Relation between Word Order of Languages and the Entropy of Mitochondrial DNA Haplogroups Distribution of the Speakers' Population in Eurasia

ユーラシア大陸における言語の語順とその話者集団の ミトコンドリア DNA ハプログループ分布のエントロピーとの関係

Terumasa EHARA 江原暉将

Ehara NLP Research Laboratory 江原自然言語処理研究室 http://www.ne.jp/asahi/eharate/eharate/

1 Introduction

We are investigating the relation between the word order of languages (we focus on OV: object verb versus VO: verb object) and the speakers' thought pattern. We have approached it through diversity of DNA of the speakers' population.

Higher diversity of DNA means that the population has the cooperative thought pattern and lower diversity of DNA means that the population has the competitive thought pattern.

The diversity of DNA was measured by the entropy of haplogroup (Hg) distribution. Our conjecture is that OV language speakers' population has higher entropy value and VO language speakers' population has lower entropy value.

Ehara (2018) showed that OV language speakers' population have higher entropy value of Y-chromosome DNA haplogroup (YHg) than VO language speakers' population. Ehara (2019) showed that OV language speakers' population have higher entropy value of Mitochondrial DNA haplogroup (MtHg) than VO type language speakers' population.

Ehara (2019) treated the data only from Europe and the surrounding area. In this paper, we will analyze the data from larger area, Eurasia.

2 Data

Data for the word order features (OV/VO) are obtained from the WALS online database (Dryer, 2013) and many other web sites. MtHg data of populations are obtained from 1000 Genomes Project (Rishishwar, 2017). From Rishishwar (2017), we can obtain the MtHg data of 2054 samples (individuals) from 26 worldwide populations. We estimate native languages spoken by these populations. We can recognize 22 languages in these data. We exclude the data that native languages aren't estimated. Populations and languages in our analysis are listed in Appendix 1 (Table A2).

The data include 26 macro MtHgs : G={ L0, L1, L2, L3, L4, L5, D, F, G, N, Y, Z, H, I, J, K, T, V, W, X, U, M, R, A, B, C } (see Table A1).

The entropy by Hgs for each language l: H(l) is calculated by

$$H(l) = -\sum_{g \in G} p(l,g) \log_{n(G)} p(l,g)$$

where p(l, g) is the probability (relative frequency of samples) of the Hg g for the language l and n(G) is the number of Hgs (in our case n(G)=26).

3 Method of the analysis

We conduct t-test for the entropy value of OV and VO word order groups. Contrary to the conjecture, t-score of OV versus VO is negative (-1.76408) shown in Table 1 (a). It means that OV language speakers' population have lower diversity of DNA than VO language speakers' population (although this statement is not significant with significant level 5%). To deal with the problem, we will use the concept of "artificial sub haplogroup".

Table	1.	Т	test	res	ults
-------	----	---	------	-----	------

	OV	VO							
Ν	9	13							
Mean	0.4369	0.4985							
Unbiased var.	0.0043	0.0059							
Т	-1.9	6385							
Two sided P	0.0636								
(a) T-test result with macro HGs									

	OV	VO						
N	9	13						
Mean	0.677	0.6507						
Unbiased var.	0.125	0.0068						
Т	0.63732							
Two sided P	0.53114							
(b) T-test result with sub HGs								
	OV	VO						
Ν	6	8						
Mean	0.7478	0.7071						
Unbiased var.	0.001	0.0009						
Т	2.48515							
Two sided P	0.02869							

(c) T-test result with sub HGs only from Eurasia

	OV	VO							
N	18	40							
Mean	0.7917	0.7429							
Unbiased var.	0.0029	0.0059							
Т	2.44	4314							
Two sided P	0.01774								
(d) T-test result with sub HGs									
C									

from Europian and sorounding areas

3.1 Artificial sub haplogroup

Hgs listed in G are macro Hgs and they have different sizes. For example, Hg M is large and Y is small. We define the size of Hg by the number of mutations, insertions and deletions in the Hg. These numbers are obtained from PhyloTree¹ (van Oven and Kayser, 2008) and listed in Table 2.

