

Peopling of the Marianas: An mtDNA perspective

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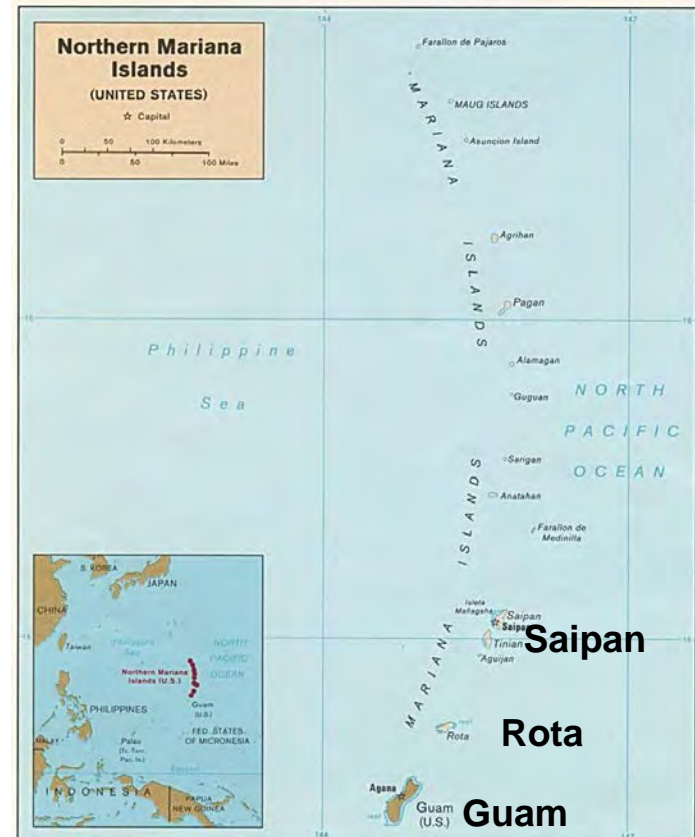
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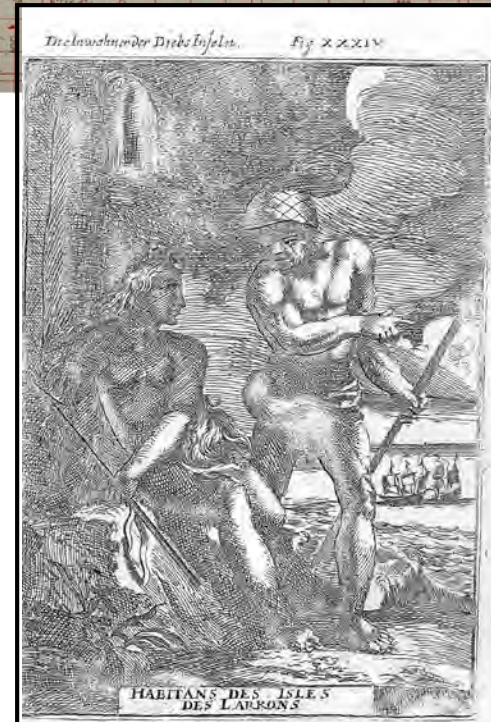
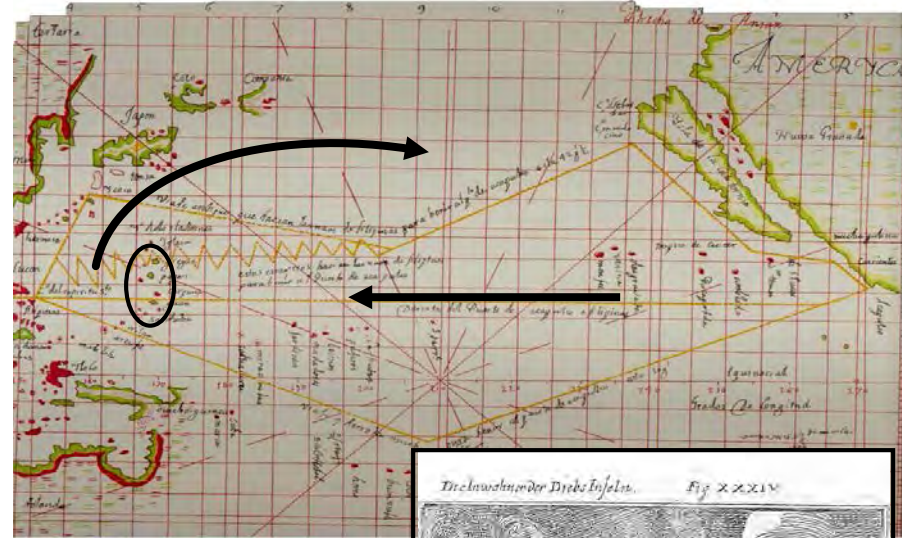
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Chamorros: The Mariana Islanders

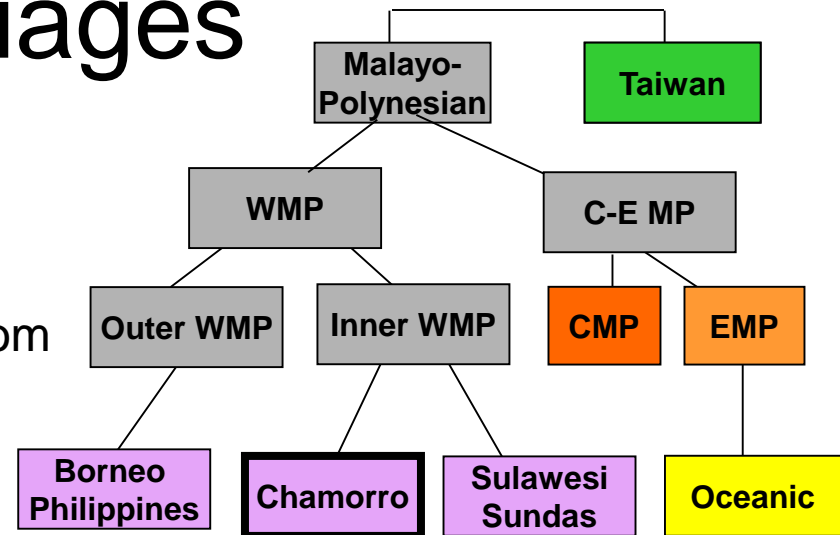
- The Marianas were the first Pacific island group encountered by Europeans. In 1521 Magellan landed on Guam. A stopping point for Spanish trade
- 1680's, during the Spanish-Chamorro wars, Spanish emptied Saipan, relocated people to Guam². Saipan was eventually resettled by Carolinians
- At Spanish contact there were as many 100,000 people , <5,000 by early 1700s³
- Spanish conquistadors described the islanders as tall, large, muscular, straight black hair, completely naked, often covered their bodies with coconut oil
- Skeletal studies of contact-time Chamorros have shown that they had muscular upper bodies¹
 - Localized bone overgrowths in the back of the skull
 - Humeral diameters larger (50% or more) than average modern humans.



