シンポジウム

日琉諸方言系統論の展望

～日琉諸方言の系統論における統計学的アプローチ～

言語距離の系統解析から ヤポネシア人の由来を考察する

SAITOU LABORATORY
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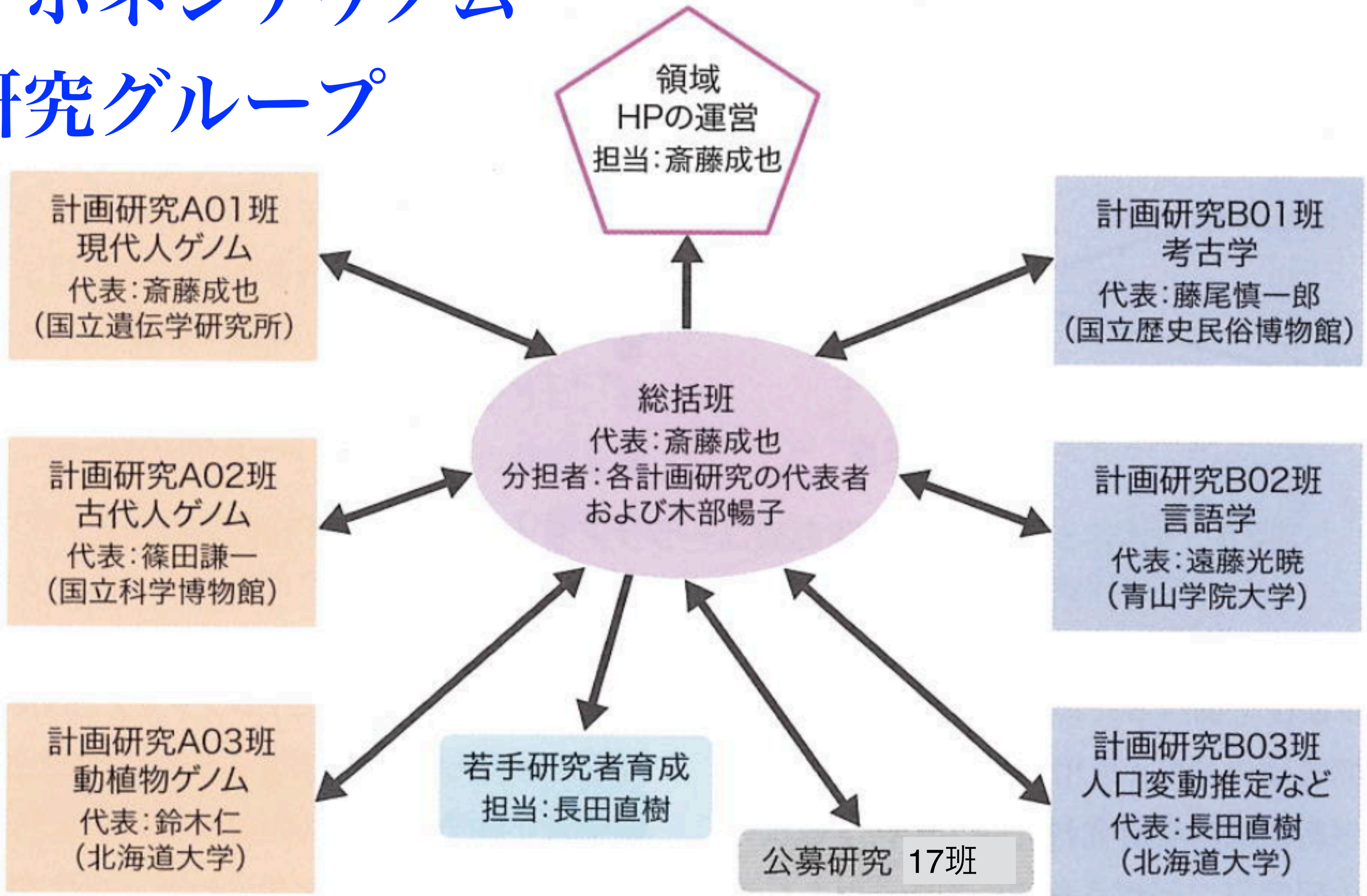
東京大学大学院理学系研究科生物科学専攻　教授 (兼任)

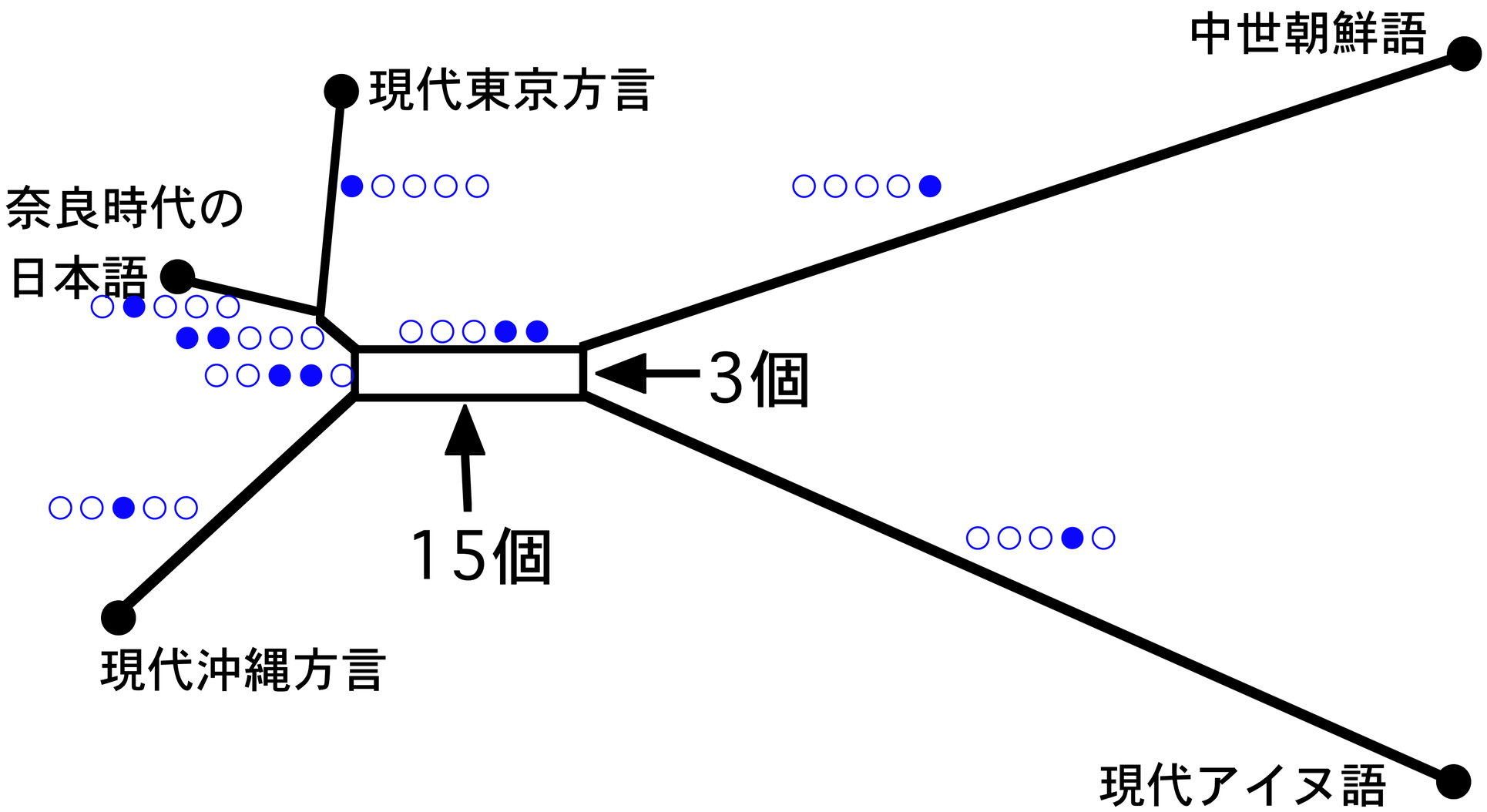
新学術領域研究「ヤポネシアゲノム」領域代表

ヤポネシアゲノム研究グループ



安本・本多 (1978)の収集した基礎語彙100語の語頭子音一致パターンに基づく日本列島周辺の言語の系統ネットワーク

斎藤成也 (2005)『DNAから見た日本人』より



Lee & Hasegawa (2011)

PROCEEDINGS OF THE ROYAL SOCIETY B

Proc. R. Soc. B (2011) **278**, 3662–3669
doi:10.1098/rspb.2011.0518
Published online 4 May 2011

Bayesian phylogenetic analysis supports an agricultural origin of Japonic languages

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Languages, like genes, evolve by a process of descent with modification. This striking similarity between biological and linguistic evolution allows us to apply phylogenetic methods to explore how languages, as well as the people who speak them, are related to one another through evolutionary history. Language phylogenies constructed with lexical data have so far revealed population expansions of Austronesian, Indo-European and Bantu speakers. However, how robustly a phylogenetic approach can chart the history of language evolution and what language phylogenies reveal about human prehistory must be investigated more thoroughly on a global scale. Here we report a phylogeny of 59 Japonic languages and dialects. We used this phylogeny to estimate time depth of its root and compared it with the time suggested by an agricultural expansion scenario for Japanese origin. In agreement with the scenario, our results indicate that Japonic languages descended from a common ancestor approximately 2182 years ago. Together with archaeological and biological evidence, our results suggest that the first farmers of Japan had a profound impact on the origins of both people and languages. On a broader level, our results are consistent with a theory that agricultural expansion is the principal factor for shaping global linguistic diversity.

