Agent-based Simulation of Population Dynamics in the Japanese Archipelago based on Osteological, Genetic, Ethnographic and Archaeological Data — A Case Study on Migration and the Spread of Rice Agriculture in the Yayoi Period

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Introduction

In this study we use an Agent-based Simulation (ABS) based on osteological, genetic, ethnographic, and archaeological data to examine demographic questions regarding the Yayoi period. Specifically, we focus on estimating the number of migrants to Japan from continental Asia and modeling the spread of rice cultivation during this period. “PAX SAPIENTICA”, an open-source GIS software with ABS functionality, was built upon and used. Multiple simulations were conducted, changing experimental variables to evaluate the validity of demographic hypotheses.

1. Simulation Structure

1.1. Spatial Dimension

The simulation area consists of Honshu, Shikoku, and Kyushu. A 10496 by 10496 cell grid was used, with each cell being 125 by 125 meters. Geographic data consists of three elements: a slope map, a land / sea map, and a region map. The boundaries of Nara–Heian period provinces were used for regions.

Agents can only occupy cells that satisfy the requirements for habitation. The cell must be on land (not sea, lake, or river) and cannot be in mountainous terrain (determined by slope). Agricultural agents must also reside in arable land, defined here as land within 5 km (40 cells) of a lake or river.

1.2. Human Agents

Human agents are composed of the following attributes:

- **ID:** Unique ID for the agent.
- **Group ID:** ID of the agent’s group.
- **Sex:** Male or Female.
- **Subsistence:** Hunter-gatherer or Agricultural
  At the start of the simulation, all agents in Japan are hunter-gatherers. Migrants from continental Asia are agricultural.
- **Longevity & Age:** Based on model tables derived from osteological data.[1] Hunter-gatherers’ life table is calculated from Jomon period human remains, while Agriculturalists’ life table is calculated from Yayoi period human remains. Data retrieved from the Kyushu University osteological database.[2] As there are few human remains of juveniles, ethnographic and historical estimates (Volk & Atkinson 2013)[3] were used to determine their mortality rate. The Child Mortality Rate (CMR; mortality rate from 0–15) was set at 50% for hunter-gatherers, and 45% for agriculturalists. Based on analysis of the life tables, we can expect a 0.1% growth rate for Jomon hunter-gatherers, and a 1.4% growth rate for Yayoi agriculturalists.
- **mtDNA:** Based on genetic research, human agents were assigned Mitochondrial DNA (mtDNA) values. Agents in Japan at the start of the simulation have values appropriate to their region from the Jomon period. Continental migrants have a random haplogroup of Asian origin that is present in Yayoi and Kofun period populations. Probability is based on the relevant haplogroup distribution.
- **Heritage:** An abstract representation of genetic heritage. Jomon = 0.0, Continental = 1.0. Children inherit the average heritage value of their parents.
- **Partner:** Records the ID, subsistence, and heritage of an agent’s spouse.

1.3. Group Agents

Group agents are a collection of human agents and represent a settlement, or a part of a settlement. Each group has a unique ID and an XYZ tile coordinate. Limited to 1 cell (125m x 125m area). When 100% of agents are of agricultural subsistence, the maximum population of a group is 80 people (based on the population density of the Karako-Kagi site). When 100% of agents are of hunter-gatherer subsistence, the maximum population of a group is 25 people. Mechanically, agricultural agents are assigned a cost of 1/80 while hunter-gatherers have a cost of 1/25, and a settlement splits when the cost value exceeds 1. When a settlement splits, a new group agent is formed in a nearby cell.

1.4 Execution Sequence

After initialization, the simulation is executed in steps. The execution sequence of each step is as follows. Group agent movement → Continental migration → Marriage→ Pregnancy & Birth → Death (end of step). 1 step is set to 1 month. Agent actions are performed in order of the array in which they appear. Agent attributes (including age in months) are updated at the end of each step.