Austronesian Languages

-The Chamorro language (Western Malayo-Polynesian)¹³ was originally grouped with indigenous languages from the Philippines. Today it is loosely grouped with languages from Greater Sundas and Sulawesi²³

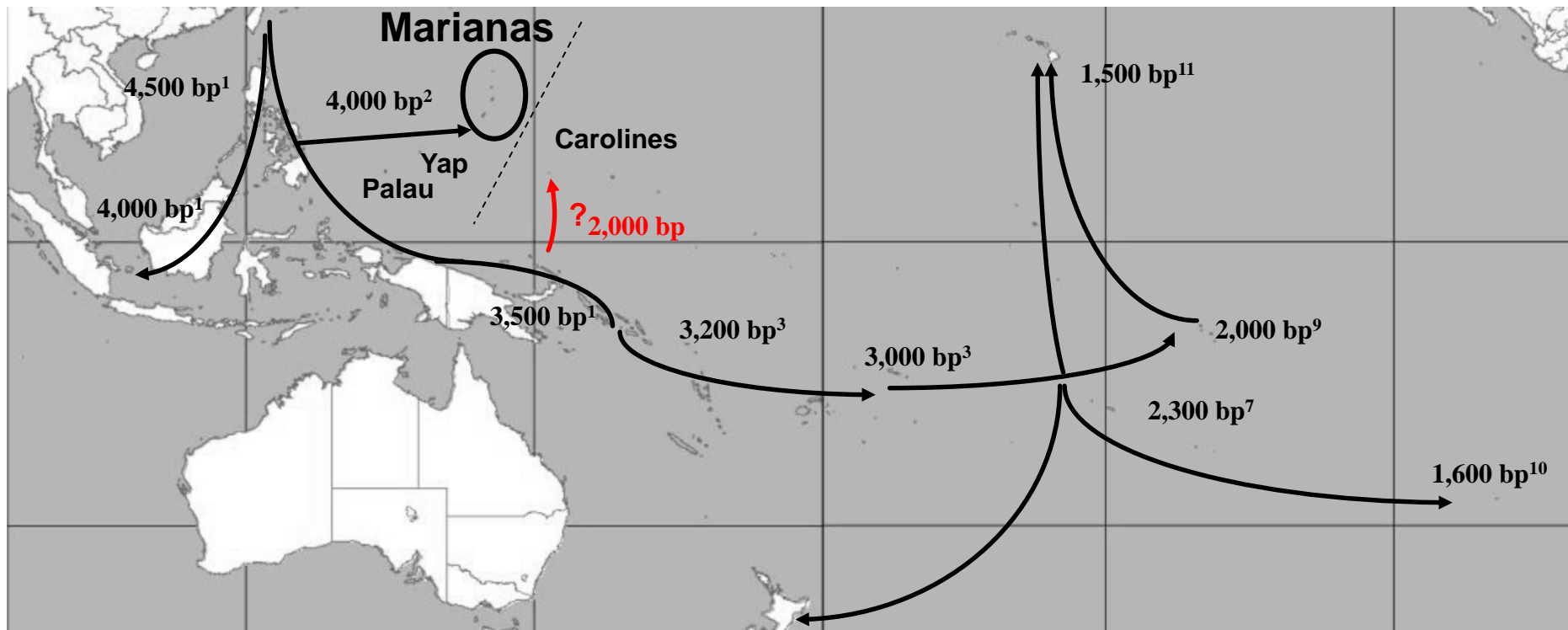
-Only distantly related to languages in the neighboring Carolines in central Micronesia



Marianas' First Settlers

-The Marianas were first settled from Island South East Asia (ISEA) around 4,000 to 3,500 BP by Austronesian-speaking sea goers². Around the same time a separate migration from ISEA moved through Melanesia to reach Polynesia by 3,000 BP. This time period was characterized by high sea levels, which would have caused complete submersion of Caroline Island atolls in Central Micronesia

-By 2,000 BP sea levels recede to modern levels, first evidence appears of settlements in the neighboring Caroline Islands¹⁹



Archaeological Evidence

Marianas pre-history (3,500 - 2,000BP) *pre-latte* period

- 3,500 BP: A distinct archaeological pottery type known as Marianas Red, similar in shape and form to contemporary pottery from the Philippines and Taiwan
 - Thin-walled lime in-filled pottery with distinct design patterns
- Sites: Achuago Point and Laulau (Saipan) 3,800 - 3,400 BP

Unique to the Marianas ~1,000 BP

-*Latte* are distinct monolith-type structures (some 5m high) possibly functioned as pillars holding up large homes or village community centers.

-First evidence of rice in the Marianas¹⁴



**Latte structures
in Tinian**



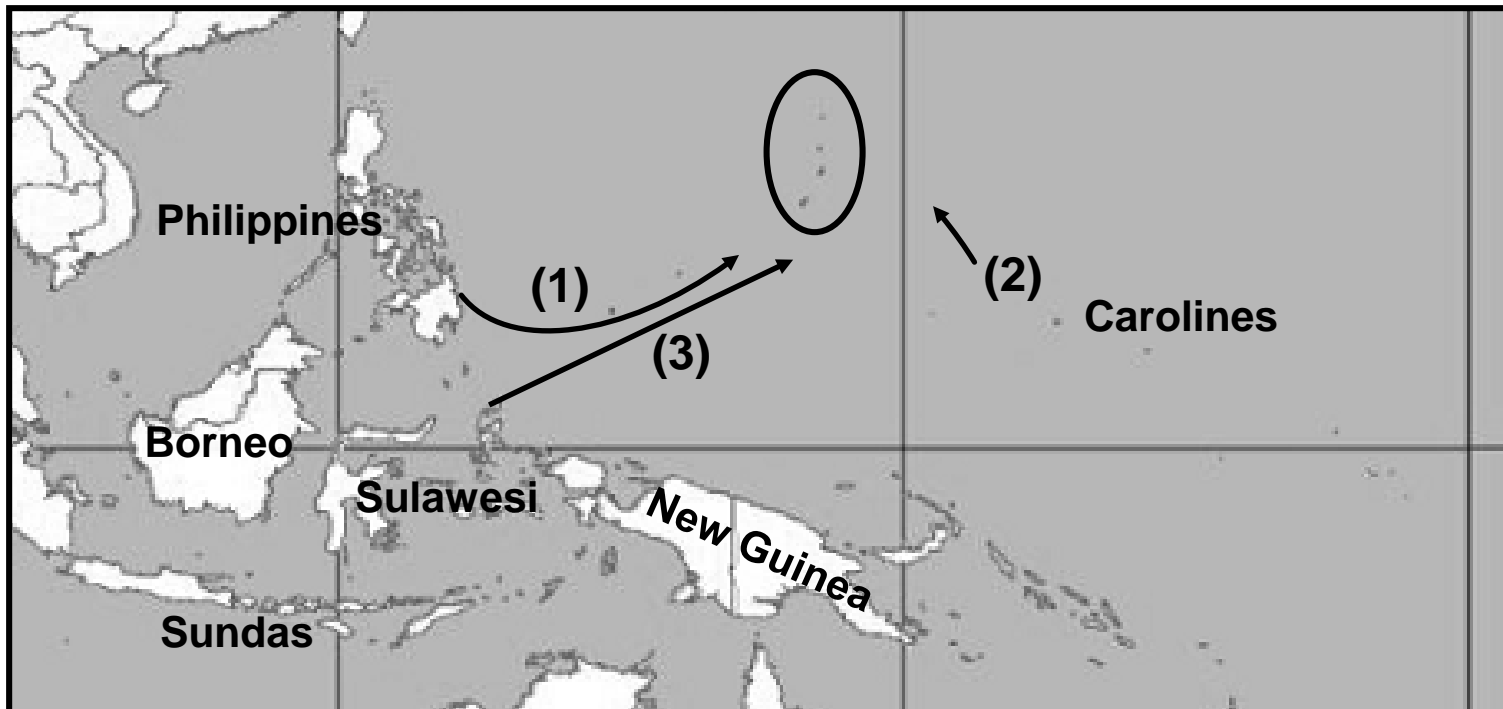
Marianas Red⁴



Rice

Hypotheses

- **(1)** In support of linguistic divisions, Chamorros are direct genetic descendants from the original settlers that arrived from ISEA around 3,500 BP
- **(2)** Gene flow from the Caroline Islands (since 2,000 BP) contributed lineages from Central Micronesia to the people of the Marianas
- **(3)** A more recent, separate ISEA migration (~1,000 BP), suggested by the appearance of rice cultivation and *latte*, contributed to the Chamorro gene pool



Field and Laboratory Methods

-We sampled DNA from 122 individuals from the islands of Guam (n=85), Rota (n=6), and Saipan (n= 31)

-Among them:

105 self-identified as Chamorros

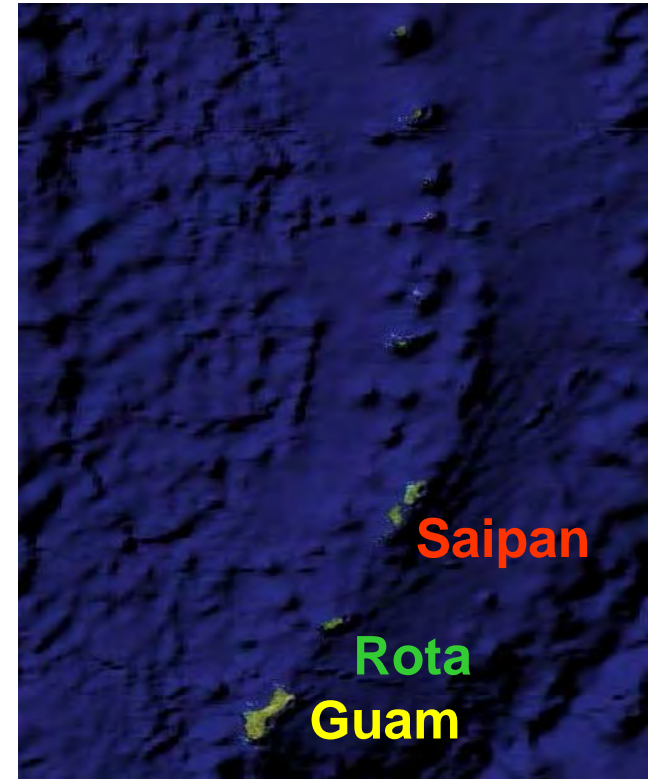
14 identified as having Carolinian ancestry

3 self-identified as Chamolinians

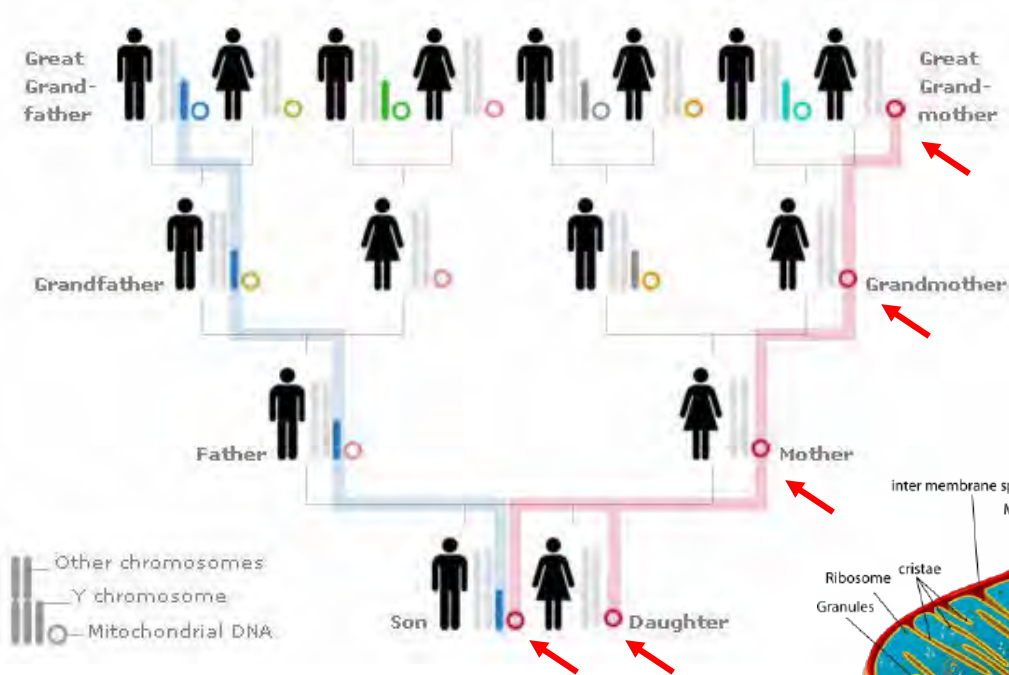
-Four-hundred bases (16000-16400) of the HVS1 region of mtDNA were sequenced. Additionally complete mtDNA genomes were done for 30 individuals

-mtDNA sequences were compared to those from populations in ISEA (Taiwan, Philippines, Indonesia), East Asia, Micronesia, and Melanesia.

-Phylogenetic Network¹⁵ diagrams were constructed to look at lineage frequency and distribution among Chamorros. Times of lineage coalescence, and thus lineage age, were estimated from these Network phylogenies.

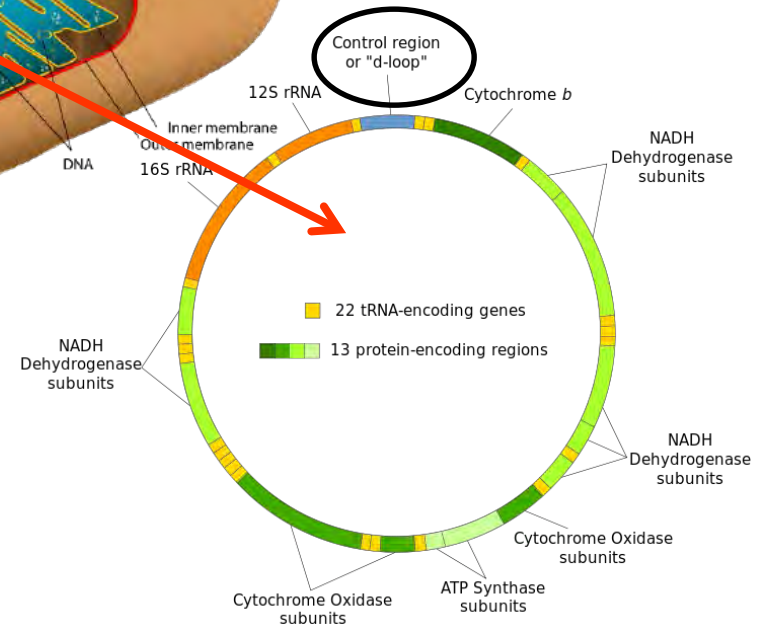
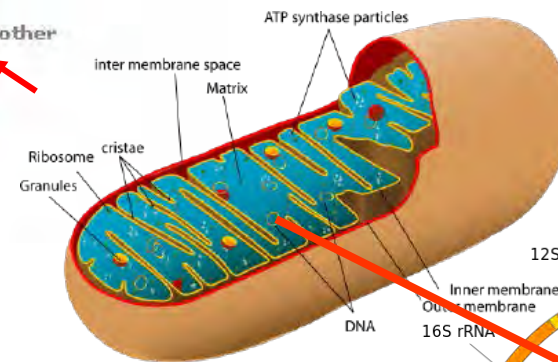


Lab methods for mitochondrial DNA (mtDNA) genetics



-Highly-mutable
very small molecule
(16,569 bp)

-Inherited maternally
WITHOUT recombination



-Control region (~1,100 bp) exhibits most mutations, and mutates at known rates.