Keywords: linguistic evolution; phylogenetics; Japonic languages

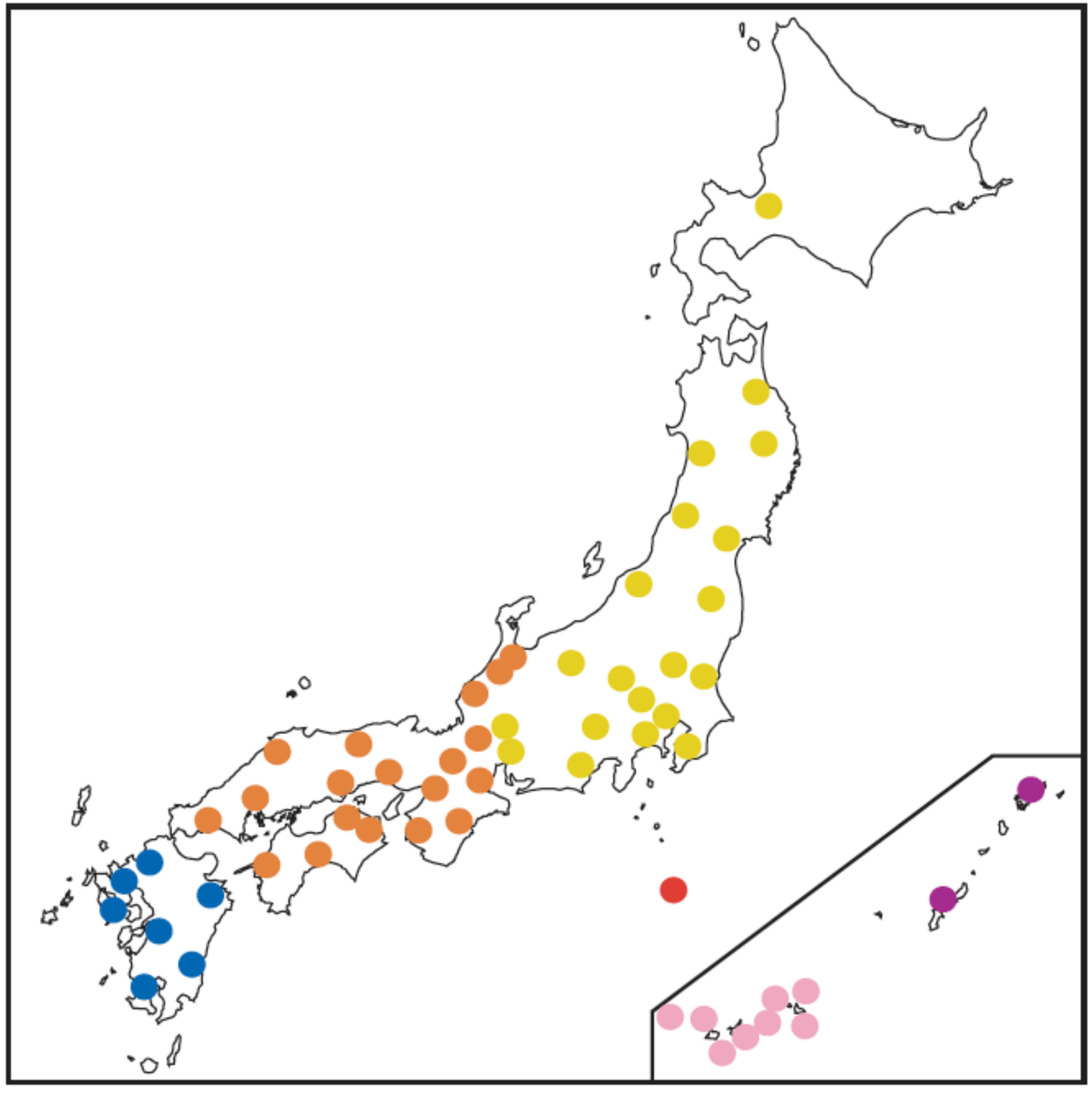
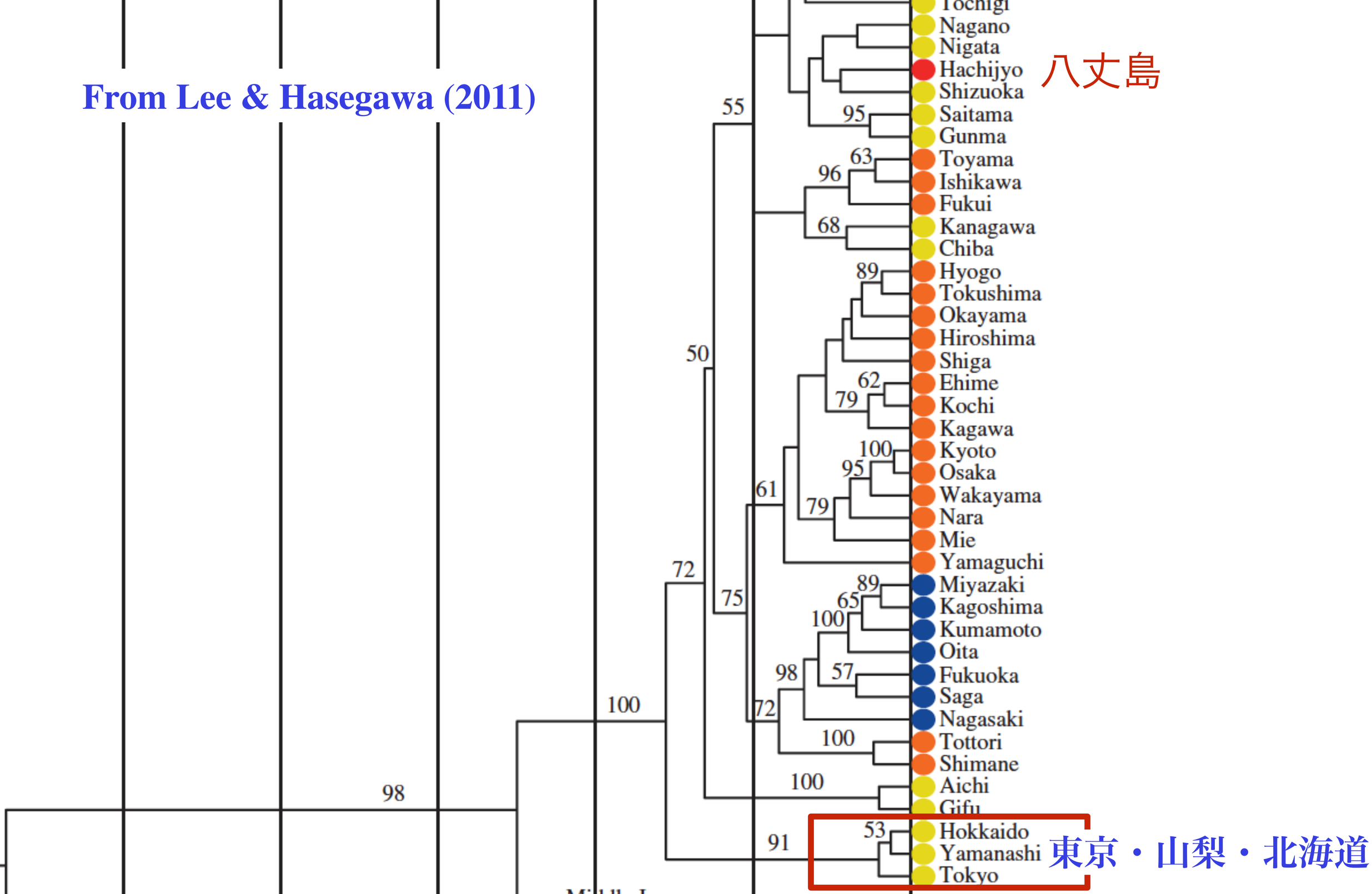


Figure 1. Map of Japonic languages. Subgroups are coded with colour circles: yellow, eastern Japanese; orange, western Japanese; red, Hachijyo; blue, Kyushu; purple, northern Ryukyuan; pink, southern Ryukyuan.

From Lee & Hasegawa (2011)

From Lee & Hasegawa (2011)



