and was originally believed to have been introduced into East Polynesia somewhere between 1000-1100 AD (Ballard 2005: 6; Clarke 2009: 211-212; Kirch 2000: 125-126). This date has been moved up to a later time frame in more recent research 1200-1300 AD (Hunt and Lipo 2006: 1605; Ladefoged and Graves 2008: 784; Wallin 2014: 102-103; Willmshurst et al. 2011: 1818). This means that the Kumara line is the sweet potato variant introduced in pre-historic times and most likely the first introduction of sweet potato into Polynesia at all (Ballard 2005: 6). That it was introduced by humans is supported by the word Kumara being used both throughout different islands in Polynesia and in South America with varieties of the word in different dialects across South America (Green 2005: 61). But whether it was South American Indians sailing to Polynesia with the plant or Polynesian voyagers sailing to South America and bringing the plant back from their voyages is still not really solved (Wallin 2014: 96).

The sweet potatoes diffusion throughout eastern Polynesia in pre-historic times is a bit more complex however. According to Green (2005), in his revision of the tripartite hypothesis, the sweet potato was first introduced to the Marquesan Islands, the Society Islands and Mangaia (Green 2005: 60-61). Even though Mangaia might seem somewhat sub-optimal as a dispersal center for sweet potato due to a low sweet potato cultivation focus (Wallin 2014: 98). From these islands, what Yen (1974) referred to as the central ellipse (Yen 1974), the sweet potato has been dispersed to other islands in eastern Polynesia, eventually reaching Hawaii, Rapa Nui and New Zealand which in one way or another marks these islands as important sweet potato locations (Wallin et al. 2005; Ladefoged 2005).

7.2.2 Camote and Batatas, sweet potato introductions in historical times
The two other lineages of sweet potato represent introductions during historic times and the sweet potatoes presence in western and northern parts of Oceania (Yen 2005: 182). The Camote lineage is believed to have been brought by Spanish sailors travelling from Mexico to the Philippines in early 16th century and then diffused throughout Oceania from the west.

Finally, European traders introduced the Batatas lineage from the Caribbean in 1492 AD and brought sweet potatoes through Europe, Africa and India to finally arrive in western Oceania in late 15th – early 16th century, which also marks a westward diffusion into Oceania (Ballard 2005: 3; Roullier et al. 2013b: 594-595; Yen 1974: 259). After these primary introductions an array of secondary dispersal events distributed these sweet potato lines further into Oceania (Roullier et al. 2013a: 2205-2206).

7.2.3 The enigmatic New Guinea
In modern times, discerning sweet potato origins is quite complicated. New Guinea is a point at which the three sweet potato lines seem to converge (Ballard 2005: 3). Sweet potato in Papua New Guinea is an important part of sustenance, accounting for roughly 60% of total crop distribution (Bourke 2005) and feeding approximately 80% of the islands inhabitants (Bourke & Harwood 2009). This means that sweet potato is wide spread across New Guinea which, in turn, means New Guinea is an important part in modern sweet potato genetic diversity in the South Pacific (Roullier et al. 2013b). The date of each lines introduction is debated, however, pollen records suggest an earlier introduction date, before any European contact, to New Guinea via the Kumara line (Haberle and Atkin 2005: 33).
7.3 The genetic approach

7.3.1 Origins

With the tripartite hypothesis mainly being based on archaeology, linguistics and history, phylogeographic studies have not really been sufficient in confirming it. By not utilizing extensive samples, most genetic studies have failed to trace the origins of South Pacific sweet potato conclusively (Roullier et al. 2013a: 2205-2206). However, by using a combination of Nuclear DNA data and chloroplast DNA data from both modern samples as well as ancient samples from herbariums, Roullier et al. (2013a) has found two separate gene pools present in the Americas, a northern group and a southern group which correlates to samples that represent phylogeographic structures in Oceania. Even though this haplogroup affinity is somewhat convoluted and plagued by admixture events between northern and southern groups in the Americas (Roullier et al. 2013a: 2207-2208).

In historic times multiple introductions has disrupted the genetic background by recombination between ancient variant of sweet potato and newly introduced ones. Meaning, what is found today is combinations of genetic backgrounds probably caused by local cultivation and admixture (Roullier et al. 2013a: 2209). There are however some patterns in modern genetic backgrounds that shows distinction between eastern Polynesia and western Pacific, as well as distinctions between Hawaii, New Zealand and eastern Polynesia (Roullier et al. 2013a: 2209).

7.3.2 A pre-historic perspective, Kumara and eastern Polynesia

Confirming the Kumara line as South American in origin would require clear affinity to the southern gene pool as defined by Roullier et al. (2013a).

Tracing chloroplast lineages and micro satellite clustering for nuclear DNA in eastern Polynesia from modern samples shows a higher affinity to the southern gene pool, but not exclusively as representations from the northern gene pool is also present. This would mean admixture and that modern samples consists of a combination of genetic origins with the exception for New Zealand and Hawaii where the lineages correlated with the southern gene pool are quite dominant (Roullier et al. 2013a: 2208).

In herbarium samples that represent early 20th century and 17th century almost all samples showed affinity to the southern gene pool through nuclear DNA clustering and chloroplast haplotype lineages. This is indicative of pre-historic sweet potato in Polynesia was indeed introduced from South America, Peru/Equador. But discerning if this is the result of one introduction or multiple is not possible from herbarium samples (Roullier et al. 2013a: 2208).

7.3.3 Historic introductions, Camote and Batatas and genetic diversity in New Guinea

For investigating sweet potato diversity on Papua New Guinea, Roullier et al. (2013b) used 369 sweet potato accessions from the National Agricultural Research Institute of Papua New Guinea, covering highland and lowland regions as well as an additional 48 accessions from the National Institute for Agrobiological Sciences in Japan whereas 30 originated from Papua New Guinea and 18 from West New Guinea, both highland and lowland regions. DNA was extracted from these accessions and then analyzed. These were then compared with another data set composed of 130 nuclear sets and 329 chloroplast sets from tropical America (Roullier et al. 2013b: 595-596).