After an agent's attributes are updated, if their monthly age exceeds their allotted lifespan (probabilistically determined at birth) then they die and are erased. When an agent’s spouse dies, they can remarry starting from the next step. The attributes of an agent’s group are updated after their death.

In this simulation, initialization begins from 1101 BC and attributes are recorded starting from 1001 BC. The initial number of agents is set to values which represent the population of the Final Jomon period, based on estimates derived from Koyama (1978).[4] Population estimates, originally divided into modern Japan’s 47 prefectures, were recalculated at a regional level (to match Nara–Heian period provinces).

1.5 Submodels

- **Continental Migration:** Migrants arrive in Chikuzen.
- **Marriage Age:** 13–60 for females, 17+ for males.
- **Marriage Rate:** Based on Washio (2018).[5]
- **Spouse Selection:** Random spouse within range.
- **Residence Pattern:** Probability of matrilocal residence.
- **Pregnancy:** Lognormally distributed between 15–50.
- **Birth:** Occurs 10 steps (months) after pregnancy.
- **Migration weight:** Agents have a higher chance of migrating in certain directions when moving over 20 km. Weights are set to encourage likely migration routes.

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[1] Details: github.com/stephenwest470/Remains2LifeTable
[2] http://db.museum.kyushu-u.ac.jp/anthropology/
[3] Volk, Anthony A., and Jeremy A. Atkinson. “Infant and Child Death in the Human Environment of Evolutionary Adaptation.” Evolution and Human Behavior 34, no. 3 (2013): 182–92.
[4] Koyama, Shuzo. “Jomon Subsistence and Population.” Senri Ethnological Studies 2 (1978): 1–65.
[5] Washio, Yuko. “Marital Customs in Changsha (A.D.235-237) : Marriage and Age”. Tōyōgakuhō: Tōyōbunko Wabun Kiyō 97, no. 1 (2018): 1-24.

2. Experiments

2.1. Evaluation Criteria (A)

- **Population at 50 AD.** Expectation: 594,000 people.[6]
- **Continental Heritage.** Expectation: 70% of population. (Expectation based on the ratio of Asian haplogroups to indigenous haplogroups in the Yayoi–Kofun period)
- **Diffusion of Agriculture.**
  Expectation: Distribution in line with Fujio (2009).[7]
  - 950 BC: N. Kyushu.
  - 750 BC: S. Kyushu, Chugoku, Kinki
  - 600 BC: Tokai
  - 360 BC: Hokuriku (and N. Tohoku)
  - 200 BC: Chubu, Kanto, and S. Tohoku

2.2. Experimental Variables (B–O)

See Figure 1.

2.3. Comparative Analysis

The central value for each experimental variable was chosen to form the base model (B). A simulation was run for each variable changed from the base model. Using the evaluation criteria, the results of each simulation were compared to those of the base model in order to understand the effects of each variable. The plausibility of each simulation model was evaluated by comparing simulation results with expected values for the evaluation criteria (A).

		Population (tens-of-thousands)	Continental heritage %	Agriculture distribution
	A Expected values	59.4 ↑	70% ↑	5. to N. Tohoku
	B Base model	44.4 —	62% —	4. to S. Tohoku
	Variable	Population (tens-of-thousands)	Continental heritage %	Agriculture distribution
Migration Start Base: 950BC	C 800BC	28.5 ↓	60% ↑	3. to Kanto
Migrants per month Base: 5	D 1	17.6 ↓	39% ↓	3. to Kanto
	E 10	83.2 ↑	74% ↑	4. to S. Tohoku
Residence pattern Base:Selective	F Matrilocal	28.0 ↓	65% ↑	4. to S. Tohoku
	G Patrilocal	68.2 ↑	55% ↓	4. to S. Tohoku
Marriage distance Base: <20km	H <10km	33.7 ↓	68% ↑	4. to S. Tohoku
	I <40km	58.3 ↑	55% ↓	4. to S. Tohoku
Migration rate Base: 0.21%	J 0.14%	48.3 ↑	62% —	3. to Kanto
	K 0.42%	53.4 ↑	53% ↓	5. to N. Tohoku
Migration distance Base:<200km	L <100km	48.1 ↑	71% ↑	2. to Tokai
	M <400km	55.6 ↑	43% ↓	5. to N. Tohoku
Agriculture inheritance Base: 50%	N 25%	11.1 ↓	45% ↓	1. to N. Kyushu
	O 75%	78.3 ↑	36% ↓	5. to N. Tohoku