日本語方言の近隣結合法を用いた系統樹

東京・山梨・北海道

東北

関東

東海

北陸

関東

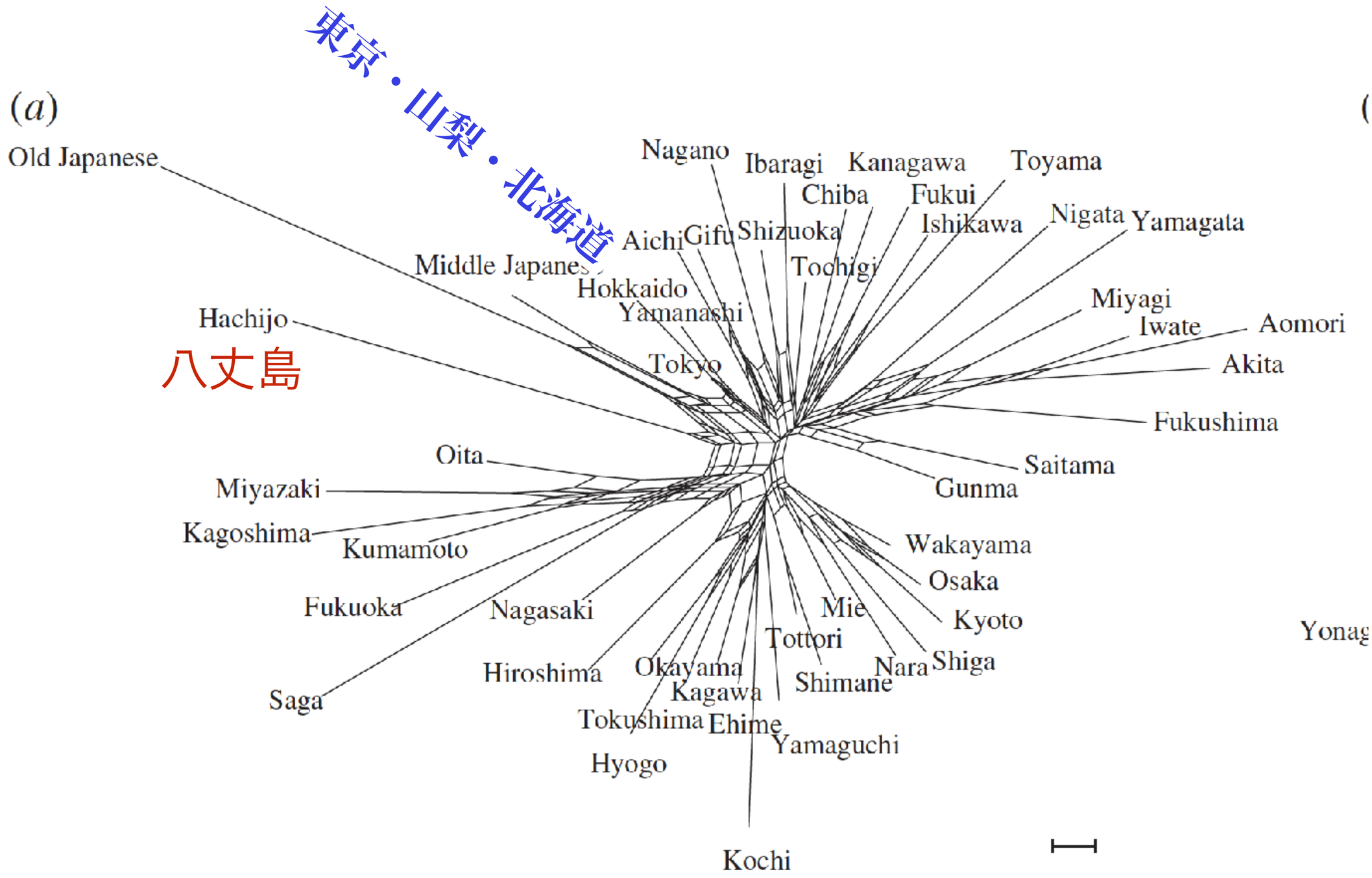
近畿・中国・四国

北九州

南九州

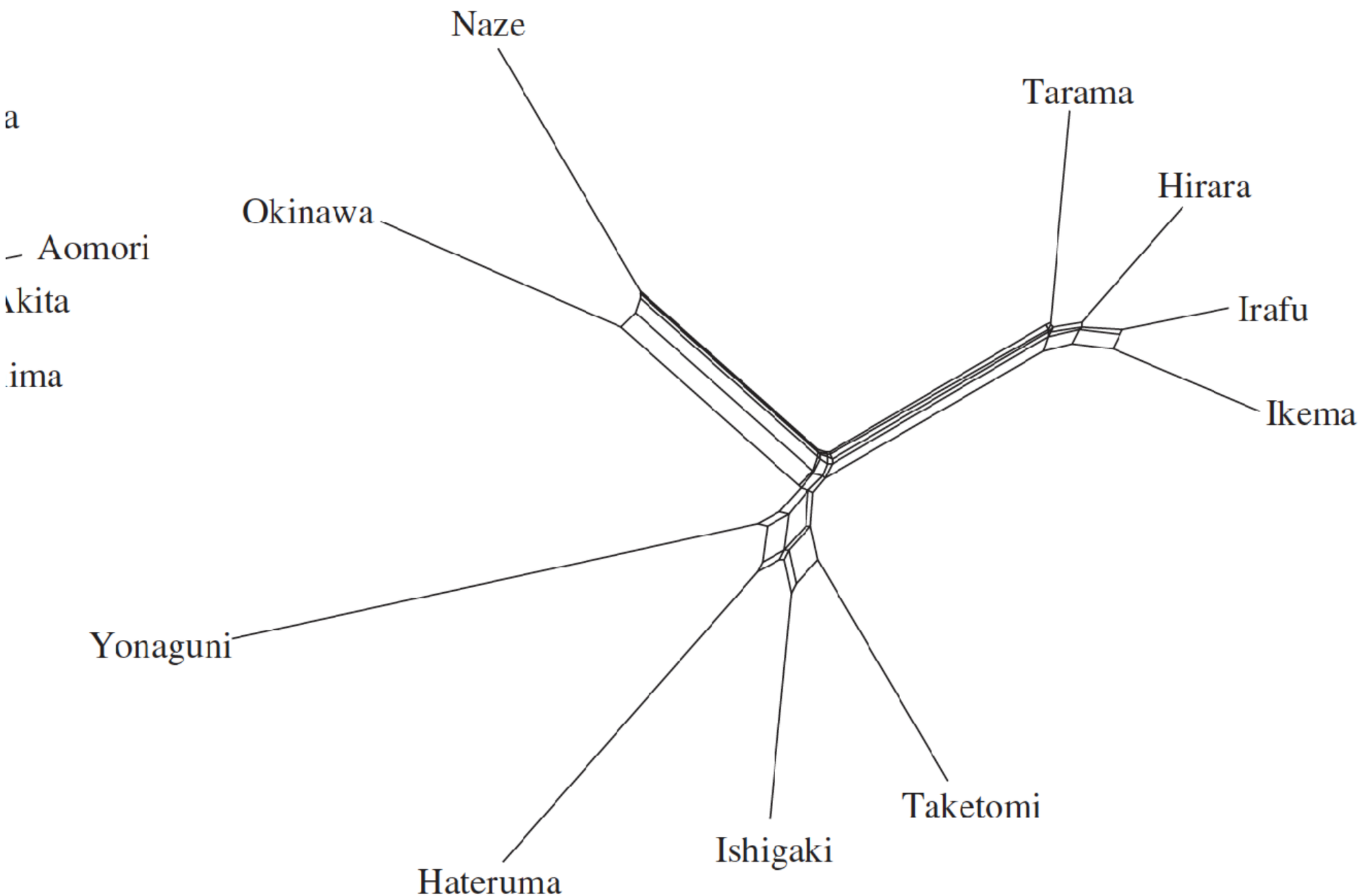
八丈島

斎藤成也監修 (2016)別冊宝島『DNAでわかった日本のルーツ』より



From Lee & Hasegawa (2011)

(*b*)



From Lee & Hasegawa (2011)

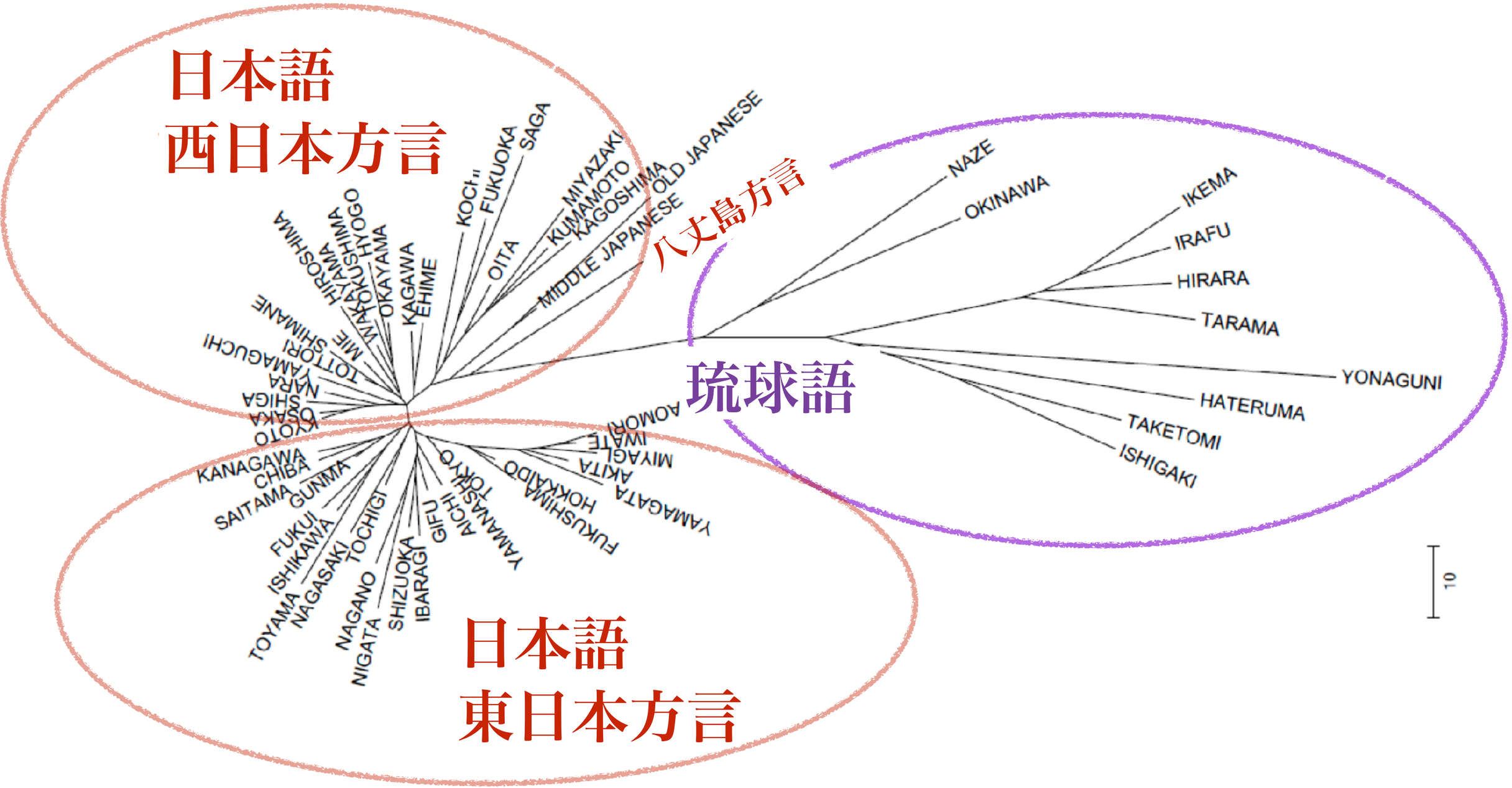
2017年１月に刊行した論文（オープンアクセス）

Man In India, 97 (1): 205–228 © Serials Publications

LANGUAGE DIVERSITY OF THE JAPANESE ARCHIPELAGO AND ITS RELATIONSHIP WITH HUMAN DNA DIVERSITY

Naruya Saitou and Timothy A. Jinam

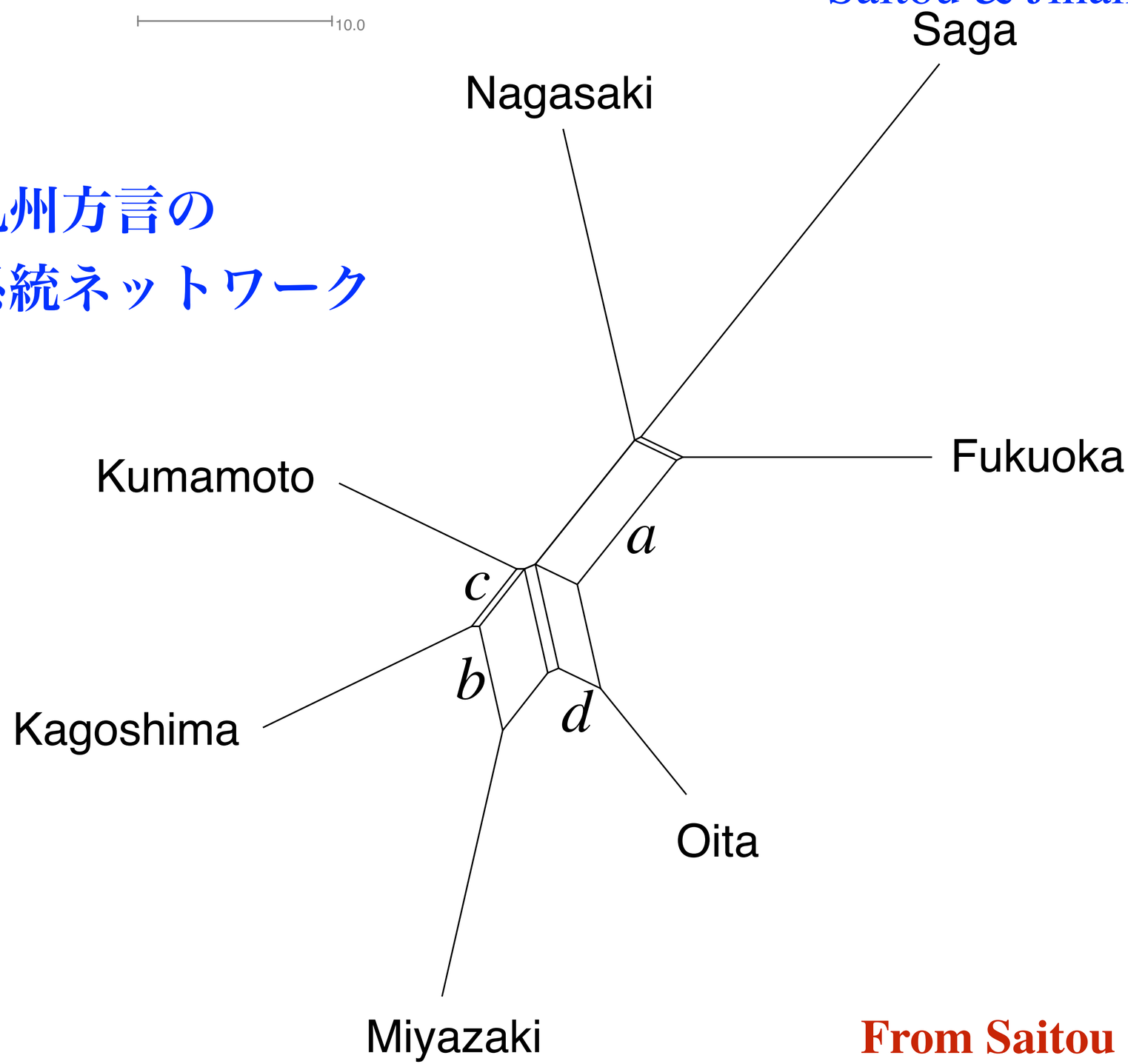
琉球語方言と日本語方言の系統樹



From Saitou & Jinam (2017)