There are different opinions on when and where the sweet potato was introduced to New Guinea, as a possible convergent point for the three lines, Kumara, Batata and Camote (Ballard 2005: 3), it is debated how much it has contributed to the sweet potato genetic
diversity of the South Pacific (Roullier et al. 2013b: 600). According to Roullier et al. (2013) the nuclear markers are not as different from Northern Americas as they are from Southern Americas. This would mean that New Guinean sweet potatoes originate from Central America and the Caribbean, via the Batata and Camote lines. But chloroplast markers show affiliation to both northern and southern groups, making it not so certain (Roullier et al. 2013b: 600-601). The presence of chloroplast haplotypes from both groups can be explained in two ways. They could have been existent in the northern genepool when they were introduced already. The most common haplotype in the southern genepool is also present in the northern genepool (Roullier et al. 2013: 601). The other explanation is an introduction directly from South America or from other parts of Oceania that would have gotten sweet potato directly from South America earlier. This is amplified by three rare chloroplast haplotypes from the southern genepool present in New Guinea that would indicate an early introduction via the Kumara line (Roullier et al. 2013b: 601). This is also supported from linguistics and paleoecological pollendata, but is in conflict with the nuclear results. The chloroplast markers do not represent the main background for genetic diversity in New Guinean sweet potato. Instead it could be argued that later introductions occurred (Roullier et al. 2013b: 601).

Earlier genetic marker studies on Oceanic crop origins have investigated sweet potato from New Guinea but only with smaller samples. These studies have shown Oceanic sweet potato to have a closer affinity with Central American sweet potato than with South American (Roullier et al. 2013b: 595). However, the sweet potato genetic diversity may be influenced from many different sources of variation, in clonally propagated crops, such as sweet potato (Yen 1974: 223), somatic mutation greatly affects phenotypic variation. Epigenetic inheritance and sexual reproduction also contributes in creating genetic diversity in South Pacific crops (Roullier et al. 2013b: 595).

The chloroplast markers and the nuclear data in sweet potato on New Guinea show reduced diversity compared to the Americas, with some exceptions for rare alleles, which is indicative of an introduction bottleneck (Roullier et al. 2013b: 601). However, before the introduction in New Guinea there was sweet potato admixture in the Americas according to data, meaning, as suggested by Roullier et al. (2013b), geneflow between northern and southern chloroplast accessions in the Americans might have led to a subset of the total genetic diversity. Leading to estimation that, an introduction of 63 clones from the northern genepool into New Guinea could explain the genetic diversity in New Guinean sweet potato (Roullier et al. 2013b: 601). However, selection, cultivation and breeding of sweet potato by farmers in New Guinea from different ecological and cultural conditions may also be a factor in creating sweet potato diversity in New Guinea (Roullier et al. 2013b: 595). Roullier et al. (2013b) data also show that most genotypes in New Guinean sweet potato are from local admixture between different introduction variants, this could be an explanation for observing a difference in chloroplast and nuclear origin signals (Roullier et al. 2013b: 601-602).

Overall, New Guinea seem to have little genetic differentiation as there is weak correlation between genetic diversity and geographic structure, no region acts outlier in genetic diversity. This could be explained by a recent introduction of sweet potato and a high rate of moving variants back and forth across the island and thus maintaining a high rate of admixture (Roullier et al. 2013b: 602).

In conclusion Roullier et al. (2013b) have through both chloroplast and nuclear genetic data showed that sweet potato on New Guinea most likely originate from Central America and the Caribbean, with some South American variant probably introduced during the 20th century by missionaries or whalers rather than by Polynesians at an earlier time (Roullier et al. 2013b: 603).
7.4 Analytic discussion

7.4.1 Finding a scale
Different disciplines approach different aspects of the sweet potato dilemma on different levels. On macro levels there is the introductions, origins and dispersals through time. In what order the sweet potato reached each island in the South Pacific and from where. The genetic studies support the Tripartite hypothesis in that the Kumara line represents a westward dispersal of sweet potato from South America before any European contacts (Roullier et al. 2013a: 2209). The traces of this introduction has been shuffled by later introductions but it still seems clear that eastern Polynesia with Hawaii, New Zealand and Rapa Nui has sweet potato derived from a South American variant. This means that macro level pre-historic distribution of sweet potato is basically solved as there is differences in genetic affinity between Polynesia and the western Pacific (Roullier et al. 2013a: 2208).

On New Guinea, genetics have ruled out hypotheses of earlier Kumara introductions and shifted the consensus towards later introductions, with the genetic traces of South American variants most likely introduced at later stages and admixed into the current gene pool.

Micro levels make this issue more complex as even the date of introduction is debated, the general consensus used to be an introduction somewhere around 1000 AD but as Wallin (2014) suggests, the consensus of an introductory date have shifted to be around 1200-1400 AD (Wallin 2014: 102-103). Looking at the micro level of dispersals in Polynesia genetically it is not really possible to be specific. The absence of ancient samples to extract aDNA from, leaves only modern and herbarium samples. Which in turn are distorted by reintroductions of sweet potato variants and local admixtures giving only a general, macro level diffusion picture. There is also the issue of later introductions mixing with local variants and shifting genetic affinity towards a different origin but keeping a typical phenotypic expression. Meaning that new variants keeps a name representative of their appearance but group together with another genetic origin (Roullier et al. 2013a: 2209). This could be seen as somewhat of a criticism of modern linguistic approaches for micro level diffusions as the words following variants of sweet potato may take different paths than their genes.

So is one scale preferable over the other in deciding the best representation for the history of sweet potato in the South Pacific? The short answer to this question is no. To elaborate,

7.4.2 Cultural impacts and the sweet potato revolutions
So with the introductions and origins of sweet potato basically covered, another question remains. What actually happens when a new crop is introduced? Wallin et al. (2005) explores sweet potato introduction to Rapa Nui by analysis of archaeological activities on monuments (Wallin et al. 2005: 86-87). There is evidence of a huge escalation of construction activities after 1200 AD which would not have been possible without dedicated agriculturalist sustaining a work force (Wallin et al. 2005: 88).

The scale of time also becomes an important factor, if an evolutionist approach explains monuments and artefacts as an evolution of culture, the time span as argued in a previous chapter is a single dimension entity. But how does a cultural landscape change when “infected” by a new variable that has the ability to sustain a workforce (as in Rapa Nui, Wallin et al. 2005)? How fast does this change happen if it can be termed as a revolution of culture (New Guinea sweet potato revolution).

The genetic studies are quite elusive on the cultural impact aspect of the sweet potato dispersals. But it is more of an ontological limitation as these aspects are not covered by the scope of their studies. It would not change the results or conclusions and it would not change the chronology investigating the why and how.