Figure 1: Experimental Variables and Results

3. Discussion

3.2. Start date of migration from Asia (C)

As there is no consensus on the start date of the Yayoi period, the start date of migration from Asia is unclear and was made an experimental variable. The C-Model (800 BC start) resulted in an unrealistically low population, but the proportion of continental heritage did not change significantly. Later start dates likely require a higher number of continental migrants.

3.1. Continental migrants per month (D, E)

The B-Model resulted in a population somewhat lower than the expected value, while the E-Model resulted in a population slightly higher than the expected value. Although there are other influential variables, we can estimate that the number of continental migrants was between 5–10 people per month, or 60–120 people per year.

3.3. Marriage residence pattern (F, G)

The F-Model (matrilocal residence) saw lower population growth and higher spread of continental heritage and mtDNA, while the G-Model (patrilocal residence) showed the opposite trend. The cause of the population discrepancy is unclear and may be the result of an error.

3.4. Marriage distance (H, I)

There is a positive correlation between population growth and marriage distance, and a negative correlation between continental heritage spread and marriage distance. Limiting marriageable distance increases the number of agents who cannot marry, thus inhibiting population growth.

3.5. Migration rate (J, K)

The monthly chance of group migration affects the speed and extent of the diffusion of agriculture. In the J-Model (0.14%; approx. 1/60 years), agriculture spreads as far as Tokai, in the B-Model (0.21%; approx. 1/40 years) it spreads to S. Tohoku, and in the K-Model (0.42%; approx. 1/20 years) it spreads rapidly, reaching N. Tohoku. The B-Model was most consistent with Fujio (2009).

3.6. Migration distance (L, M)

A lower migration distance maximum (L-Model; <100km) led to a lower dispersion of agricultural subsistence, while a higher maximum (M-Model; <400km) led to a higher dispersion. When migration distance is increased, agriculture is able to spread to Jomon agents at an earlier stage, leading to higher reproduction and a higher proportion of agents with Jomon-heritage. The B-Model (<200 km) most closely matched the evaluation criteria.

3.7. Agricultural inheritance rate (N, O)

Applies when an agriculturalist and hunter-gatherer produce offspring. At 25% (N-Model), agricultural subsistence fails to spread beyond N. Kyushu and continental-heritage hunter-gatherers spread across Japan. At 75% (O-Model), agriculture spreads extremely quickly and predominantly Jomon-heritage agriculturalists become the majority population of the Japanese archipelago.

Conclusion

We were not able to replicate the expected values of the evaluation criteria, but we were able to clarify the effect of certain variables on Yayoi demography. We can conclude that during the 1000 years between the Initial Yayoi and Middle Yayoi periods there were likely 60,000–120,000 migrants from Asia, and their mitochondrial DNA and agricultural subsistence pattern was able to spread across the Japanese archipelago via periodic long-distance migration and short-distance intermarriage with indigenous hunter-gatherers. In the future we hope to improve the capabilities of the simulation so that it may better replicate the archaeological reality and test additional demographic hypotheses.

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[6] Koyama, Shuzo, and Shigenobu Sugito. “A Study of Jomon Population : Computer Simulation Analysis.” Bulletin of the National Museum of Ethnology 9, no. 1 (1984): 1–39.
[7] Fujio, Shinichiro. “Details of the Research, the Results and Issues.” Bulletin of the National Museum of Japanese History 149 (2009): 1–30.

GitHub YouTube Details