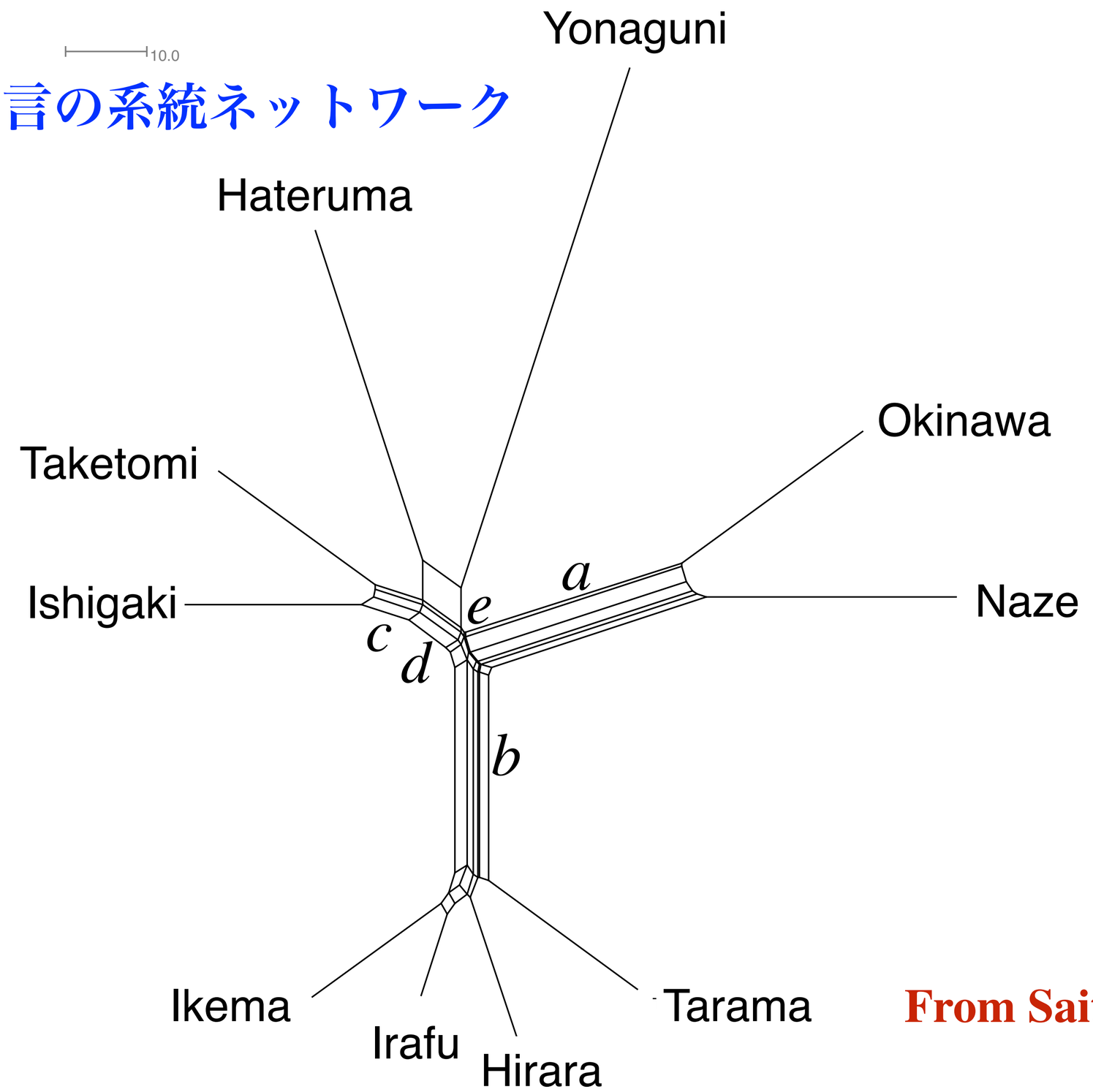
Saitou & Jinam (2017)より

九州方言の
系統ネットワーク



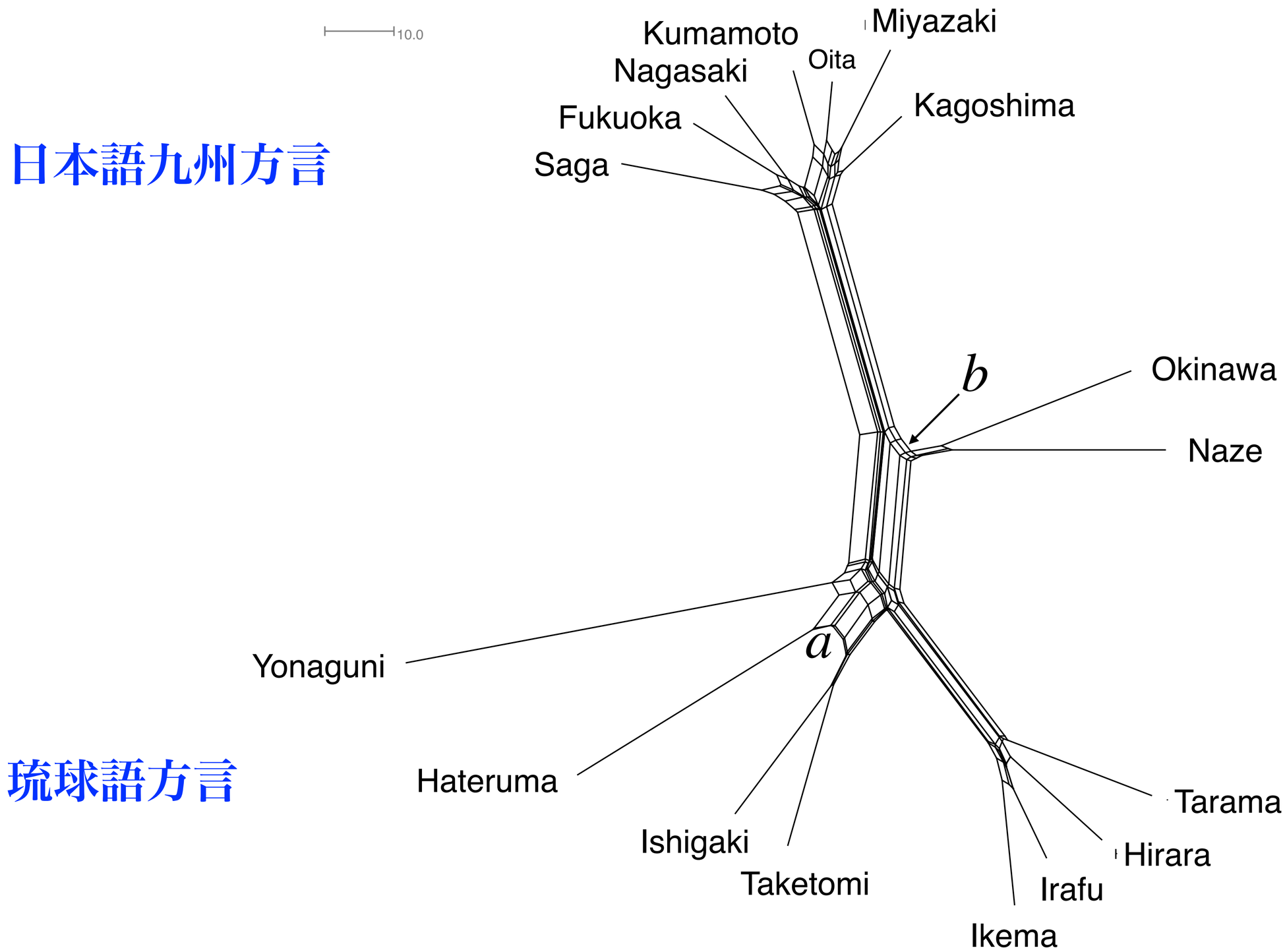
From Saitou & Jinam (2017)
Figure 6

琉球語方言の系統ネットワーク



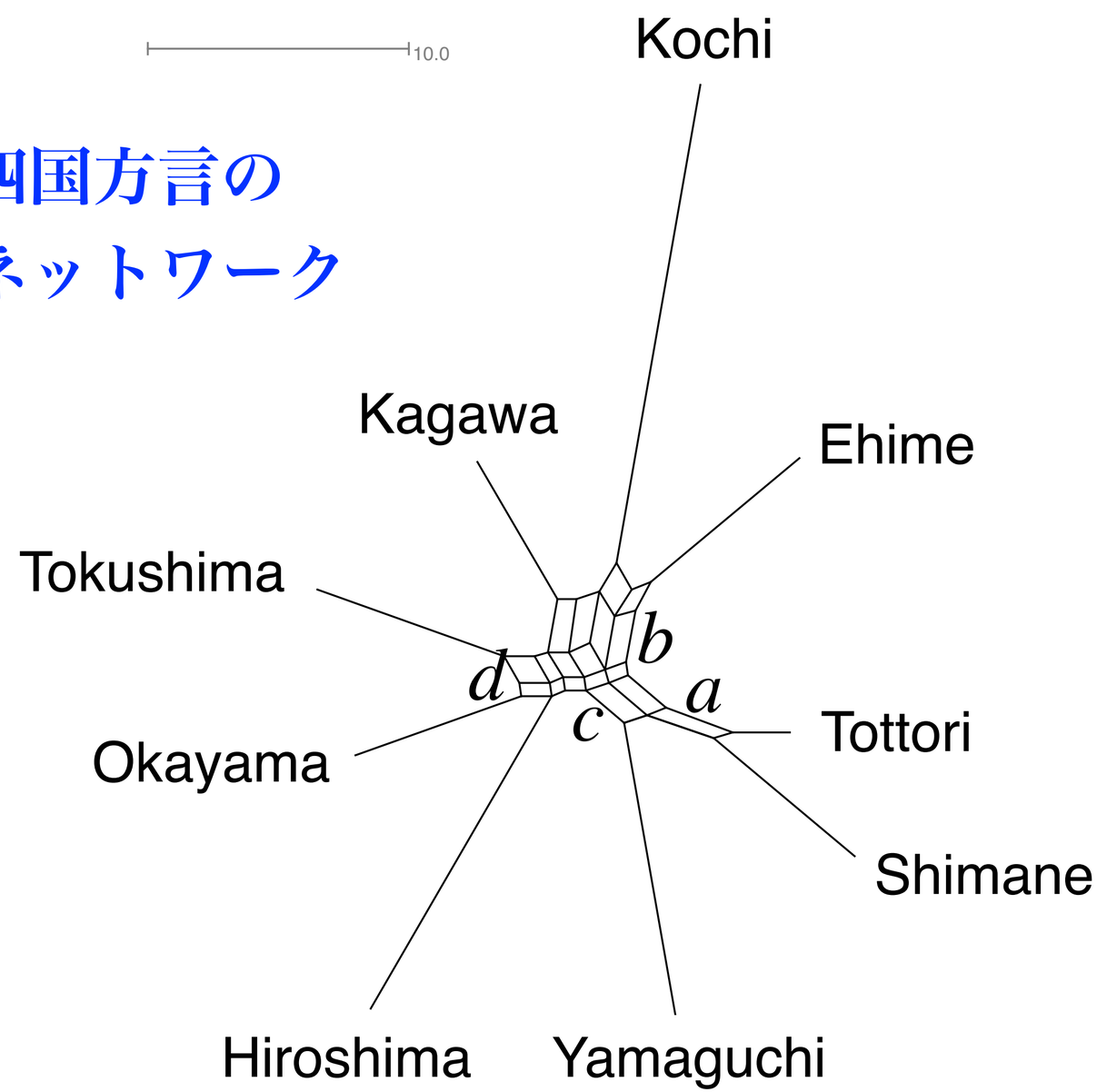
From Saitou & Jinam (2017)