-We study mtDNA diversity by looking at haplogroups, or groups of related lineages in human populations

-Different haplogroups originate and are commonly found in different world regions

mtDNA Control Region

-Two major regions (two simple reactions)

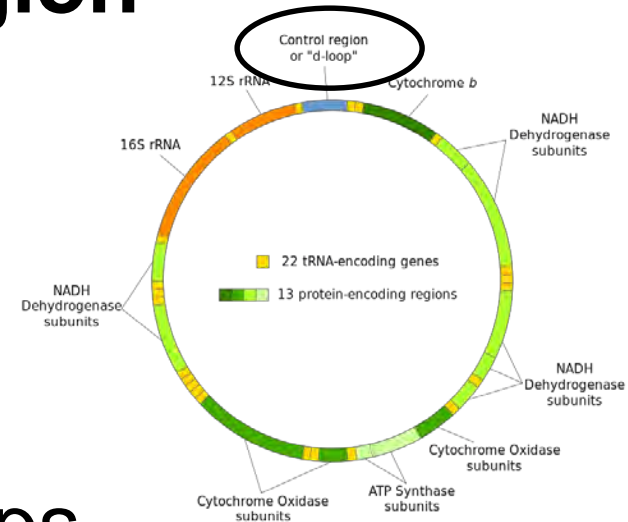
HVS1: 16025 - 16400

HVS2: 70- 500



-Comparative data exists for hundreds of thousands of individuals worldwide

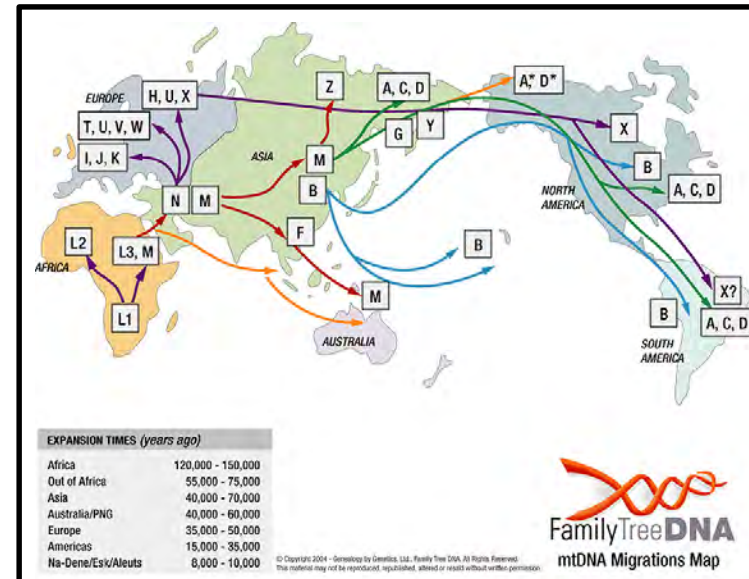
-The region is non-coding, thus mutations are NOT affected by natural selection, they accumulate at a constant rate through time



mtDNA Haplogroups

Haplogroup	Subgroup	(HVS1) Mutations
A		16223, 16290, 16319
	A2	16111, 16223, 16290, 16319, 16362
B		16189, 16217
	B4a1a	16189, 16217, 16247, 16261
C		16223, 16298, 16327
E		16223, 16362, 16390
	E2	16051, 16223, 16362, 16390

- B4a1, E, M, P and Q Pacific Islanders
- A-D and X2a Native Americans
- H-K , N and T-X2b West Eurasians
- L0, L1, L2, and L3 Sub-Saharan Africans
- A-G, M-S, Y-Z Asians and Australians



Median-Joining Network¹⁵

122 Individuals

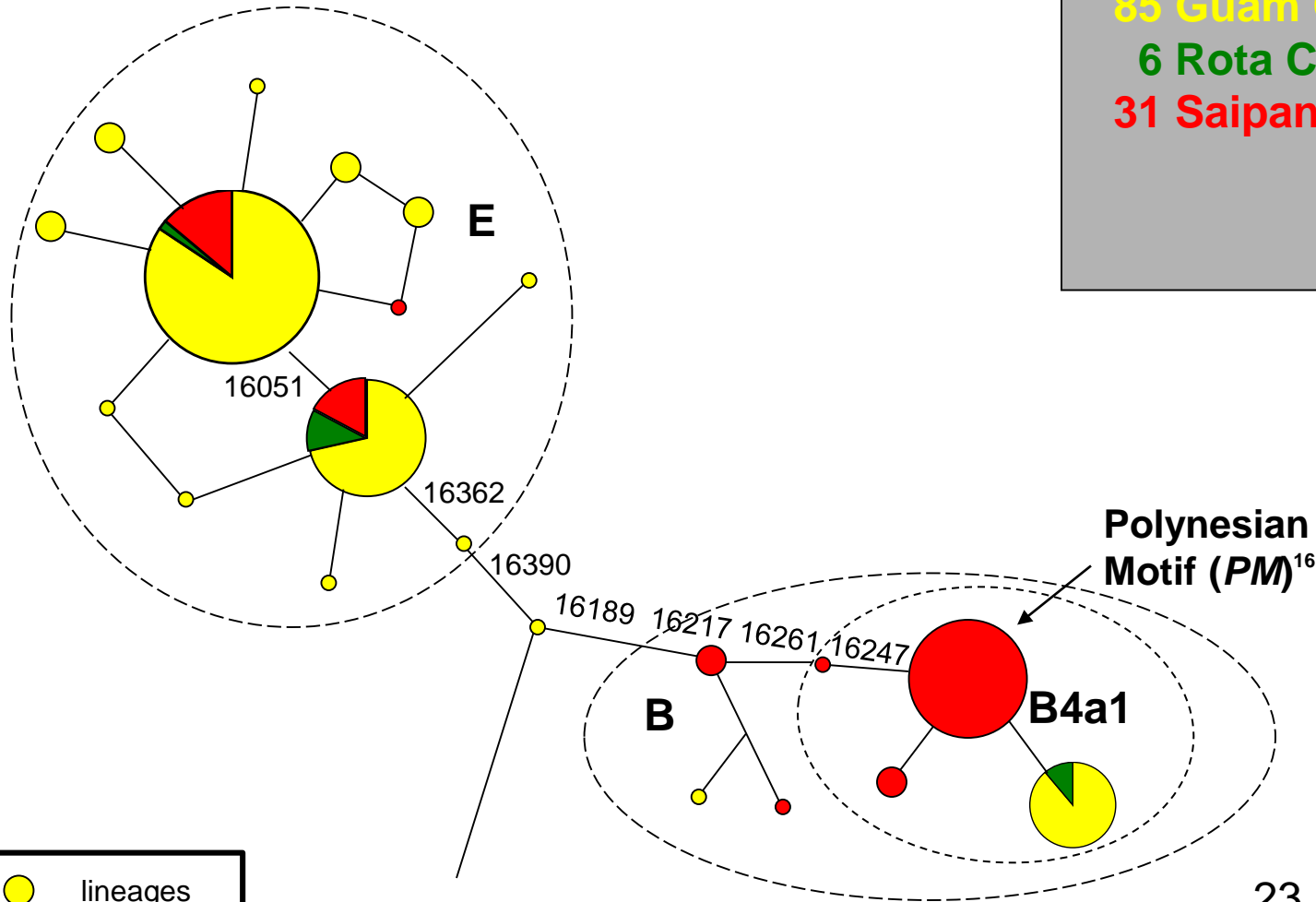
85 Guam Chamorros

6 Rota Chamorros

31 Saipan 14 Chamorros

14 Carolinians

3 Chamolinians



Haplogroup E:

16223, 16362,
16390

Haplogroup B4a1:

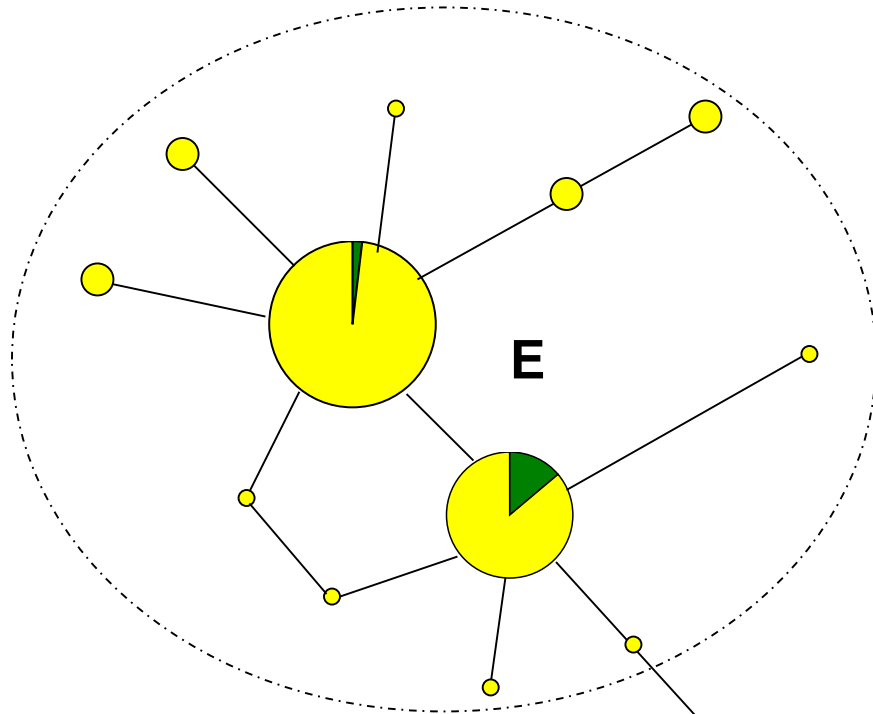
16189, 16217,
16261

Haplotype B4a1a(PM)



16189, 16217, 16247,
16261

23 unique haplotypes
25 polymorphic sites
across HVs1

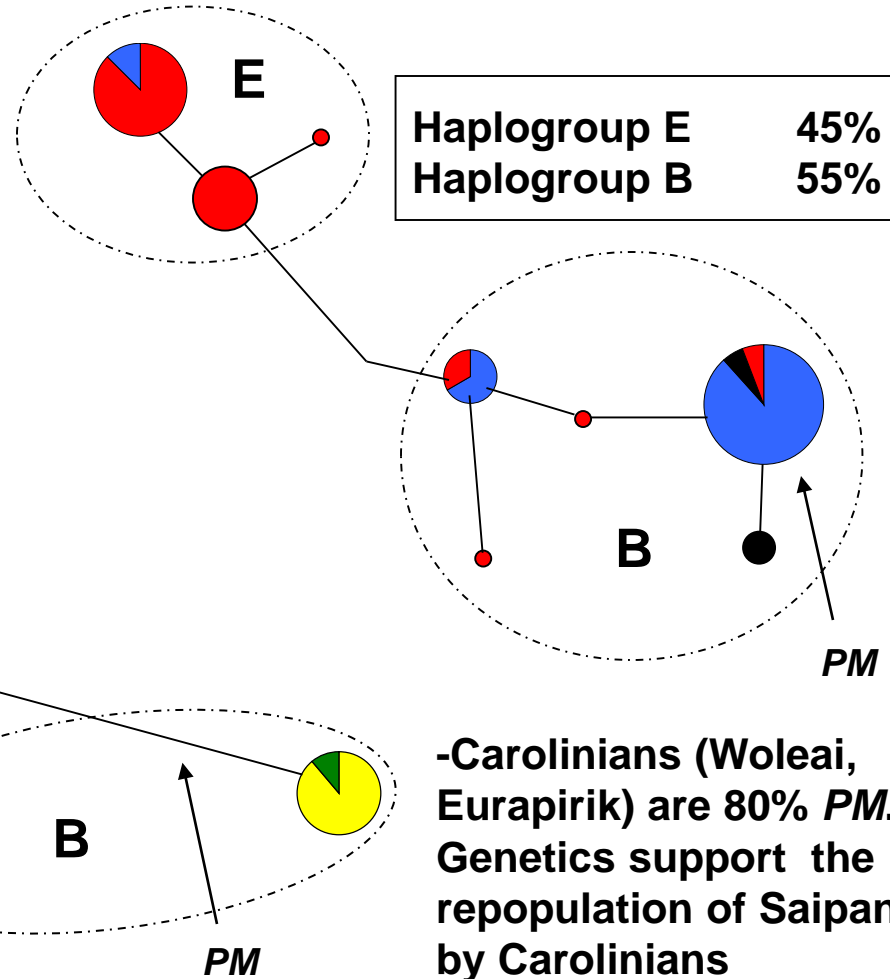
Guam and Rota



Haplogroup E	89%
Haplogroup B	11%

	lineages
	mutations

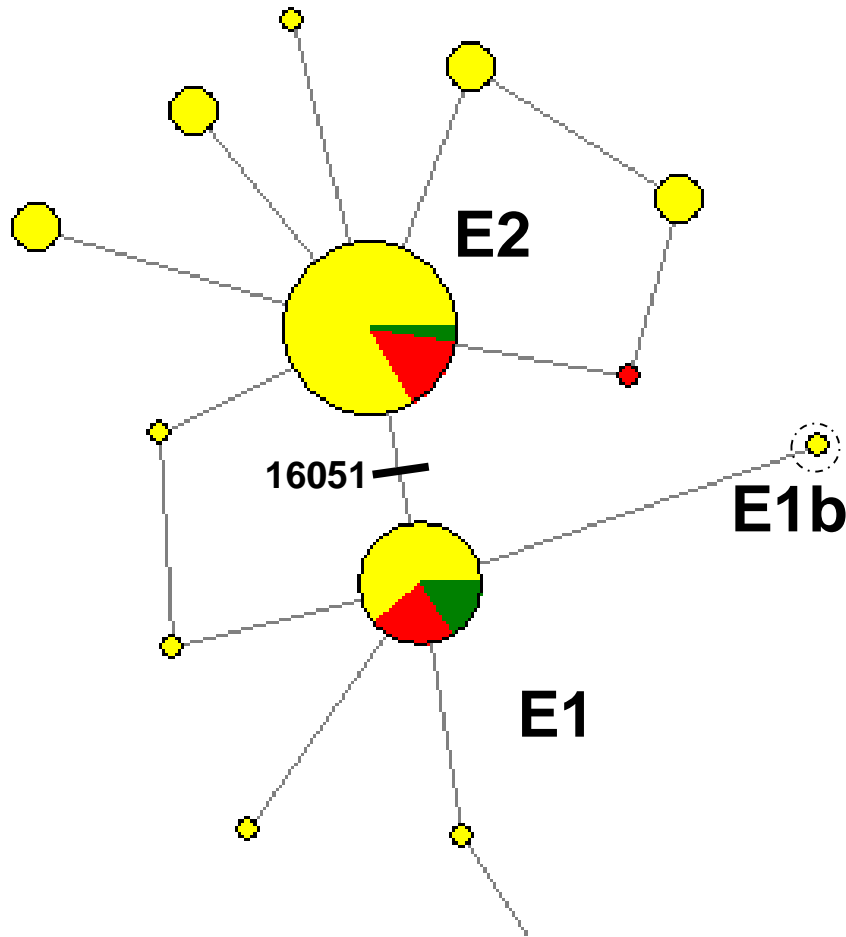
Saipan Chamorros, Carolinians Chamolinians



Haplogroup E	45%
Haplogroup B	55%

-Carolinians (Woleai, Eurapirik) are 80% *PM*.
Genetics support the repopulation of Saipan by Carolinians

Chamorro Haplogroup E

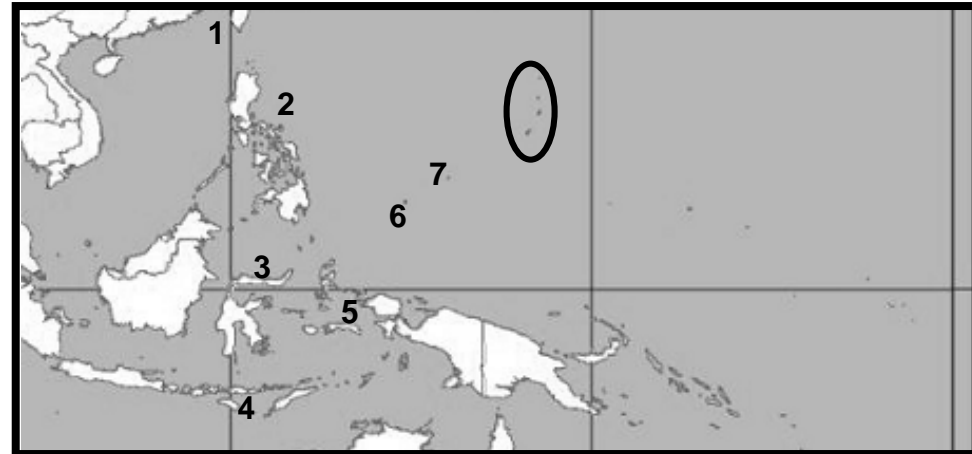


-E1 and E2 differ by one HV1 mutation (16051)