8.1 Introduction

Major human migration movements have become a hot topic in the past decade or so. Working with human DNA to uncover migration patterns and continuity between populations has gained a lot of notoriety for its potential to interpret major human events in time. As methodology in genetics advances, so do the potential results of these studies. In Neolithic Europe, scientists have been utilizing ancient and modern DNA samples to create different models for revealing human migrations and continuity/discontinuity between populations spatially connected. Origins can be deduced from studying modern mtDNA haplogrouping or by finding persistent haplogroups between ancient and modern populations (Bramanti et al. 2009; Malmström et al. 2009; Haak et al. 2010; Brotherton et al. 2012; Skoglund et al. 2012; Brandt et al. 2013). These genetic studies provide a new take on archaeological dilemmas and as they may change the consensus of how we understand past events and populations, the current position of research is sometimes reviewed (e.g. Pinhasi et al. 2012).

As presented earlier, human migrations in the Pacific is in constant flux, new data provide new interpretations of human origins and colonization patterns and the general consensus changes (e.g. Kirch 2000; Andersson et al. 2012). With genetics investigating human origin questions in the Pacific, things are changing again. A review of the current research position on Pacific genetics was conducted by Elizabeth Matisoo-Smith in 2015. In this chapter I aim to deconstruct this review in order to determine the general genetic discussion from an archaeological perspective. This review has been selected as it summarizes the current debate in genetic research concerning human migrations in the Pacific. It summarizes this research from the perspective of a geneticist working with archaeological dilemmas.

This deconstruction is significant in finding out what concerns a geneticist in this position and how they might view the schism between archaeology and natural sciences (as in Lidén & Eriksson 2013). The purpose of this chapter is to examine the dialogue between archaeology and genetics on these topics and to accentuate archaeology’s role in Pacific migrations. To find out how archaeology functions as a science in these questions and to propose a discussion of how archaeology should utilize its strengths to complement these issues in multidisciplinary approaches. This chapter aims to answer the research question of how the current research on genetics and material culture is discussed and to provide results in terms of answering where the current genetic and archaeological research stand on human migrations in the South Pacific.

Matisoo-Smith’s review (2015) also covers some of the discussion on plant and animal DNA in the Pacific.
8.2 What’s it all about, a summary

8.2.1 Introduction and background (Matisoo-Smith 2015: 1-5)
The Pacific is the last place on earth that has seen major human migrations, from reaching the east coast of Asia 60,000 years ago and expanding into the reachable continent Sahul by crossing Wallacea (Figure 8) due to lower sea levels 45,000-50,000 years ago. Colonizing most of what today is Near Oceania by 30,000 years ago and then colonizing the most remote islands of eastern Polynesia 1000 years ago.

The interaction between modern humans and Denisovans in ancient times and the island landscape of the South Pacific being isolated from the rest of the world by a vast sea makes this area play an important role in studying evolution. Ancient DNA has been a troubled topic as the interest in origins and relations of Pacific people has been high since the first arrival of Europeans. This interest leading to some highly questionable methods resulting in a divide based on fear and mistrust between science and indigenous people. Therefore, population studies have been limited to collections not subjected to concern of local indigenous groups.

Genetic and linguistic variation in Near Oceania is most likely based on hunter/gatherer groups being isolated due to the largeness of Australia’s landscape and isolation of the island landscape around New Guinea. For remote Oceania, settlement began roughly 3000 years ago, based on archaeological sites, and is defined by the Lapita Cultural Complex. The Lapita is identified by a specific type of pottery as well as a Neolithic ‘package’ including domestic animals and plants. The Lapita is also connected to the spread of Austronesian language originating in Taiwan. Archaeologically there is no real point of origin for the Lapita Culture. The expansion of Lapita Cultural Complex reached Samoa and Tonga about 3000 years ago and expansion further did not continue until 1200 years ago with the most remote islands of Hawaii, New Zealand and Rapa Nui settled last, 1200-1000 years ago for Hawaii and 750-800 years ago for New Zealand and Rapa Nui.

Figure 8 Map of Sunda, Wallacea and Sahul.
The consensus for settlement in Oceania has been subject to change over the last 30 years due to modern archaeological, genetic, and molecular research. From belief in Thor Heyerdahl’s theory of a South American origin for Polynesian people to blood protein data and mitochondrial DNA disproving this possibility.

Mitochondrial and Y-chromosome DNA regional haplotypes correlated with archaeological and linguistic evidence for two large colonization waves into the Pacific. The first initial wave during the Pleistocene and the second wave consisting of Neolithic Lapita people, speaking Austronesian languages, which has become the general accepted model for Pacific colonization. The Lapita people has then been termed the direct ancestors of modern Polynesian people based on linguistics and culture, which has also been identified through mtDNA mutations found throughout Oceania and Polynesia in particular (these mtDNA mutations were characterized by specific single nucleotide polymorphisms (SNPs) and a nine base pair (bp) deletion composing the haplogroup B4a1a1a). The haplogroup B4a1a was identified with clear Taiwan affinity and supporting a Taiwanese origin for Polynesia.

However, the origin of B4a1a1a has been criticized as it is not at all present in Taiwan or the Philippines. The Polynesian haplotypes has been argued to have evolved in the Bismarck Archipelago 6000-8000 years ago which predates the Lapita Culture in that area. How reliable these estimates of coalescence dates are, has also been debated and there is a possibility that haplogroup B4a1a1a has been present although at a low frequency.

From yDNA data there is a more complex history however, where haplogroups K, M, S and C originates in Pleistocene Near Oceania and are generally only found in Pacific populations. The branch for haplogroup O, which is also found in Pacific populations and widespread in Asia, is believed to have been introduced during the Holocene as part of the Austronesian expansion. These Near Oceanic Y-chromosomes are significantly present even where mtDNA lineages are derived from Asia. This has been explained by Lapita societies having a structure for matrilineal descent and patterns for matrilocal residence. In Tonga and Samoa yDNA variation for a certain haplotype has been linked to an indigenous Taiwanese population giving the first biological evidence of a Taiwan-Polynesian connection. But for Polynesian populations, only a few have been sampled in Pacific genetic studies, and Y-chromosome variation may be affected by slave traders removing men from populations in historic times.

As whole genome studies are becoming more standard, there have not yet been any drastic changes to the origins or admixture events proposed by mitochondrial or Y-chromosome studies. But as a strong Asian component has been identified in eastern Polynesian populations it has been hypothesized about a post-Lapita expansion into Central and East Polynesia from Samoa. Whole genome studies on modern Polynesian populations and ancient DNA analysis is, however, needed to investigate this further. But employing ancient DNA studies requires multidisciplinary approaches to access key issues of Lapita origins and Remote-Near Oceanic connections. There also needs to be further collaboration with local communities.