Figure 5



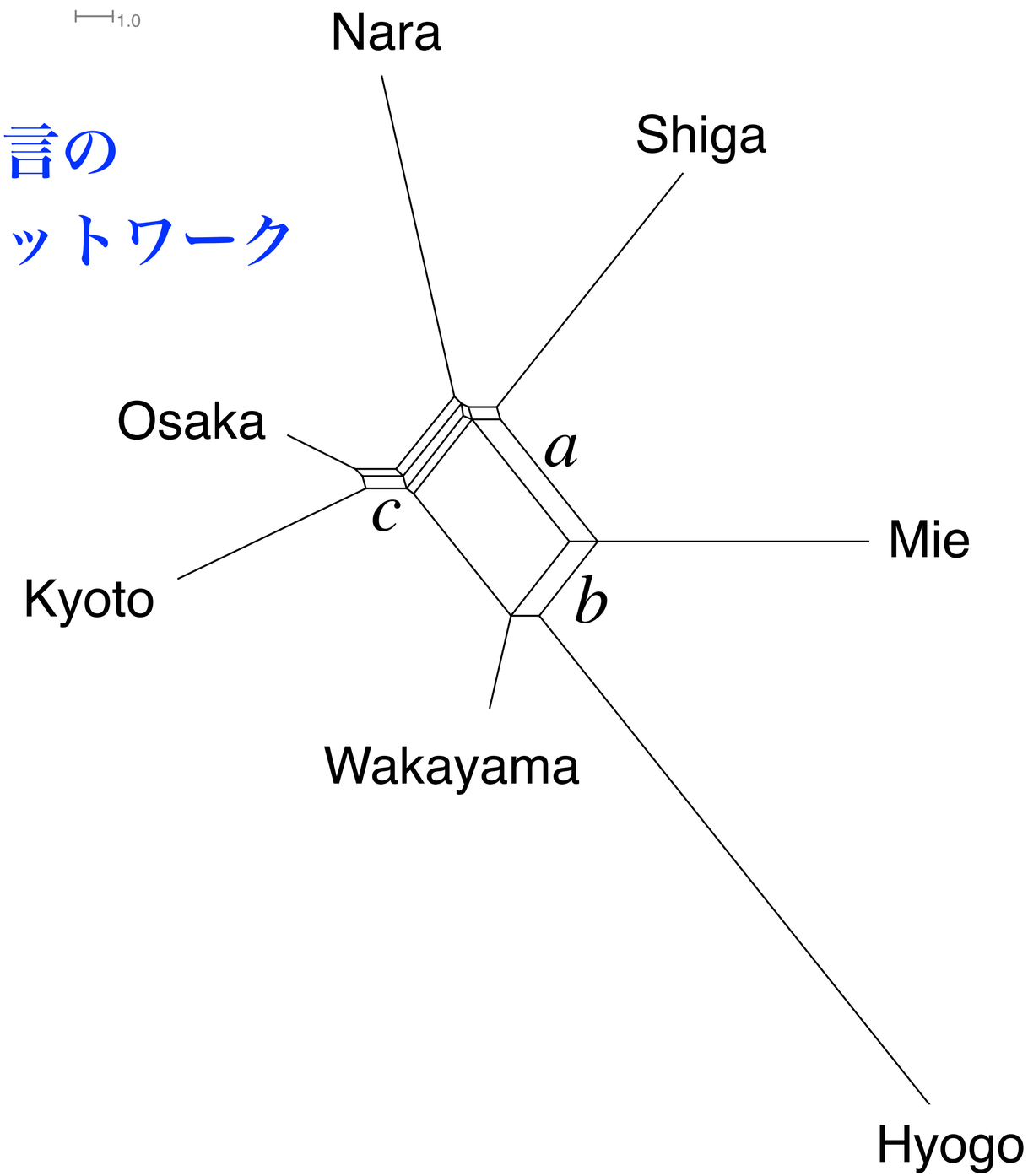
From Saitou & Jinam (2017) Figure 12

中国四国方言の系統ネットワーク



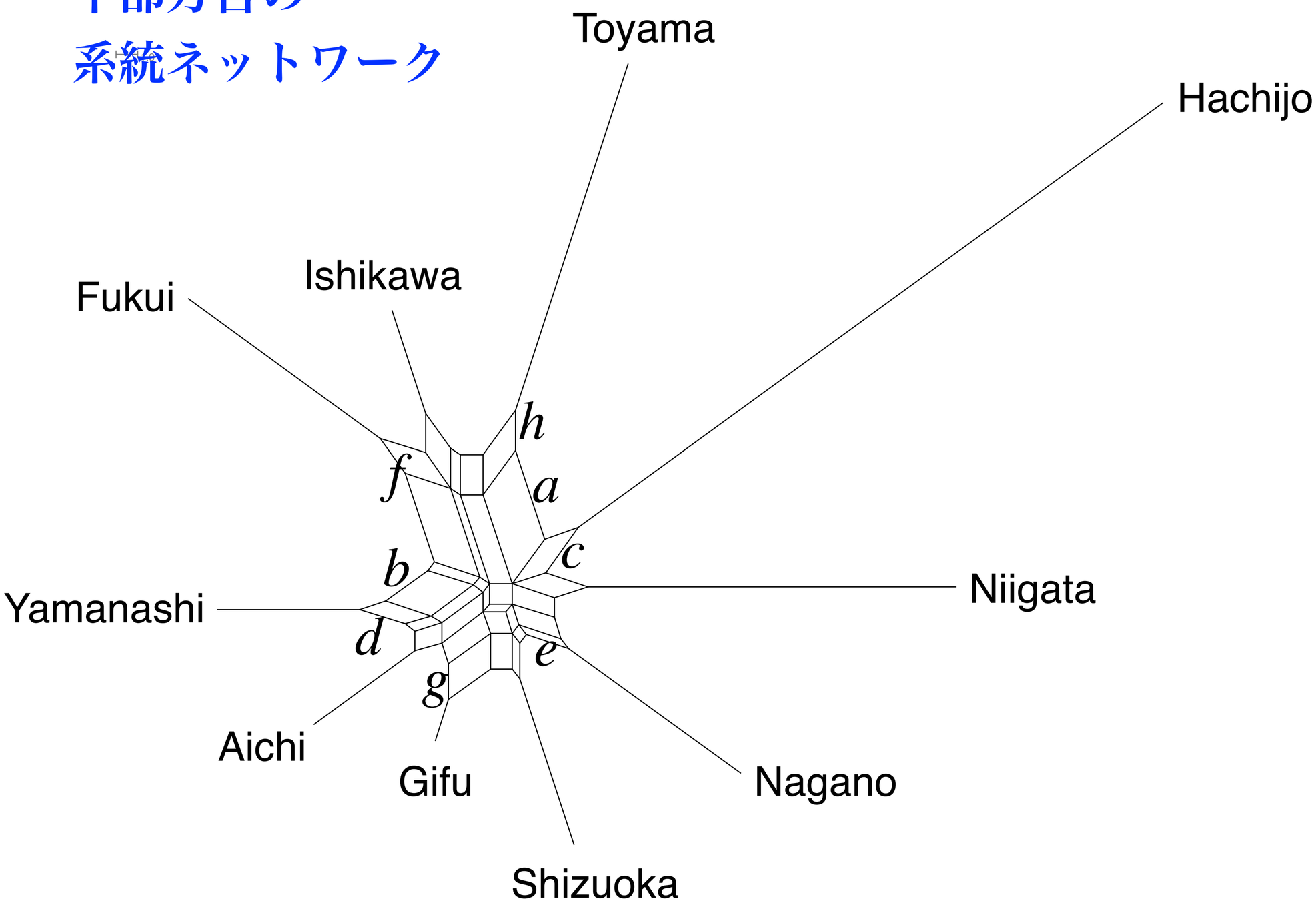
From Saitou & Jinam (2017) Figure 7

近畿方言の系統ネットワーク



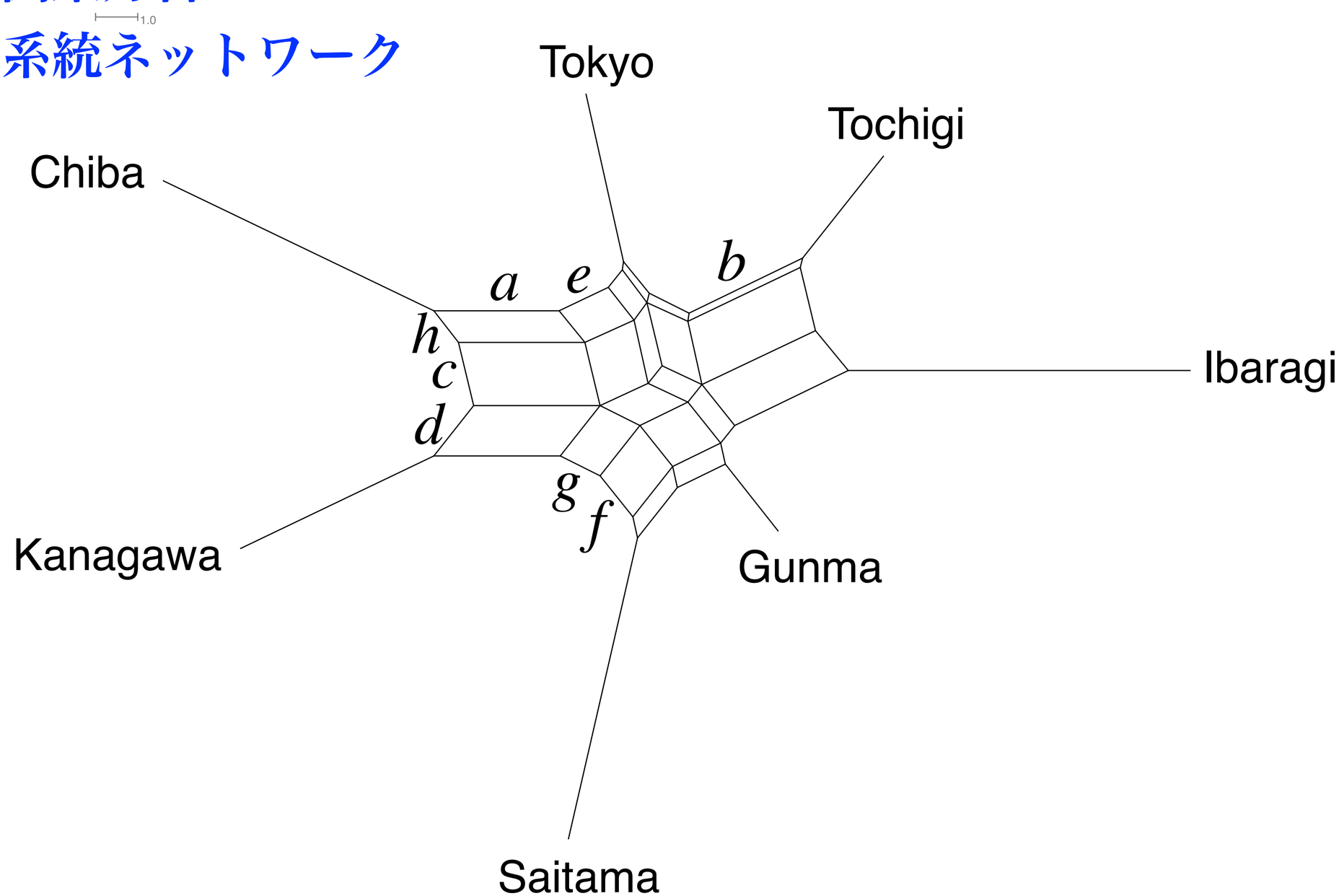
From Saitou & Jinam (2017) Figure 8

中部方言の系統ネットワーク



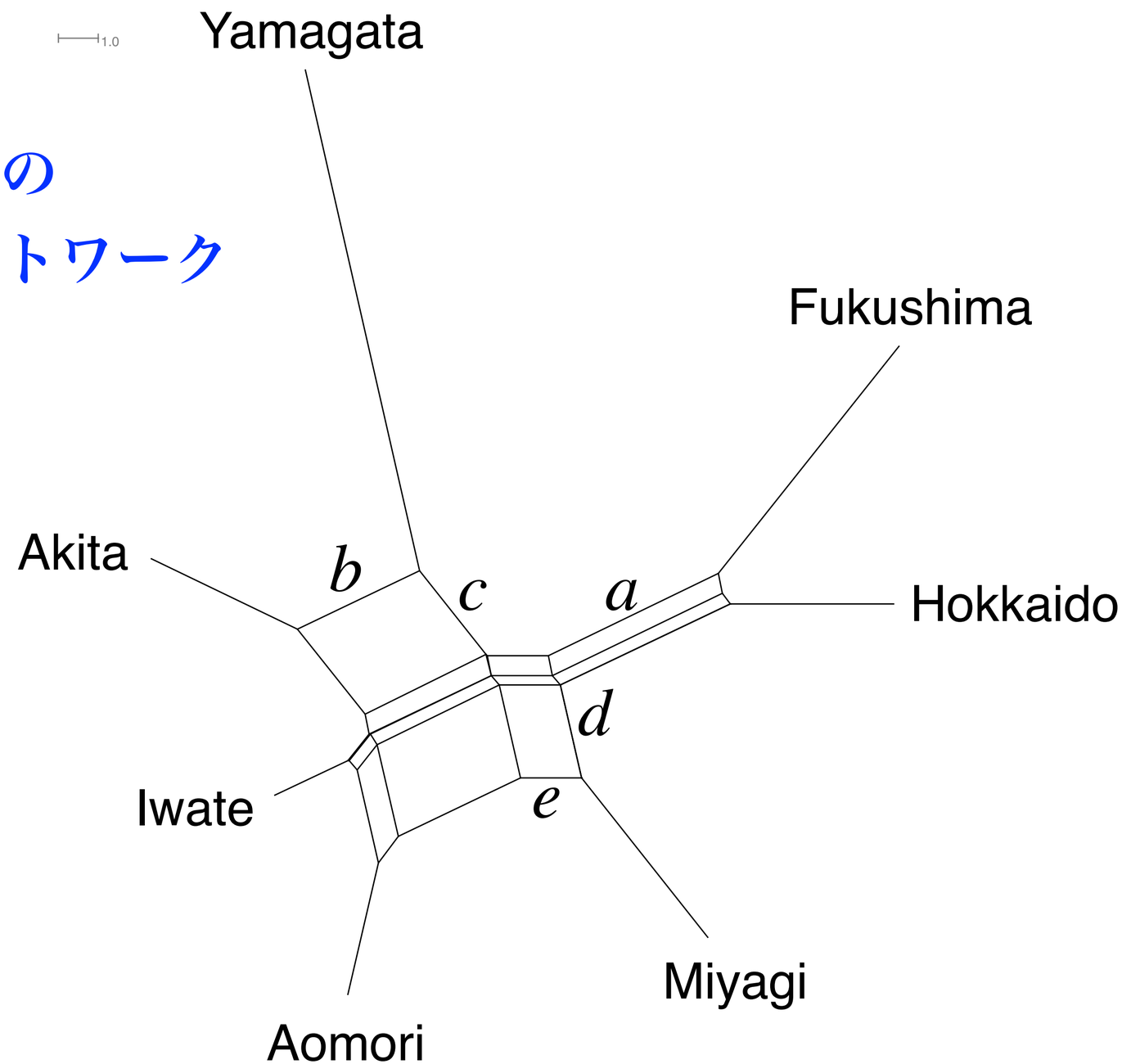
From Saitou & Jinam (2017) Figure 9

関東方言の系統ネットワーク



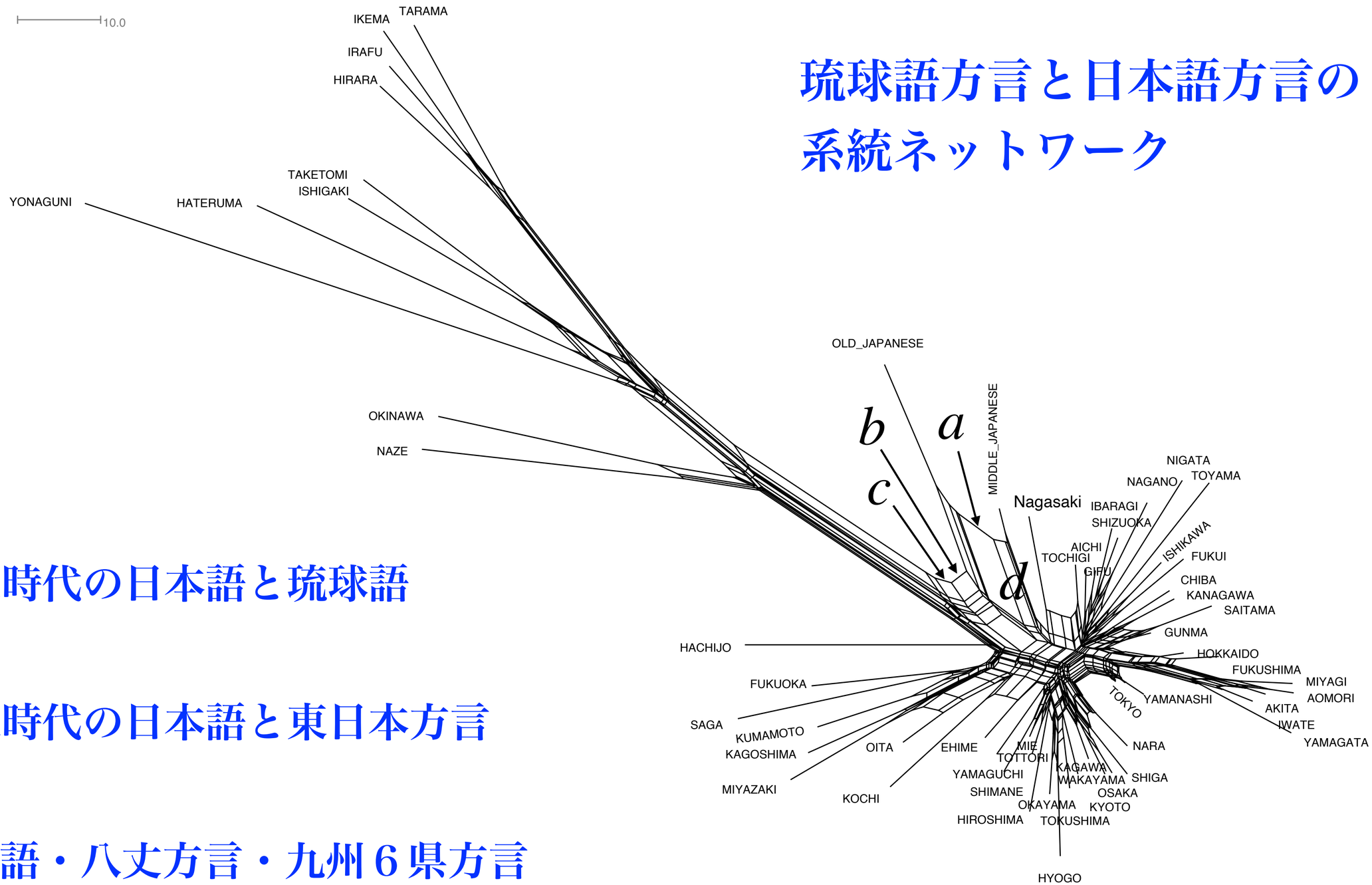