Table 2.	Macro	haplogroups	and	their	sizes
----------	-------	-------------	-----	-------	-------

Hg	А	В	С	D	Е	F	G	Η	HV
Size	389	725	300	750	53	254	167	1395	181
Hg	Ι	J	JT	K	L0	L1	L2	L3	L4
Size	131	443	3	355	615	421	368	564	99
Hg	L5	L6	М	N	0	Р	Q	R	S
Size	108	27	2192	464	14	159	123	601	61
Hg	Т	U	V	W	Х	Y	Z	1	
Size	393	1110	80	107	188	29	70		

 $^{\rm 1}$ Actual data are obtained from

https://www.phy-

 $lotree.org/builds/mtDNA_tree_Build_17.zip.$

We define the number of sub Hgs (SHgs) of a macro Hg by the rounded up value of size/100. For example, the number of SHg of macro Hg M is 22 and macro Hg Y is 1. These SHgs are defined artificially. So, we call them "artificial sub haplogroups".

3.2 Distribution within artificial sub haplogroups

We distribute relative frequency of the macro Hg g to its artificial SHgs. Uniform distribution may be too diverse. So, we use Gaussian like distribution within SHgs. Precisely, when m(g) is the number of SHgs of a macro Hg g, i th SHg (i=1,...,m(g)) has the relative frequency r(i, g): r(i, g)

$$= \begin{cases} cdf(-3+6i/m(g)) \times R(g) & (i=1) \\ \{1-cdf(-3+6(i-1)/m(g))\} \times R(g) & \\ (i=m) \\ \{cdf(-3+6i/m(g)) - cdf(-3+6(i-1)/m(g))\} \times R(g) \\ (else) & \\ \end{cases}$$

where cdf() is the standard Gaussian cumulative distribution function and R(g) is the relative frequency of macro Hg g.

The equation of entropy calculation is not changed except for G is the set of all artificial SHgs.

4 Results

4.1 Results from the data of the present paper

Using artificial sub haplogroups, we re-calculate the entropy for the data and re-conduct ttest. The result are shown in Table 1 (b). The Tvalue is positive (0.63732), however, two sided P is extremely large and the conjecture is not significant by these data.

We restrict the data only from Eurasia, excluding four data from Africa (Esan, Mandinca, Luhya and Yorba) and three data from America (Arawak, Zapotec/Chontal and Quechua/Aymara). The result is shown in Table 1 (c). The Tvalue is positive (2.48515) and two sided P is small enough which is significant with significant level 5%. The detail of the calculation results are shown in Appendix 1.

Figure 1 shows the ranking of the entropy values for each language speakers' population from

lower to higher. African and American populations rather have lower entropy value.





4.2 Results from the data of previous paper

Applying our artificial sub haplogrouping method to the data of previous paper (Ehara, 2019), we obtain the result shown in Table 1 (d). The T-value is positive (2.44314) and two sided P is small enough which is significant with significant level 5%.

5 Conclusion

Relation between word order (Object (O) / Verb (V)) of languages and the entropy of Mitochondrial DNA haplogroups distribution of the speakers' population is examined. T-test results using "artificial sub haplogroup" show OV word order language speakers' population tend to have higher entropy value than VO word order language speakers' population.

The languages used in this analysis are not exhaustive. The number of languages are only 14 from Eurasia. The number of languages in the world are more than several thousand. Analysis using the data from these language speakers is the remaining issue.

References

- Matthew S. Dryer. 2013. Order of Object and Verb and Order of Adjective and Noun, *In: Dryer, Matthew S.* & Haspelmath, Martin (eds.) The World Atlas of Language Structures Online. Leipzig: Max Planck Institute for Evolutionary Anthropology. (http://wals.info/chapter/83 and 87, Accessed on 2015-3-23).
- Terumasa Ehara. 2018. Relation between Word Order of Languages and the Entropy of Y-chromosome Haplogroup Distribution of the Speakers' Population, *Proceedings of The 24th Annual Meeting of The Association for Natural Language Processing*, P10-8, pp.1019-1022, March 2018.
- Terumasa Ehara. 2019. Relation between Word Order of Languages and the Entropy of Mitochondrial Haplogroups Distribution of the Speakers' Population, *Proceedings of The 25th Annual Meeting of The Association for Natural Language Processing*, P2-9, pp.490-493, March 2019.
- Lavanya Rishishwar and I. King Jordan. 2017. Implications of human evolution and admixture for mitochondrial replacement therapy, *BMC Genomics*, Vol. 18, pp.140-150, 2017.
- Mannis van Oven and Manfred Kayser. 2008. Updated Comprehensive Phylogenetic Tree of Global Human Mitochondrial DNA Variation, *HUMAN MUTATION Mutation in Brief*, #1039, 30:E386-E394, Sept. 2008.