Times of Coalescence

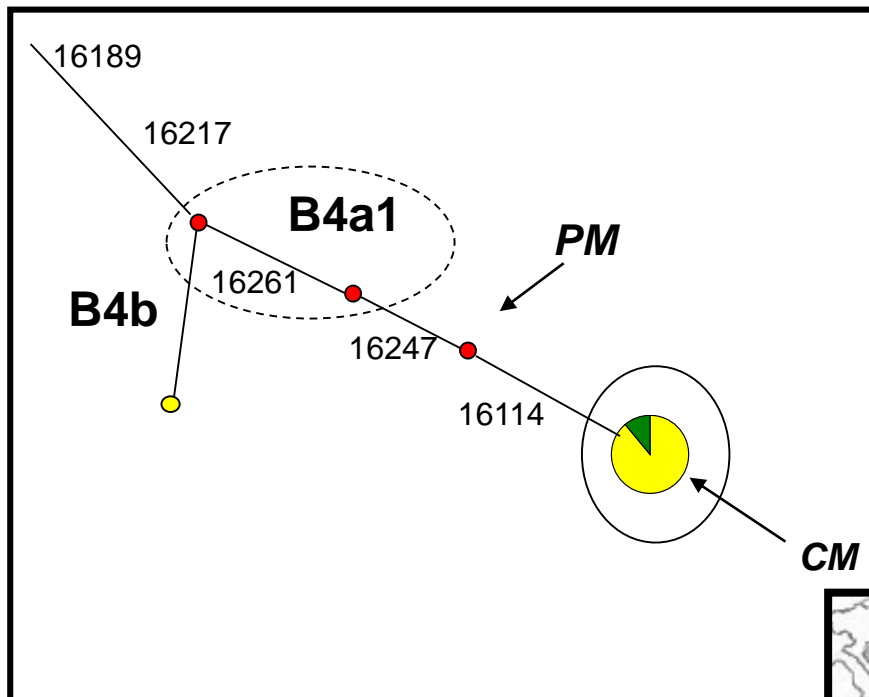
E1	2,777 +/- 1,241 years
E2	5,720 +/- 2,667 years
E	9,963 +/- 5,486 years

	E	E2	E1	E1b
Chamorros	.89	.61	.28	.01
1 Taiwan ¹⁶	.12	.03	.09	-
2 Philippines ¹⁶	.10	.02	.08	-
3 Sulawesi ¹⁶	.26	.03	.23	.03
4 Sumba	.16	.02	.14	.12
5 Moluccas ¹⁶	.17	.05	.12	-
6 Palau ¹⁸	.03	-	.03	-
7 Yap ¹⁸	.06	-	.06	-



-Chamorros frequencies are very different to Yapese and Palauans

Chamorro Haplogroup B4a and the Chamorro Motif (CM)?

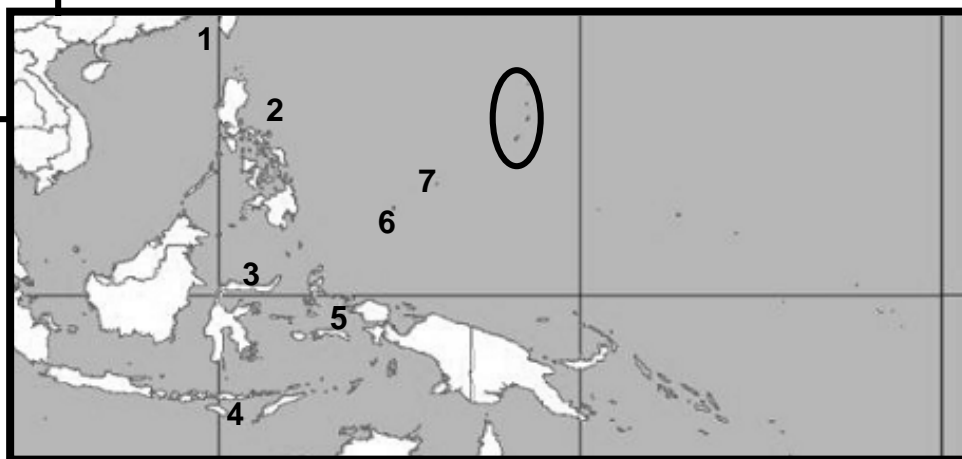


	B	B4a1	PM	CM	B4b
Chamorros	.11	.02	.01	.07	.01
1 Taiwan ¹⁶	.36	.09	-	-	.07
2 Philippines ¹⁶	.23	.11	-	-	.02
3 Sulawesi ¹⁶	.21	.05	.04	-	.01
4 Sumba ¹⁶	.02	.02	-	-	-
5 Moluccas	.28	.09	.14	-	.05
6 Palau ¹⁸	.55	.14	.42	-	.10
7 Yap ¹⁸	.72	.17	.40	-	.07

-B4a1: Taiwan, Philippines, Indonesia, Melanesia, Polynesia, East Asia

-PM: Occurs in >90% of Central/Eastern Micronesians,¹⁸ 40-42% of Yapese and Palauans, and in 30-40% of Island/Coastal Melanesians¹⁷

-The Chamorro Motif (CM) is unique to Chamorros of Guam and Rota.

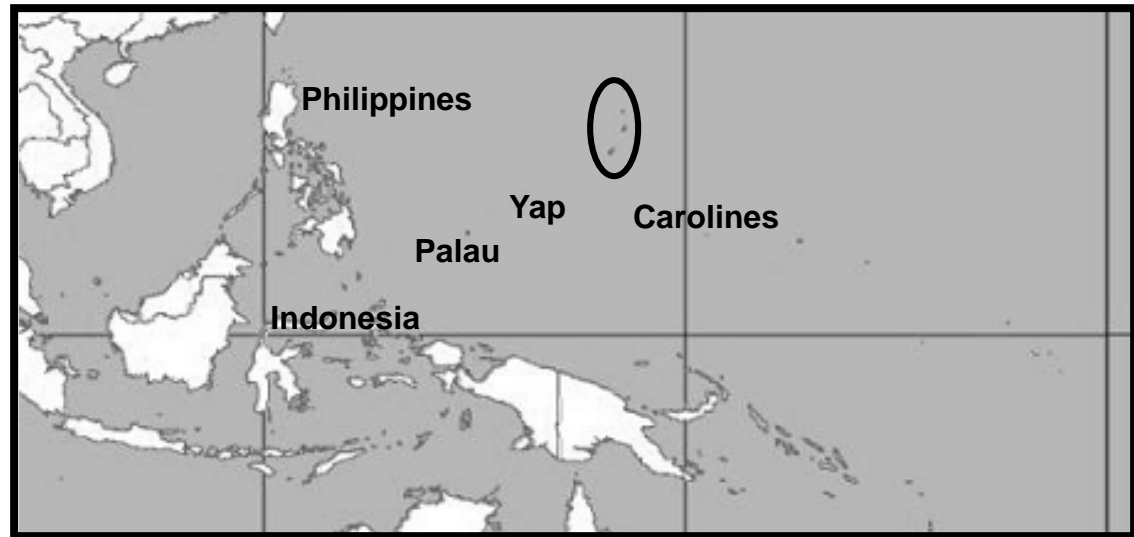


-Chamorros frequencies are very different to Yapese and Palauans

In search of the Chamorro Motif?