From Saitou & Jinam (2017)Figure 10

東北方言の系統ネットワーク



From Saitou & Jinam (2017)Figure 11

琉球語方言と日本語方言の系統ネットワーク



Split *a*: 奈良時代の日本語と琉球語 vs その他

Split *b*: 歴史時代の日本語と東日本方言 vs その他

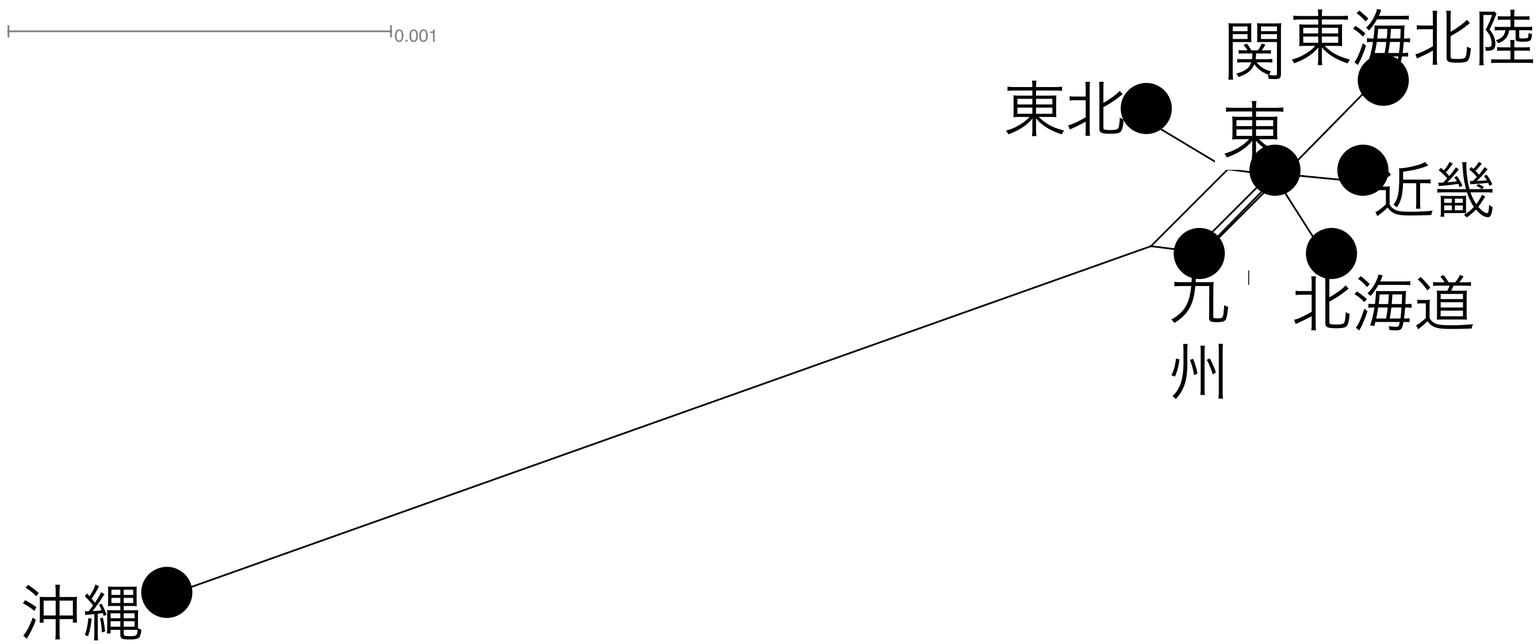
Split *c*: 琉球語・八丈方言・九州 6 県方言 vs その他

Split *d*: 歴史時代の日本語 vs その他

From Saitou & Jinam (2017) Figure 25

現在の日本列島８集団間の遺伝的近縁関係

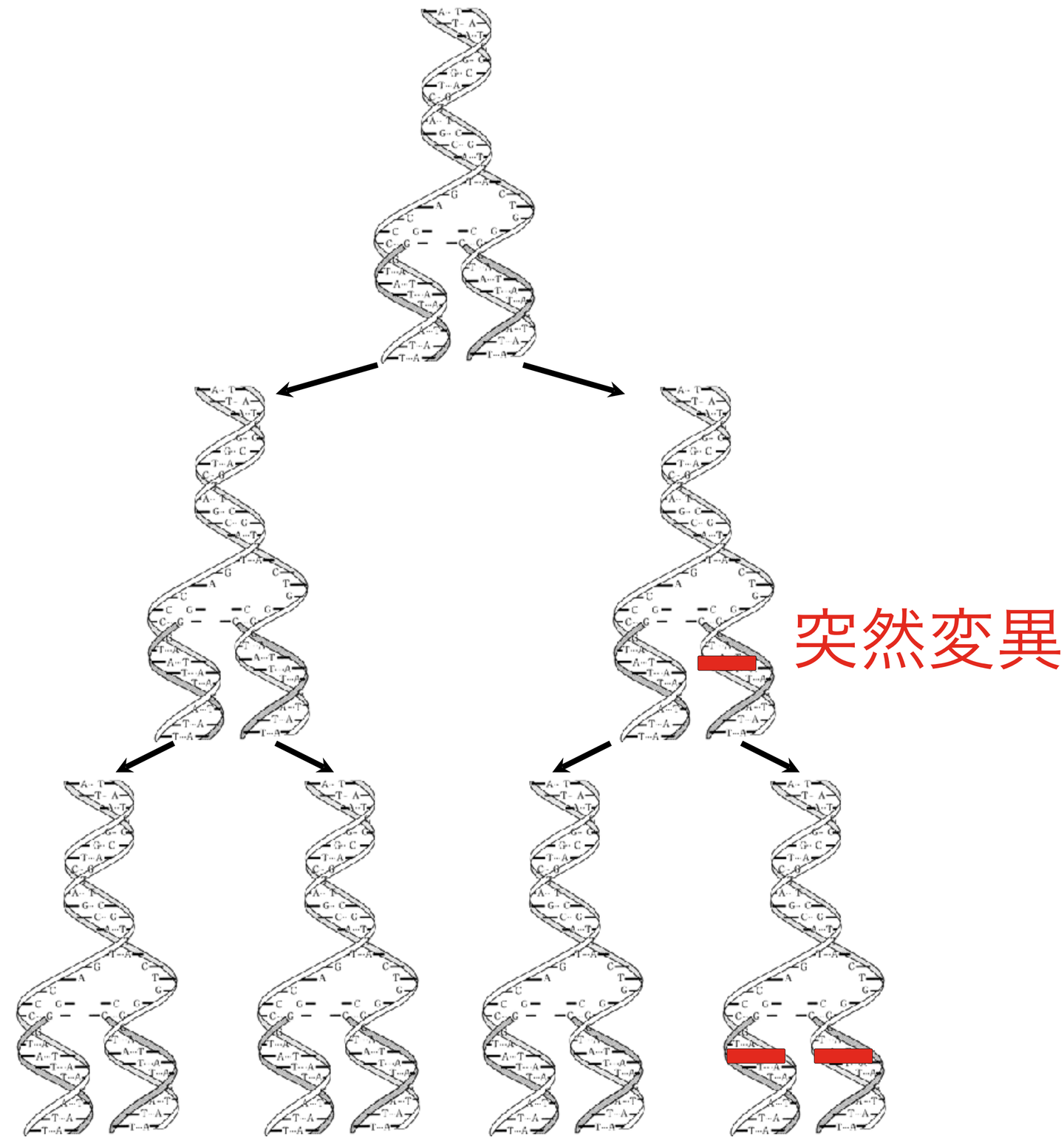
（山口・鎌谷らの論文のデータにもとづく）



From Saitou & Jinam (2017)