Appendix 1 Base data used in the research

Base data used in the research are presented in the following 2 tables.

In Table A1, N means a number of samples. L0, L1, ..., C mean name of macro haplogroup (Hg) (cell values are relative frequency (%) of each Hg in the sample). The last raw of Table A1 indicates the number of artificial sub haplogroups for each macro haplogroup.

In Table A2, feature values for O-V are OV, VO and blank (No data). Feature values for A -N (adjective versus noun) are AN, NA, NDO (No dominant order) and blank (No data). "E by Hg" means the entropy calculated by macro haplogroups and "E by SHg" means the entropy calculated by artificial sub haplogroups.

Area	Population	Ν	L0	L1	L2	L3	L4	L5	D	F	G	Ν	Y	Z	Н	I	J	Κ	Т	V	W	Х	U	М	R	A	В	С
	Esan in Nigeria	- 99	7.071	20.2	27.27	43.43	2.02	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Gambian in Western Division, The Gambia	113	0	13.27	42.48	37.17	1.77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.31	0	0	0	0	0
Africa	Luhya in Webuye, Kenya	101	17.82	7.921	11.88	46.54	4.95	9.901	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.99	0	0	0	0
	Mende in Sierra Leone	85	2.353	20	45.88	28.24	1.176	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.353	0	0	0	0	0
	Yoruba in Ibadan, Nigeria	108	4.63	15.74	35.19	43.52	0.926	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Chinese Dai in Xishuangbanna, China	99	0	0	0	0	0	0	12.12	25.25	0	0	0	0	0	0	0	0	0	0	0	0	0	24.24	14.14	0	19.19	5.051
	Han Chinese in Bejing, China	103	0	0 0	0	0	0	0	22.33	15.53	4.854	7.767	0	0.971	0	0	0	0.971	0	0	0	0	0	18.45	5.825	6.796	11.65	4.854
East Asia	Southern Han Chinese, China	108	0	0 0	0	0	0	0	21.3	14.82	1.852	9.259	0	2.778	0	0	0	0	0	0	0	0	0	17.59	10.19	5.556	14.82	1.852
	Japanese in Tokyo, Japan	104	0	0	0	0	0	0	37.5	5.769	10.58	8.654	0.962	3.846	0	0	0	0	0	0	0	0	0	13.46	0	5.769	13.46	0
	Kinh in Ho Chi Minh City, Vietnam	101	0	0	0	0	0	0	1.98	26.73	0	3.96	0.99	0	0	0	0	0	0	0	0	0	0	32.67	10.89	0.99	20.79	0.99
	Utah residents with NW European ancestry	99	0	0	0	0	0	0	0	0	0	0	0	0	51.52	1.01	8.081	3.03	10.1	3.03	5.051	0	18.18	0	0	0	0	0
Furana	Finnish in Finland	- 99	0	0 0	0	0	0	0	0	0	0	0	0	0	37.37	2.02	7.071	6.061	3.03	4.04	2.02	2.02	36.36	0	0	0	0	0
Europe	British in England and Scotland	92	0	0 0	0	0	0	0	0	0	0	0	0	0	42.39	3.261	10.87	5.435	10.87	0	2.174	5.435	19.57	0	0	0	0	0
	Iberian populations in Spain	107	0	0.935	0	0.935	0	0	0	0	0	1.869	0	0	54.21	0.935	3.738	6.542	7.477	5.607	0	0	16.82	0	0.935	0	0	0
	Toscani in Italy	108	0	0.926	0	0	0	0	0.926	0	0	0	0	0	50	0	7.407	8.333	12.04	1.852	3.704	0.926	13.89	0	0	0	0	0
	Bengali in Bangladesh	86	0	0	0	0	0	0	2.326	1.163	0	0	0	0	1.163	0	2.326	0	0	0	2.326	0	12.79	67.44	9.302	1.163	0	0
	Gujarati Indian in Houston, TX	106	0	0	0.943	1.887	0	0	0	0	0	0	0	0	6.604	0	0.943	0.943	1.887	0	1.887	1.887	14.15	38.68	30.19	0	0	0
India	Indian Telugu in the UK	103	0	0	0	0	0	0	0	0	0	0.971	0	0	1.942	0.971	0.971	0.971	3.883	0	4.854	0	13.59	59.22	12.62	0	0	0
	Punjabi in Lahore, Pakistan	96	0	0	0	0	0	0	0	3.125	2.083	0	0	0	7.292	0	1.042	0	3.125	0	2.083	1.042	11.46	57.29	11.46	0	0	0
	Sri Lankan Tamil in the UK	103	0	0	0	0	0	0	0	0	0	2.913	0	0	11.65	0	0.971	0	0	0	0	0	13.59	48.54	21.36	0.971	0	0
	African Caribbean in Barbados	96	4.167	21.88	39.58	27.08	1.042	0	0	0	0	0	0	0	1.042	0	1.042	0	0	0	0	0	1.042	0	0	1.042	1.042	1.042
	African Ancestry in Southwest US	66	10.61	24.24	21.21	36.36	0	0	1.515	0	0	0	0	0	0	0	0	0	0	0	0	0	1.515	1.515	0	1.515	0	1.515
America	Colombian in Medellin, Colombia	94	1.064	2.128	2.128	4.255	0	0	2.128	0	0	0	0	0	1.064	0	0	0	2.128	0	0	0	0	1.064	0	42.55	35.11	6.383
	Mexican Ancestry in Los Angeles, California	67	0	0	0	0	0	0	13.43	0	0	0	0	0	7.463	0	0	0	0	1.493	1.493	0	2.985	0	0	37.31	22.39	13.43
	Peruvian in Lima, Peru	86	0	0 0	1.163	2.326	0	0	15.12	0	0	0	0	0	1.163	0	0	0	0	0	0	0	0	0	0	16.28	46.51	17.44
1	Puerto Rican in Puerto Rico	105	1.905	4.762	3.81	9.524	0	0	0	Ő	0	Ő	0	0	1.905	0	5.714	0.952	0.952	0	0	0	3.81	0	0	36.19	6.667	23.81
Number of	artificial SHg		7	5	4	6	1	9	8	2	9	C	1	1	14	9	5	4	4	1	9	9	19	24	10	4	9	4