8.2.2 Ancient animal and plant DNA (Matisoo-Smith 2015: 5-7)

With ethical problems of sampling indigenous populations and acquiring ancient samples, animals were instead used as a proxy for studying human migrations. As animals was brought as part of a colonization package during the Lapita expansion and are represented by dogs, chickens, pigs and rats. Remains from these animals were also recovered to a greater extent than human remains at archaeological sites as well as a belief that mtDNA variation was higher among animals in the Pacific. This approach became known as the commensal
approach and the first animal to be studied extensively was the Pacific rat (*Rattus exulans*). The Pacific rat is native to Island Southeast Asia and its remains are found at the earliest archaeological sites in Polynesia and remote Oceania. In mtDNA analysis of the Pacific rat, two interaction spheres in the Polynesian triangle were identified, a northern and a southern. Both originating in the Cook Islands and the Society Islands.

Ancient DNA studies on rats and archaeological records could together deduce an origin hypothesis which did not coincide with the Austronesian origin of Taiwan. Meaning that the rats were picked up along the way and not part of the initial expansion.

As for pigs, it appears one lineage was introduced into the Pacific with origins in Vietnam. Dogs on the other hand were introduced through two mtDNA lineages, separate from the introduction of the Australian dingo. However, there seems to be a lack of dog remains from early Lapita sites (3500 years ago), the frequency of recovered dog remains picks up from about 2000 years ago. This is suggestive of dogs not being a central part of Lapita culture.

The chicken is found throughout both Near Oceania and Remote Oceania in the earliest Lapita sites and show two separate mtDNA lineages. Chicken bones from pre-European contexts found in Chile has shown direct affinity to mtDNA lineages in Polynesia suggesting a Polynesian-South American connection and a Polynesian introduction of chickens to South America instead of the previously believed hypothesis of a European introduction into South America. The study concluding this connection has been heavily criticized but supplemental studies still make it valid. Alongside there has been morphological studies of human crania found in vicinity to the chicken bones in Chile, also suggesting Polynesian presence. But the strongest and most accepted evidence of a Polynesia-South America connection comes from the sweet potato.

The sweet potato being of South American origin and found throughout Polynesia in pre-European contexts is also accompanied by the word Kumara, which stems from the South American word for sweet potato, cumar. The samples of sweet potato obtained though, do not yield aDNA. This pre-European variant of sweet potato has been replaced by later introductions during the 16th century. This makes it difficult to identify origins of pre-historic variants. From European herbarium samples some progress has been made. Suggesting multiple variants was brought back from South America and multiple introduction of sweet potato into the Pacific while also confirming the tripartite hypothesis of three main lines of sweet potato introductions.

Other plants, bacteria and DNA from teeth may also in the future provide data for tracking human migrations in the Pacific.

### 8.2.3 Ancient human DNA (Matisoo-Smith 2015: 7-9)

In recent years, collaboration between researchers and local Pacific people has evolved to become more inclusive and of interest for indigenous groups. The earliest aDNA studies on human remains utilized the 9bp deletion as an indication of authenticity as this deletion is expected in Polynesians descending from East Asia. In a study including ancient samples to investigate relationships of Polynesians and Lapita people, only East Polynesian samples and one sample from Tonga (300 years old) contained the 9bp deletion while Lapita samples did not. This leads to hypothesis of Melanesian origin for Lapita culture. This was criticized however and the lack of the 9bp deletion expected in contaminated samples. The results have never been replicated and the bad preservation conditions for aDNA in the South Pacific make it likely they never will.

Another, more recent, study outlined data for mtDNA variation in East Polynesia while also using ancient samples dated 1300-1600 AD to find these sequences fell into two lineages. Most of the modern samples and most of the ancient samples contained the Polynesian haplogroup B4a1a1a while in the rest of the samples haplogroup Q1 was identified.
Haplogroup Q1 originates in Near Oceania and had been found at low frequencies throughout Remote Oceania as far as Samoa and Cook Islands. These results means that haplogroup Q1 was spread further eastward than first believed and it was also present before any European contact, most likely by the founding group of the Gambier Archipelago thus highlighting continuity between ancient and modern populations.

In a different continuity study, this time focusing on European impact in the Solomon Islands, samples of teeth and hair were collected and analyzed for mtDNA sequences. Out of 21 samples, 17 yielded positive haplogroup assignment whereof 12 samples were of B4 variants, three were the 30 000 years old M27 and one was Q1. The results of haplogroup frequencies correlate to modern populations from western Solomon Islands meaning that the impact of disease from contact with Europeans in late 1800s and early 1900s, did not affect Solomon Islands as severely as other Melanesian island groups.

On New Zealand in accordance with a Maori tribe at one of the oldest archaeological sites on New Zealand dated to 1285-1300 AD, the employment new technologies have yielded complete mtDNA genomes from two individuals and two almost complete mtDNA genomes from two other individuals buried at the site. These data showed significant variation in mtDNA in the first settlers of New Zealand which did not coincide with earlier studies on Maori mtDNA variation. Based on these results there are indications that genetic variation and human migration patterns in Polynesia have been greatly underestimated.

Another complete genome from ancient mtDNA has been made possible by employing next generation sequencing technologies, this genome is from an Australian Aboriginal man whose lock of hair was stored in a collection at the University of Cambridge. This DNA sample showed a previously unidentified sub-group of haplogroup O as well as Denisovan and Neanderthal DNA. This is indicative of a division between Australian Aboriginals and Eurasian populations somewhere 77 000-64 000 years ago. This divergence is earlier than a different dispersal that is responsible for most modern East Asian populations. Another study showed gene flow between Australian Aboriginal populations and Indian populations during the Holocene. But the geographically limited samples mean this contact needs to be further investigated.

The Polynesian mtDNA markers (9bp deletion and specific SNPs) have also been found in 19th century Brazilian remains. However, there is a haplogroup found in Madagascar populations that also contains the Polynesian markers which was not screened for in the Brazilian study until more recently. This proved the samples were, in fact, Polynesian but radiocarbon dates predate slave trade in the Pacific. Meaning, the remains may have been mislabelled in the collections.