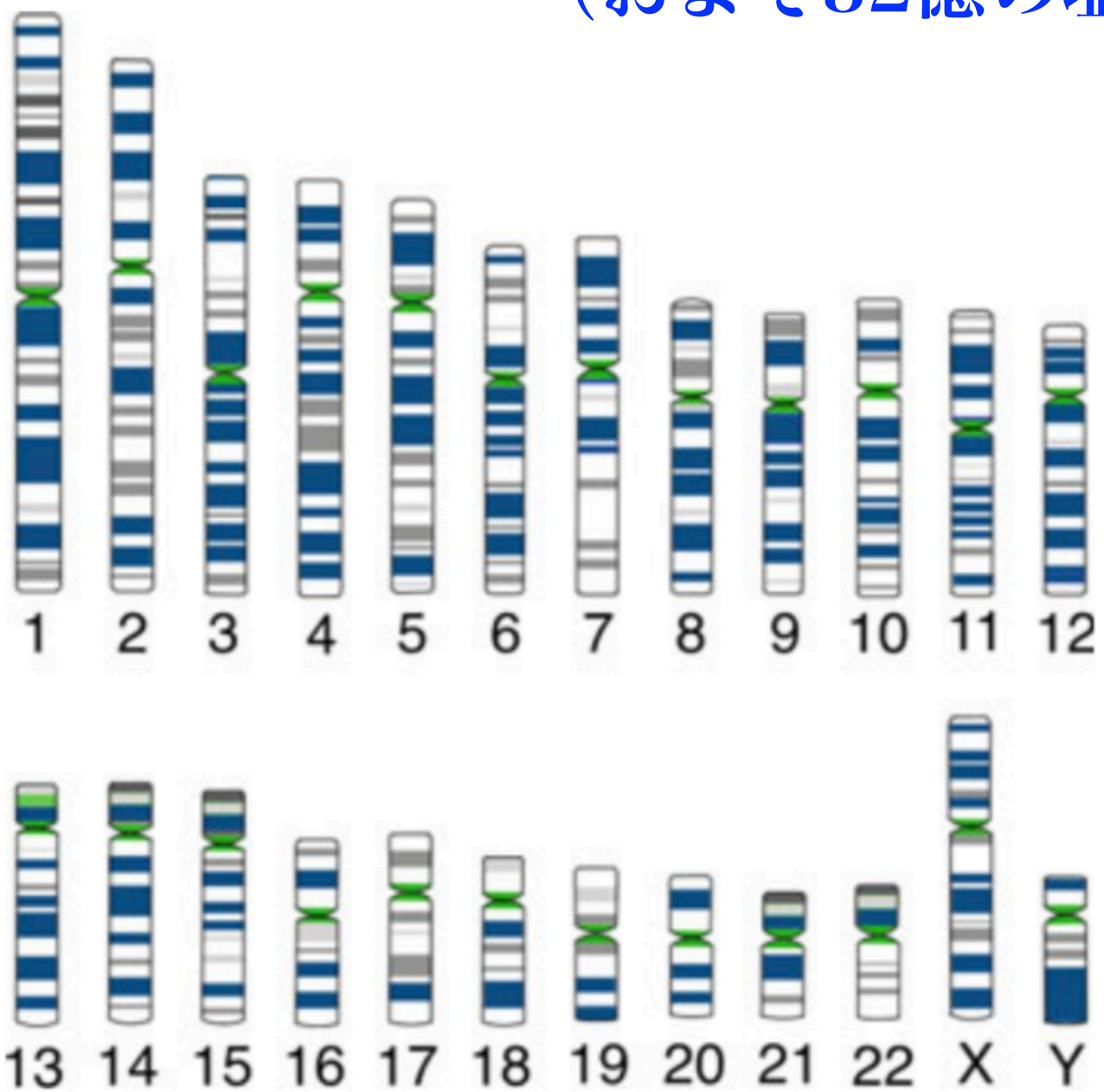
進化の根本

DNAが自己複製を
繰り返しながら
突然変異を蓄積



ヒトの細胞核内の常染色体と性染色体

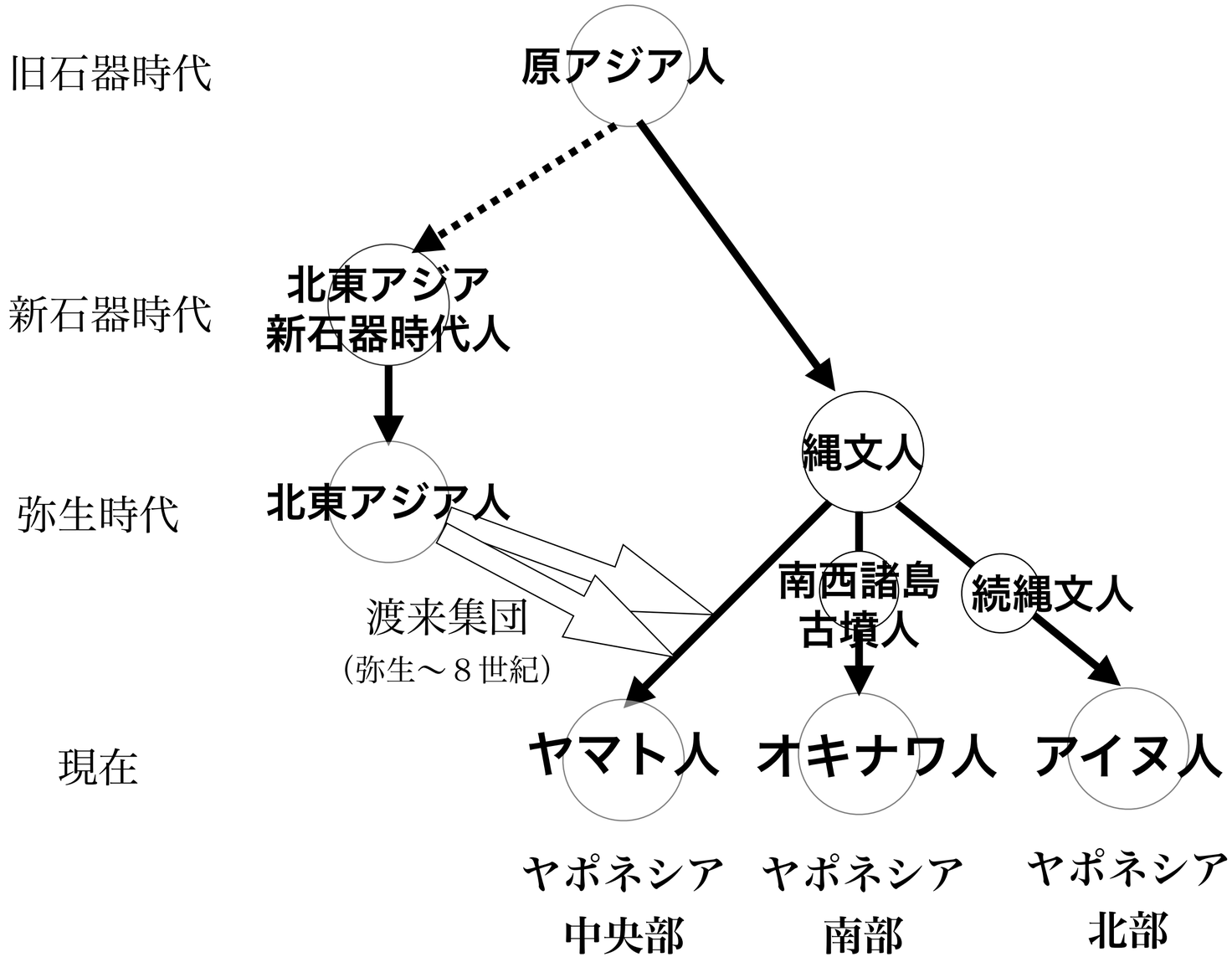
（およそ32億の塩基＝ゲノム）



ミトコンドリアDNA
(およそ16,500塩基)

Saitou (2018)より

二重構造モデル（埴原 [1995]にもとづく）



斎藤 (2020)より

二重構造モデルについて

支持できる点：

◎アイヌ人とオキナワ人に遺伝的な共通点がある

◎稲作農耕開始以降、多数の人々が大陸から渡来

◎ヤマト人は縄文人と弥生時代以降人の混血