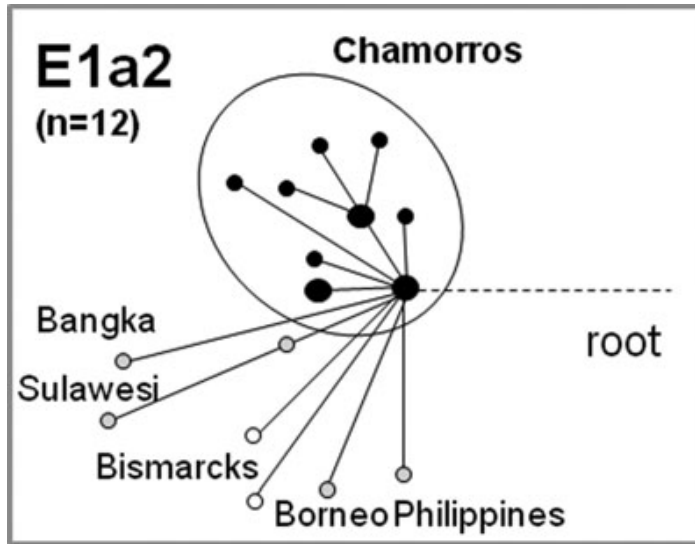
16114, 16189, 16217, 16247, 16261

- More than 270 haplogroup B4a1 individuals from Micronesia were sampled:
 - 141 from the Outer-Islands of Yap/ Carolines (Ulihi, Woleai, Eurapirik)
 - 80% *PM*, 0 *CM*
 - 72 from Yap proper
 - 40% *PM*, 0 *CM*
 - 60 from Palau
 - 42% *PM*, 0 *CM*
- Eastern Indonesia
 - 4 - 14% *PM*, 0 *CM*
- Philippines
 - 0% *PM*, 0 *CM*

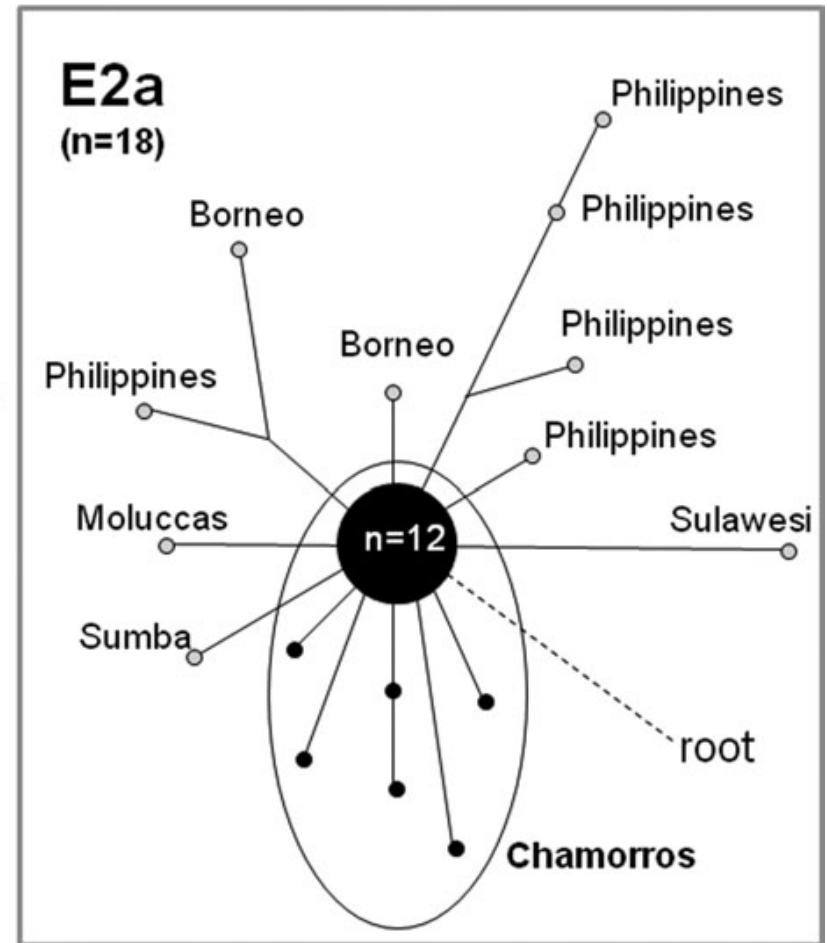


Did the Chamorro Motif arise on the Marianas?

Complete mtDNA genome analyses (n=30)



- n=1
- n=2
- Chamorros
- ISEA
- Oceania

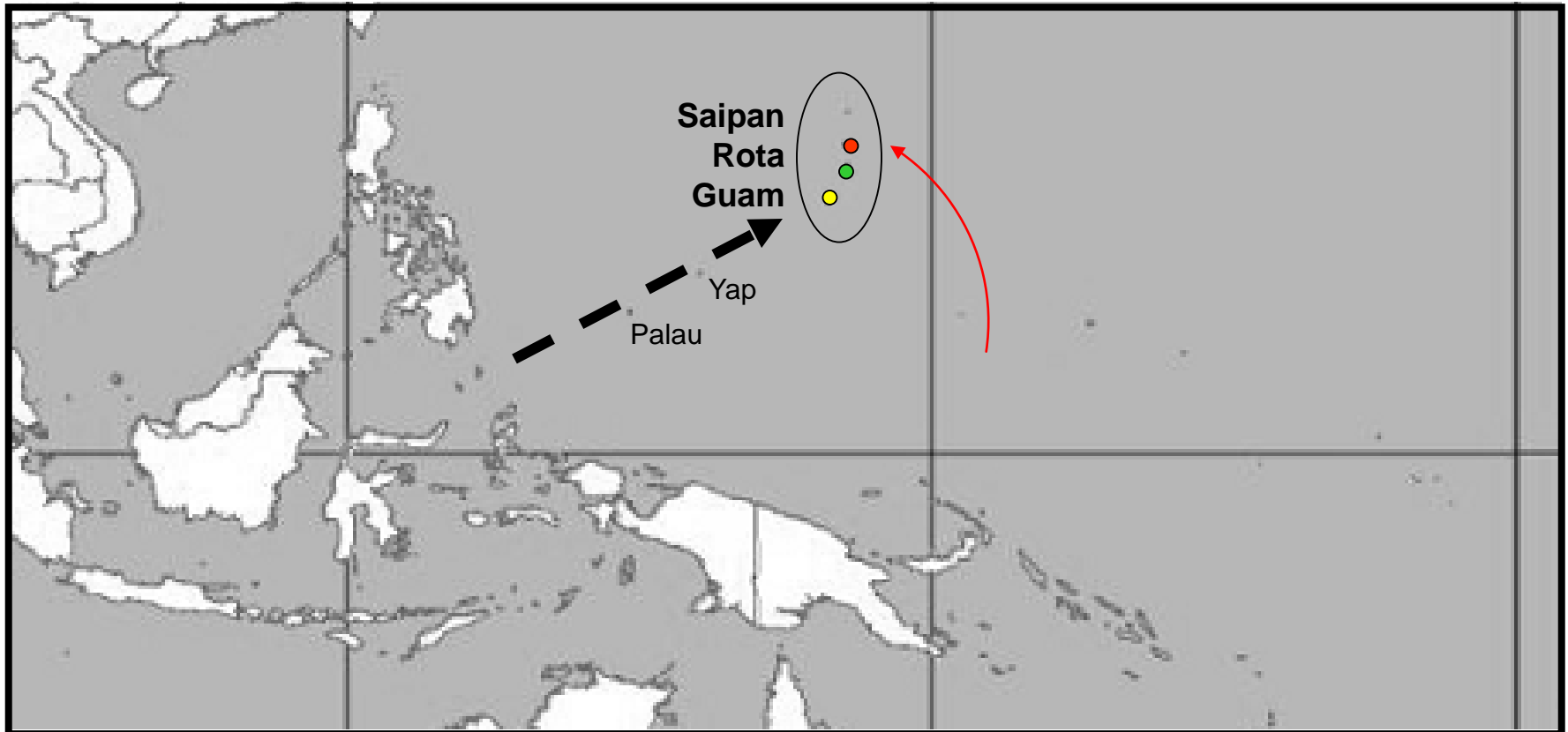


-Seven HVR1 haplotypes (3 E1, 4 E2) yielded sixteen unique mtDNA complete genome haplotypes. None of these haplotypes are shared with any other populations.