8.3 The deconstruction

8.3.1 The main theme and general comprehension

There are three main components to Matisoo-Smith’s (2015) article, an introduction and background that outlines the current consensus of pre-history and history in the Pacific. There is a review of animal and plant, ancient DNA studies and how these facilitate discussion on Pacific migrations. The final component is a review of ancient DNA studies on humans, issues with these studies and what the future might hold for genetic researchers in the field of South Pacific ancient DNA. There are also some key points and themes that are discernible, (1) what has led up to the current consensus, (2) genetic methodology and criticism and how biology helps shape the discussions of human migration, (3) complexities regarding mtDNA and yDNA, (4) animals and plants as proxies for human migration, (5) ethical aspects of working with human samples in Pacific cultures and (6) what the future may show in terms of genetic analysis.
There is a clear bias in the main theme of the article, as is expected for a genetic review, towards the methodological issues with the work that is in review. There is also a clear macro scale bias as pinpointing when and where is of greater importance than why and how. The implications of dealing with when and where in macro scales are defining a sense or order of things occurring. A time line is produced and events occur on this line. Later events are explained by another event taking place prior. The result creates a very clear picture of human migration through time. However, this clear picture is actually not very clear at all as each event is plagued by discussion and disagreement among scientists and the consensus of each event is often changing. This of course is the spinning wheel of science, as new data is encountered, new hypothesis arise and the consensus model change.

The introduction and background is a reiteration of what is currently in vogue. While not wrong, it certainly gives a very general, and somewhat simplified, picture of the discussions on human migrations in the Pacific. It is also important to note that many of the archaeological-linguistic discrepancies presented are points where genetics could provide new data, or where it already has, and basically “solve” these disagreements. For example, this pertains to the discussion on Lapita origins and New Guinea/Australia genetic diversity (Matisoo-Smith 2015: 3-4). Whether this way of arguing is intentional makes little difference as it highlights the focus on a genetic perspective on these topics.

There have been many occurrences where biological methodology has stepped in and proven or disproven certain hypothesis proposed by archaeology, anthropology or linguistics. Like blood protein data falsifying Heyerdahl’s hypothesis of an expansion from South America into Polynesia (Matisoo-Smith 2015: 3). It is however, the molecular and genetic data that provide conclusive evidence to debated topics in the examples used by Matisoo-Smith. There are other opinions on Heyerdahl’s hypothesis as well that are not included in these examples, Thorsby (2014) suggests, based on HLA markers, that there indeed was an eastward expansion from South America to Easter island before Europeans. It was just not the initial colonization, as Heyerdahl thought (Thorsby 2014: 129).

Things clear up and become more specific once genetic history is discussed. Lapita people are, linguistically and culturally, the direct ancestors for Polynesian people which also, was originally supported by mtDNA (Matisoo-Smith 2015: 4). This support has since been debated with the advancement of genetic methodology and the employment of complementary studies, which is richly reiterated. The genetic side of the story is critically reviewed with the complications of the B4a1a haplogroup, meanwhile the other side of scientific analysis is presented rather perfunctory. This shows the interest and knowledge bias of the author for the biological side of science on these topics.

By further examining the complexities of mtDNA and yDNA the review changes its scope. From the big picture, macro scale analysis to a more micro level discussion about group compositions and social structures. This discussion is very short however and suggest matrilineal institutions of residence and descent for Lapita societies as cause for the difference in genetic origins referencing Hage and Marck (2003). A different cause for mtDNA and yDNA difference in origins is also discussed, moving the review back to the macro scale focus, in that Polynesian populations are underrepresented in Pacific genetic analysis. There is also a third possible cause presented by Matisoo-Smith, historic events where Polynesian men were taken as slaves that may affect difference in maternal and paternal genetic origin. These last two possible causes shift focus from micro scale, multidisciplinary analysis to strictly genetic sampling biases. These causes can also be seen as rather deterministic in that everything is explained through population genetic concepts like genetic drift (i.e. all men are randomly removed by slavers). Thus, the cause for genetic variation is explained by biology rather than human agency and culture.

Despite the affinity for biological perspectives and explanations there is still an interest in questions related to culture and interactions between communities.
Despite the acceptance of this general model of Island Southeast Asian origins for Polynesians and their Lapita ancestors, questions still remained: How was the Polynesian Triangle itself settled? What were the immediate origins of the New Zealand Maori or the people of Rapanui? How much interaction was there between the Lapita peoples in western Remote Oceania with the Papuan populations of Near Oceania? Where was the homeland of the Lapita peoples and their culture? Ancient DNA provides a unique opportunity to address many of these questions but requires a multidisciplinary approach and collaboration and engagement with local communities. We might also be able to further engage with and encourage Pacific communities to participate in whole genome studies (both ancient and modern) to begin to address questions about how Pacific populations might have adapted genetically to the range of Pacific environments and specific challenges. These approaches could help us better understand why Pacific communities today suffer from higher than normal rates of particular diseases such as diabetes, gout and other metabolic disorders… (Matisoo-Smith 2015: 5).

Even though there is a call for multidisciplinary approaches it seems to be founded in expanding the biological knowledge of the Pacific rather than interpreting material culture and understanding the people of the past and their culture that has shaped the Pacific into what it is today.

8.3.2 Animals and plants
The review of the commensal model, or animal and plant DNA in Pacific contexts, is heavily reliant on Matisoo-Smith’s own work, primarily Pacific rats (Rattus exulans) and Polynesian chickens (Gallus Gallus), and to some extent dogs (Canis familiaris). Which is evident by examining references in each domesticates respective paragraph. The chicken bones presented by Storey et al. (2007) have been heavily debated (as argued in chapter 6) and in this review Matisoo-Smith summarizes this debate in favor of her own work.

Moving on to plants the sweet potato is primarily used as an enhancer for the previous paragraph about chickens and the South American-Polynesian connection argued for by Storey et al. (2007; 2008; 2010; 2014). As the sweet potato also is an indication of a South American-Polynesian connection in pre-history (as presented in chapter 7). Sweet potato from the archaeological record is poor, however, as conditions for preservation in the Pacific is atrocious for aDNA. The argument used here is again a promotion of a biological perspective and a reduction of archaeology to a provider of specimen. It could prove interesting to utilize landscape analysis of the archaeological record or viewing change in the material culture to argue the impact of sweet potato introductions (as argued in chapter 7). But this is a perspective bias as the primary focus in this review lies upon macro scale origin discussions.

Most other species of the commensal model, not part of Matisoo-Smith’s own work, is not as carefully reiterated. They are also critiqued as plants are most commonly only obtainable through modern samples with complicated reintroduction histories (Matisoo-Smith 2015: 6). But there is a genuine interest in what can be accomplished by continuing work with these species and also with bacteria and viruses associated to humans. This might be an outcry for more researchers to join the field of Pacific population genetics.