Table A1. Populations, macro haplogroups and relative frequencies (%)

Table A2. Languages, word order and entropy

Area	Population	Language	OV-VO	AN-NA	E by Hg	E by SHg
	Esan in Nigeria	Esan	VO	NDO	0.401	0.525
Africa	Gambian in Western Division, The Gambia	Mandinka	ov	NA	0.377	0.506
Arrica	Luhya in Webuye, Kenya	Luhya	VO	NA	0.473	0.570
-	Mende in Sierra Leone	Mende	OV	NA	0.388	0.508
	Yoruba in Ibadan, Nigeria	Yoruba	VO	NA	0.370	0.503
	Chinese Dai in Xishuangbanna, China	Tai Lue	vo	NA	0.519	0.696
	Han Chinese in Bejing, China	Mandarin	VO	AN	0.650	0.756
East Asia	Southern Han Chinese, China	Cantonese	VO	AN	0.633	0.752
	Japanese in Tokyo, Japan	Japanese	OV	AN	0.570	0.690
	Kinh in Ho Chi Minh City, Vietnam	Vietnamese	vo	NA	0.500	0.696
	Utah residents with NW European ancestry				0.459	0.673
E.	Finnish in Finland	Finnish	VO	AN	0.480	0.689
Lurope	British in England and Scotland	English	VO	AN	0.515	0.695
	Iberian populations in Spain	Spanish	VO	NA	0.472	0.686
	Toscani in Italy	Italian	VO	NA	0.492	0.687
	Bengali in Bangladesh	Bengali	OV	AN	0.358	0.735
	Gujarati Indian in Houston, TX	Gujarati	OV	AN	0.496	0.775
India	Indian Telugu in the UK	Telugu	OV	AN	0.421	0.752
	Punjabi in Lahore, Pakistan	Panjabi	OV	AN	0.454	0.771
	Sri Lankan Tamil in the UK	Tamil	OV	AN	0.428	0.764
	African Caribbean in Barbados				0.466	0.562
	African Ancestry in Southwest US				0.490	0.598
America	Colombian in Medellin, Colombia	Arawak	vo	NA	0.465	0.583
	Mexican Ancestry in Los Angeles, California	Zapotec/Chontal	vo	NA/AN	0.511	0.621
	Peruvian in Lima, Peru	Quechua/Avmara	OV	AN	0.440	0.592
	Puerto Rican in Puerto Rico				0.587	0.639