-Two Migrations? (1) Diversity of E1 and E2 indicate a old (*pre-latte*) introduction. Anthropologists (Soares et al 2008) suggest E1a and E2a originate in Eastern Indonesia between 5,000 and 10,000 years ago, thus a likely source for the E1a and E2a types among Chamorros. (2) B4a haplotypes (*CM*) are younger, likely new migration.

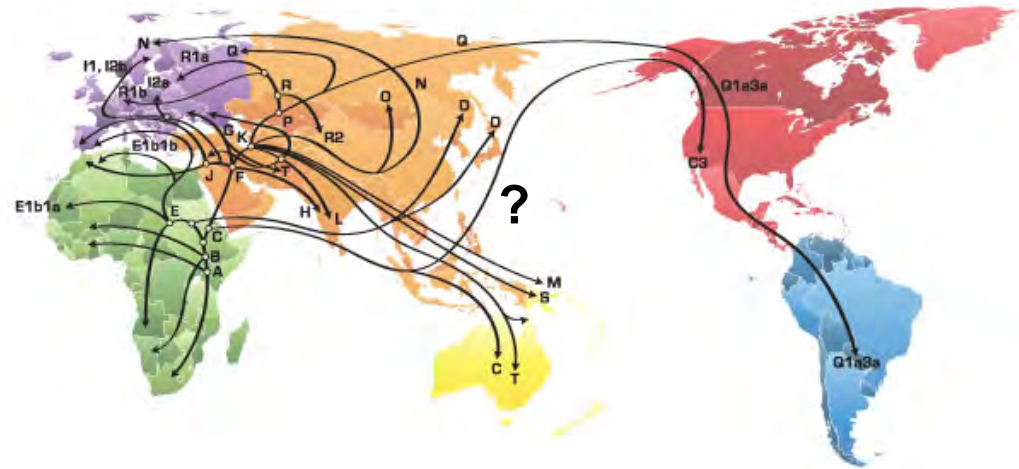
Conclusions

- Genetics support the linguistic and archaeological evidence of a Chamorro origin in ISEA
- E1 and E2 came to the Marianas early (~4,000BP) already differentiated and reached their unique high frequencies found in the Chamorros through genetic drift, followed by isolation.
- Limited gene flow from the Carolines, Yap, and Palau to Guam and Rota, but strong connection with Saipan supports replacement on Saipan, but nowhere else
- The *CM*, which has no known variants, possibly came more recently from ISEA with the appearance of the *Latte* structures and rice
- It likely arrived with the 16114 mutation, since there is no ancestral *PM* in Guam and Rota

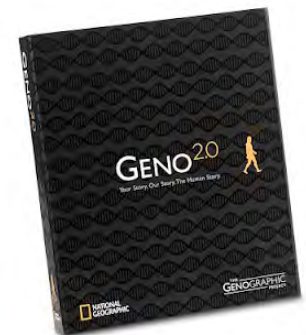


New Questions & Future Directions

- Y Chromosome DNA variation
 - Strictly inherited by father to son
 - Will it be similar to mtDNA?
 - Will is how admixture with Spain, Philippines and/ or Mexico?
 - What was the impact of historic depopulation on the Y-chromosome DNA?



- Autosomal DNA variation
 - Will be analyzed through SNPs microarray
 - Earlier work on autosomal STR found some similarities between Chamorro and Filipino populations. Will SNP analysis show the same pattern?
- Through a recent NGS grant we will begin looking at autosomal diversity (GenoChip), and this study will help answer questions of genetic admixture



GenoChip Autosomal SNPs

GenoChip is a chip based assay for SNP (mutation) detection designed to identify known anthropologically relevant mutations (130,000 SNPs)

Example from Puerto Ricans (20 participants)

24% SubSaharan African

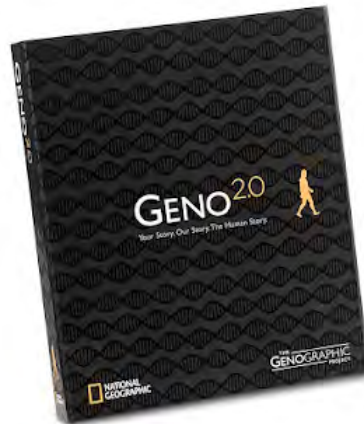
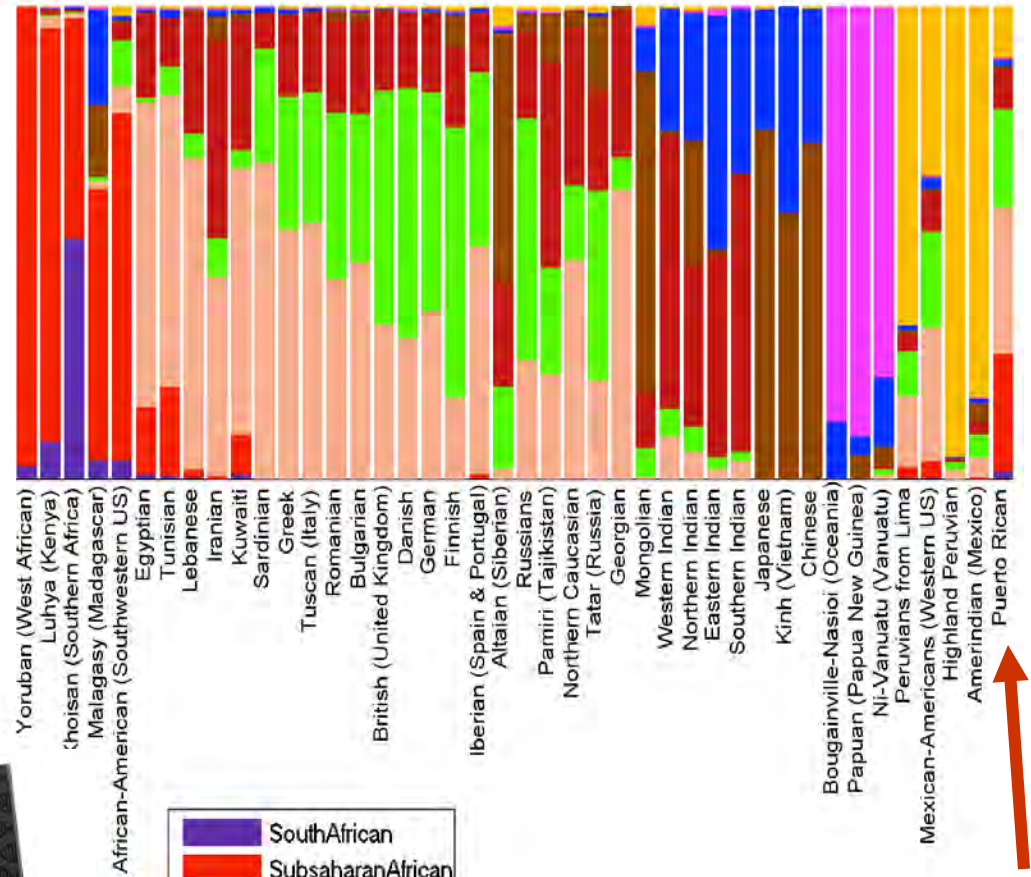
32% Mediterranean

18% Northern European

9% Southwest Asian

14% Native American

3% Other



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Thank you!