8.3.3 Human DNA
Moving on to human ancient DNA, this is presented through five cases of successful aDNA sequencing using modern methods. These cases are all focused on what may be further researched in the future as these methods could help in conducting more complex analysis on more difficult materials. It is also important to note the wide time span of ancient DNA as aDNA is DNA from dead organisms (Hofreiter 2001: 353) and not necessarily “ancient” as in the meaning of the word. The cases represent samples from 13th century up until 20th century from various regions in the Pacific. These samples provide much information to help
understand the genetic variety in modern Pacific as well as understanding the spread of certain haplogroups before European arrivals. It also helps understand the impact of Europeans in the Pacific with diseases and slavery. Of course in a very biological way as once again the cause of genetic variation is considered through a biological perspective rather than cultural and human agencies.

The case with the oldest obtained samples draws heavily from archaeological conclusions that the site initially was settled by East Polynesians and was a founding populations on New Zealand (Matisoo-Smith 2015: 8). Archaeology in this case seem to have been mostly concerned with finding an origin for New Zealanders. As full mitochondrial genomes were sequenced from this site, the origins of New Zealanders turned out more complex than previously thought (Matisoo-Smith 2015: 8). It appears that material culture do not hold the same origin history that genetic variety does, therefore perhaps archaeologists should reconsider putting too much emphasis on migrations and origins of people and instead consider the cultural aspects in a broader range.

As many ancient genomes are being produced, Matisoo-Smith (2015: 9) brings up an interesting point in that applying the same methods to screen for Polynesian contacts in South America. So far only mtDNA has been obtained, showing the limitations of only obtaining female lineages as Polynesian traders and explorers quite possibly could have been men. If mtDNA shows no gene flow from Polynesia to South America it is not conclusive evidence of no contact. In this case material influences could provide a solid complement, at least until nuclear genome or Y-chromosome genomes are obtained. Then material influences can be examined for human interactions and explore a different narrative all together, one that biology can not quite penetrate.

8.4 Concluding remarks

The biological perspective is quite clear, a geneticist’s view on Pacific prehistory is mostly concerned with origins and grand population movements. With rapidly improving methodology and advancements in technology, aDNA studies will very likely continue to map dispersal history in the Pacific despite the poor preservation conditions for aDNA. But archaeology’s role is not quite clear as it is interpreted and used by geneticists mostly as a background for their research or a provider of specimen to be sampled.

What then, would be an appropriate way to conduct archaeology if it is to complement genetic studies? An evolutionary approach seems to promote a macro scale thinking, in order to discuss material culture in the same manner as genetics. A problem with this is that it becomes reductionist and superfluous as there will be little difference to genetic consensus and if it is, will it be as conclusive as genetics? I believe archaeology need to reconsider the macro scale origin perspective and instead focus on how human influences each others through contact other than in the biological sense. Material culture has the potential to provide a vastly different story than that of biological data, it can also show influences and trade connections to a greater extent than studies based on biological data. Archaeology needs to establish itself as a mediator of material culture rather than trying to explain the same macro scale, human origin perspectives currently provided by ancient DNA genetics.

Working with interpretation of material culture means applying an agency based approach rather than an evolutionary approach as the biological perspective is accounted for in genetics.

Comparing Matisoo Smith’s (2015) review to Anderson et al.’s (2012) summary of Pacific history. A different reasoning and different arguments is shown. Anderson et al. (2012: 21) draws on equivocal pottery directionality as an example of contrasting biological modelling. They also suggest the development of regional interaction and trading networks during the Holocene as motivations for increasing migrations. Societal status and opportunities presented by seafaring are also considered in motivations as to why people
migrated (Anderson et al. 2012: 21-22). What drives migrations is more in focus and these motivations are best approached through an agency perspective. This stands in stark contrast to Matisoo-Smith’s (2015) review where motivations and status is most often not even considered in the discussions. The human factor of migration, that which motivates people to leave their homes and seek something else, is left aside for biological systems. Human dispersal is measured through genetic variety and people leaving their home is a genetic bottleneck that explains the genetic variation in modern people.
Part IV, Reaching a consensus

Figure 9 Gauguin, P., (1892) Tahitian: Mata Mua, [painting] accessed 2016-05-30 from https://commons.wikimedia.org/wiki/File:Paul_Gauguin_-_Mata_Mua.jpg
9. Discussion and interpretation

9.1 Archaeology versus genetics

The goal of genetics seems clear, outline human migrations through time based on genetic markers. In many cases, ancient DNA studies pick up where archaeology has left off, continuing or re-shaping the consensus. By basing their studies on archaeological backgrounds however, a lot of faith is put in that the archaeological conclusions are solid interpretations. This creates somewhat of a dilemma for archaeology and a divide in ontological perspectives. On the one hand, agency based interpretation investigates why the archaeological record is constituted the way it is. On the other hand, evolutionary archaeology strives to be a natural science, drawing conclusions from the material record that are empirically grounded. In acting as a natural science, archaeologists of the latter perspective hope to bridge the gap between archaeology and the natural sciences, creating a common ground for both parts to facilitate discussions. What I find interesting in all of this is that the material culture and genetic data seem to tell different stories in Pacific migration histories where one often act as background for the other. The problem I see is that instead of working together in figuring out certain sites or approaching the same material from different perspectives, everyone is trying their best to create grand narratives. The main concern is always figuring out Pacific settlement as a whole. In order for archaeology and genetics to create something together, both fields need to concentrate on their strengths respectively. Archaeology needs to perhaps take a step back as the main way of interpreting prehistory, genetics has the potential to map human migration patterns by working with modern and ancient DNA in ways archaeology can not, in a biological way. That is to say, the biological perspective is not the same as the cultural, and it should not be. Material culture has its own story to be interpreted and is not reachable through biology, only through interpretation. If archaeology succumbs to being an objective, generalizing science, what role can material culture play in the grand scheme of Pacific prehistory?

There are some potential cases where archaeology and genetics stand to gain something from each other that could prove very interesting. The sweet potato introductions I believe is one such case. The biological perspective highlights origins and dispersals together with linguistics to a degree not affirmative by material culture. The cultural perspective can however highlight what happens culturally when this crop is introduced, how the cultural landscape change, be it monument building or transforming the landscape to support agriculture to a greater degree. This is an example of material culture changing due to the introduction of something biologically traceable, but changes in material culture do not have to be a repercussion of biological phenomena. Material culture change and disperse independently of genes as well and this is where genetics and archaeology needs to meet. Questions of why cultural change occur and how these changes can be interpreted are important aspects and can be a great complement to understanding migration patterns.

As evidenced by deconstructing Matisoo-Smith´s review, geneticists view the material record in an evolutionary perspective whether they have actively considered it or not. Material culture is a stepping stone that always lead to how genetic variation is constituted within a population and human agency is not considered as a factor in shaping it. Instead human agency is equaled to a biological phenomenon such as genetic drift or a founder effect, taking human individuality and the human ability to shape their own societal role out of the equation.

What I would like to see in Pacific archaeological contexts is multidisciplinary approaches where genetic results show the origin of a population and archaeological results
show what has changed culturally, interpreting why and how this could be the case. They both need to be very aware of the other which so far, seem truest for archaeology taking to heart what geneticists conclude on dispersals.

9.2 Archaeology versus archaeology

How then, should archaeologists approach the archaeological record? I have become quite the advocate of agency-based archaeology through this thesis as I find it evident that genetics tell a better origin story than archaeology. If archaeology aims to explain the same models as genetics by typologies and serializations of material culture, the final picture will be overly reductionist as two dispersals, perhaps not similar, try to map out how humans have dispersed through time in the Pacific. The only measure is that of change through time which only shows from where something comes and how that has changed. Change in human culture is not a straight line however, as sometimes things change back to a state they were earlier. Hybridization does not “evolve” culture, it only changes and hybridization is a constant influence. This is often seen in modern cultures as well as, for example, fashion trends change to incorporate features that has been forgotten or out of style for decades. The interesting part is not that this happens but why it happens. Why is something that can not be explained by serialization or typologies no matter how many samples are found. Why is not always explained by biological phenomenon either. Why is, however, explained by interpretation and the employment of hermeneutic theory and this is where I believe archaeology should be, especially when working with natural sciences.

The human factor of humans is difficult as we are aware of our state and role in society. If cultural evolution were truly measurable in our everyday existence and quantifiable to the point that human actions are calculable. Humans made aware of such a system and how it works, would consciously act against that system in order to separate themselves from the quantifiable mass, rendering the newly found system completely useless. If this is the case, then what is the point in explaining human action through cultural evolution at all? Conscious decision making needs to be factored in to the equation as human agents are aware of their surrounding societal structures and how they shape it by acting within it.

Another way to look at this is by considering how archaeology and genetics complement each other. I would argue that if archaeology employs an evolutionary approach, it would become a complement to genetics. As genetics explore human migrations and origins, archaeology complements this by showing the “migration” of material culture and how the material culture has changed over time. As the main focus of research lie in how migration events happened in the past, studying change in the archaeological record is not the best way to deal with these questions, genetics is hence, archaeology will become a complement to genetics.

There is much complexity in the archaeological record that seem disregarded in genetic research. If the main focus instead lies in interpreting what drives these migration events in the past, genetics become the complement archaeology instead. If the goal is to interpret and understand a site from its material culture, genetics can provide data on origins and relations at that site. This can be utilized as a complement when interpreting how this site has been shaped to what can be excavated. I think it important for archaeologists to take the lead and use genetics as methodological complement, however, in order to utilize genetics, archaeologists need to fully understand how these methods work and how these models are created lest archaeologists make use of something “magical” that shows exactly what they want or else it will be disregarded.

Archaeologists obtain a material record that can be utilized by other scientists regardless of how archaeologists work with this record. If conclusions are to be drawn, I strongly believe
interpreting the material record and using results from genetics or other sciences can be supplementary to archaeology’s interpretations.

9.3 Merging the cases
In the grand narratives the generalizing effect of drawing conclusions from incomplete data has the possibility to create misguided pictures of history. Missing out on bits of information can create a history far from what actually happened. At the same time smaller narratives focusing on subjective interpretations may seem irrelevant to understanding the grand history of a place. Genetics seem to rely heavily upon conclusions made by archaeology as a base for their studies. There is never much critique involved in utilizing this base as suggested from the analysis in this thesis. Of course the same is true the other way around as archaeology often takes results from genetics as truths in support of their hypotheses. The “filter” from Lidén and Eriksson (2013) seems close at hand in these cases. There seems to be a common theme for all the discussions highlighted in this thesis however, where the archaeological record is taken for granted as a background for genetic research. The material culture or the dispersal events of humans are viewed as biological phenomena and not results of human agency. But in many cases perhaps they should be. If the chicken was introduced to South America by Polynesians voyaging east before Europeans arrived (which seems highly plausible), what influences can be seen by that introduction and what was taken back to Polynesia, if they ever went back?

The case of the sweet potato argues something similar and it is not permeated by disagreements on authenticity and methodology as in the case of chickens. The South American – Polynesian connection is confirmed but it is still problematic and complex. DNA in the case of sweet potato is limited to modern samples and, to a substantial extent, herbarium samples that represent 20th and 17th century sweet potatoes. These were collected by Europeans exploring the Pacific and can represent origins of Polynesian sweet potato in a general sense (i.e. they are of South American origin), they can not really derive the complex dispersal history within Polynesia and the Pacific as these are clouded by later reintroductions distorting genetic affinity. The timeframe of sweet potato introductions seems to match that of chicken introduction to South America however. As sweet potato was introduced to Polynesia around 1200 – 1400 AD and chicken samples in Chile derived from Polynesian chicken ancestry dates to around 1200 – 1400 AD as well.

This can hopefully be investigated further by studying human genomes in the future by hopefully moving beyond mtDNA genome sequencing to full autosomal genomes which will be required if we presume the traders and explorers were in fact men. In the meantime, what this means for group consistency and seafaring culture could prove interesting.

9.4 Where do we go from here?
I argue that archaeology in the Pacific should zoom in to consider micro scale cultural interactions and implications that can be interpreted through the material record. Working closely with geneticists in their pursuit to map out prehistoric migrations in the Pacific. Meanwhile geneticists need to consider the archaeological perspective and start thinking about how the impact of cultural dispersal can be interpreted by mapping biological origins. They also need to consider a different perspective on working with human dispersals as not everything can be explained by biological phenomena, possibly with the help of archaeologists as mediators of both macro scale studies and micro scale studies. Not to say
there is a lack of interest as geneticists and archaeologists are working together in many cases and this collaboration is constantly improving.

Another way to move forward is by exploring the possibilities of a new educational system, one which specializes in both genetics and archaeology in order to promote a new generation of “archaeogeneticists”. These researchers would preferably be educated in population genetics and bioinformatics to understand computer modeling and how to interpret genetic data as well as the interpretive element of archaeology. I believe genetics will continue to influence archaeological research to a great extent and even though “archaeogenetics” is achievable by close collaboration between scientists, making sure these scientists understand both fields would perhaps mean a different approach and more intricate motivation for studying human migrations.
10. Conclusions

10.1 Answering my research topics

Answering the research topics posed in this thesis no longer feels as important as the discussion is deeper than what conclusions can be drawn from the general consensus of different scientific approaches. The current consensus is very likely to change continuously as genetic methodology improve and the archaeological record is expanded and interpreted. This might seem obvious as it is a goal of science but it rings especially true in Pacific prehistory.

• Where does the current genetic and archaeological research stand on human migration patterns in the South Pacific?

• How is the current research based on animal DNA discussed to investigate human migrations in the South Pacific?

• What does genetic and archaeological research conclude on sweet potato dispersal patterns in the South Pacific?

• How is the current research of genetics and material culture discussed in Pacific contexts?

10.1.1 The first question

This question was aimed to summarize the research consensus on Pacific migrations from both an archaeological and a genetic perspective. However, there is much disagreement on specifics and generally, with the poor preservation conditions for aDNA in Pacific environments, the specific complexities of migrations in Pacific can not be understood through one sciences’ endeavors alone. By an intricate collaboration and exploration of different ontological approaches to these questions however, this dilemma might be untangled in the future. As of now, the current consensus that can be approached through the selected cases in this thesis is that of a South American – Polynesian connection before European contacts. There appears to be a point of contact within 1200 – 1400 AD but it is not obtainable to find out from which part initial contact was sought.

10.1.2 The second question

The second question aimed to investigate in what manner animals was represented and how they could be used as a proxy for studying human migrations. As it turns out, the discussion on animal DNA is mostly concerned with methodological issues. Can the discussion pass that state of arguing of authenticity and unite in a consensus, chickens as a proxy for human migrations can move on to begin explore what effects on Polynesian and South American cultures there has been. As for other domestic animals, this thesis has not really been able to cover them all. But mtDNA lineages show origins and dispersal routes and dates of introductions to different sites that can help further investigate how humans have migrated in
the Pacific. Humans have actively brought these animals with them but what they have been used for can only be interpreted through the archaeological record.

10.1.3 The third question
Through the third question, the aim was to investigate sweet potato as a representative of domestic plants in a similar manner to that of animals. The sweet potato origin history has basically been solved from a genetic perspective, the tripartite hypothesis has been confirmed by investigating herbarium samples as ancient DNA yielding sweet potato samples are absent from the archaeological record. This has been the suggested truth for a long time however based on multidisciplinary studies. But the dispersals are a complex matter, and to fully understand them more research is required. Preferably from multidisciplinary studies. Genetics have shown its prominence in working with dispersal patterns and archaeology can show what the result of the cultural impact has been as this crop has been introduced. How societies change and what happens in the material record.

10.1.4 The fourth question
The fourth question is not easily summarized as it is wildly different for different sciences and for different scientists. The purpose of it was to act as a foundation for discussing theoretical perspectives. What I can conclude, mostly from deconstructing a genetic review, is that generally, the research is discussed as biological phenomena, from a biological perspective. There are discussions of motivations and reasons for migrations but they are often overcome by the urge to understand origins of Pacific people through dates and routes. Further, this question was also supposed to promote discussion of how archaeology should position itself as a science in order to utilize the material record in complement to other scientific research. What I propose is that an agency-based approach stand the most to gain in multidisciplinary studies as it outlines a whole different set of questions not approachable through any other perspective.
11. Summary

Over the past few years in Swedish and Scandinavian archaeology, there has been extensive discussions on where archaeology is headed in terms of a new paradigm. Kristiansen (2014) argues we are moving into a “post-paradigm” where processual and post-processual schools of thought are being mixed together. In the heart of these discussions is genetics, how this science influence archaeology and how archaeologists and geneticists interact. In Pacific archaeology however, this type of discussion has been absent as geneticists have studied migration patterns based on genetic data. The Pacific is an exemplary case as the island landscape create natural bottleneck effects for both genetic variation and for material culture. Preservation conditions for aDNA in Pacific environments are atrocious and if aDNA samples are obtainable they are severely damaged leading to most research being based on modern DNA.

This thesis has aimed to investigate the discussions on archaeology and genetics in Pacific contexts through three case studies. The first case explored the debate on an ancient DNA sample obtained from a chicken bone at an archaeological site in Chile (Storey et al. 2007). The sample showed a mitochondrial haplotype present in Polynesian chickens inferring a Polynesian – South American contact. As the site pre-dates European arrivals in South America this would mean that Polynesian seafarers (or South American seafarers) sailed between Polynesia and South America 1200 – 1400 AD. This pre-European connection has also been argued in the second case in this thesis, the sweet potatoes presence in Polynesia. As sweet potato is a South American plant originally, this has been the consensus for a long time. In recent studies (Roullier et al. 2013a; 2013b) confirmed the hypothesis by genetics, showing the strengths of genetic research in migration studies. There is potential for interpreting the material culture and how the sweet potato introduction during 1200 – 1400 AD impacted the social environment that can not be studied genetically.

The third case in this thesis was aimed to discuss how the archaeological record and human culture is viewed from a geneticist’s perspective. This was explored by deconstructing a review of genetic research on migrations in the Pacific (Matisoo-Smith 2015). The conclusions drawn from this deconstruction was that human culture and human agency is often explained as biological phenomena and sources of genetic variation. Migration events are explained as bottlenecks and European slavers abducting men from Pacific islands is equaled to population genetic concepts like genetic drift. There is also a tendency for viewing archaeology as a background for where to begin genetic research and the archaeological record only as samples to extract DNA from.

I argue that human migrations are not the same as cultural spread and that archaeology needs to take a leading role in working with these questions in Pacific contexts. The best way to take the lead I believe is through an interpretive archaeology where finding what drives migration is more important than mapping peoples origin. I also argue that to fully utilize genetics in archaeology, archaeologists need to be educated in genetics or geneticists need to be educated in archaeology. Either way, a new major direction for archaeological education would be archaeogenetics where the interpretative, critical aspects of archaeology is combined with the statistic analysis and bioinformatics of population genetics.
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*Figure 7.* Thévet, A., (1557) Ipomoea batatas [drawing], accessed 2016-06-01 from https://commons.wikimedia.org/wiki/File:Hetch_Thevet_1557_53r.png Licence: https://creativecommons.org/publicdomain/mark/1.0/….29

*Figure 8.* Map of Sunda, Wallacea and Sahul, illustration by Tom Johansson….40

*Figure 9.* Gauguin, P., (1892) Tahitian: Mata Mua,[painting] accessed 2016-05-30 from https://commons.wikimedia.org/wiki/File:Paul_Gauguin_-_Mata_Mua.jpg Accession number: CTB.1984.8 Photographer: Colección Carmen Thyssen-Bornemisza depósito en el Museo Thyssen-Bornemisza Licence: https://creativecommons.org/publicdomain/mark/1.0/….48