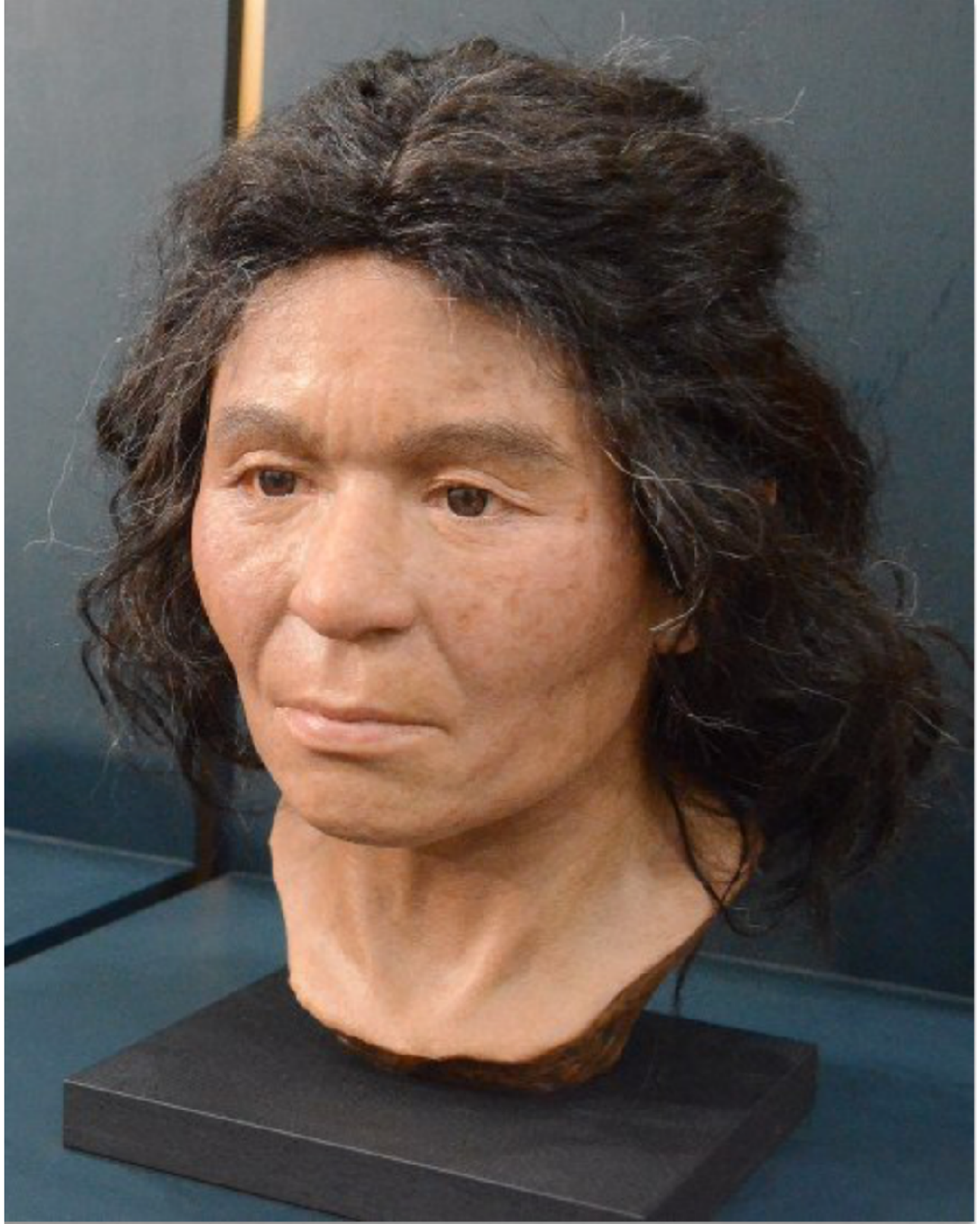
支持できない点：

◎オキナワ人はヤマト人にかなり近い

結論：二重構造モデルは一次近似としては支持できる

（ただし「アイヌ沖縄同系説」から自然に導かれる仮説）

礼文島
船泊遺跡
出土縄文人
F23
女性の復顔



本土日本人 (ヤマト人) に伝えられた縄文人ゲノムの割合

神澤ら (2019)： 13% {船泊縄文人}

神澤ら (2017)： 12% {三貫地縄文人}

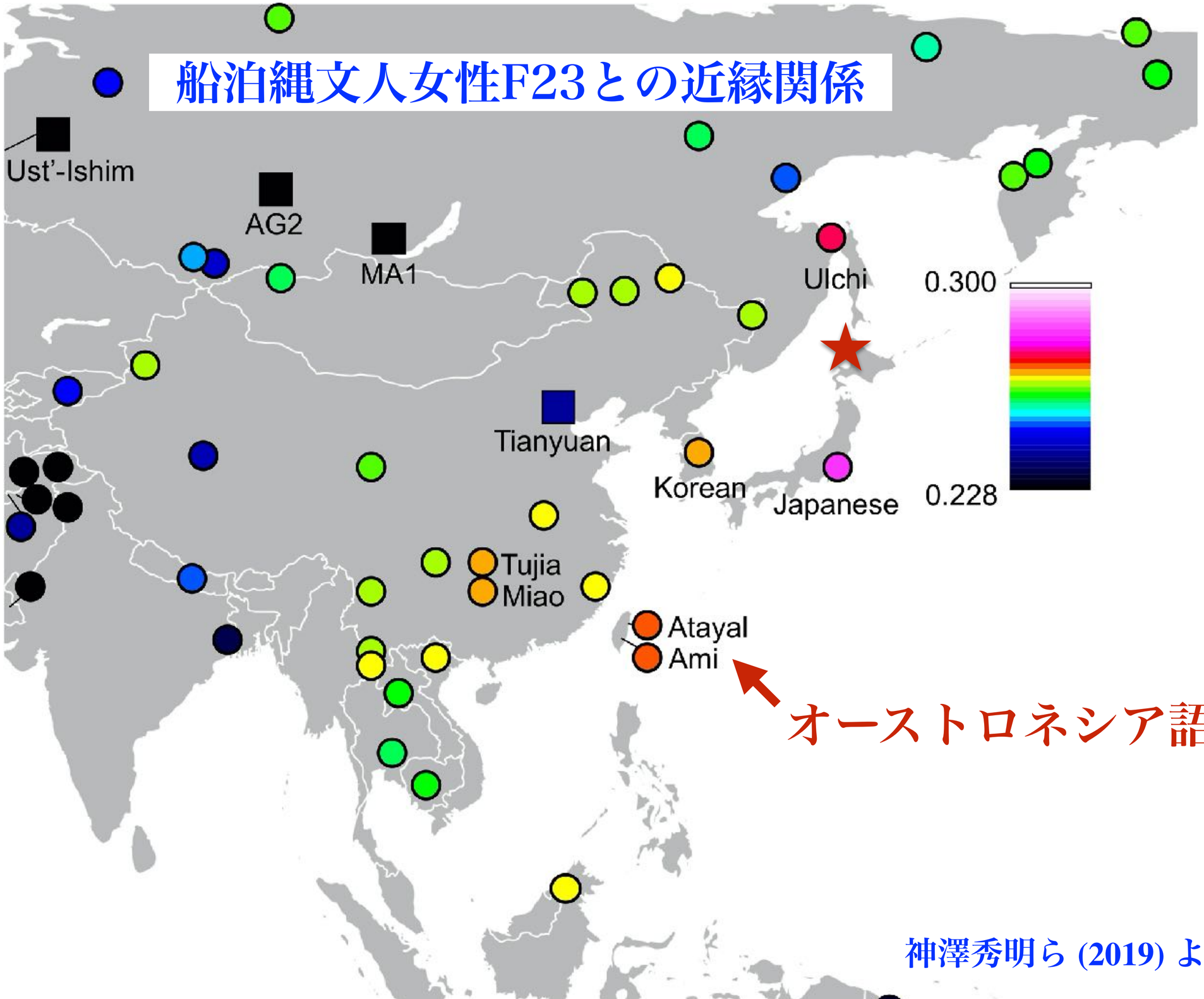
Jinamら(2015): 14–20% {現代人のみ}

アイヌ人とオキナワ人に伝えられた船泊縄文人ゲノムの割合

アイヌ人へ： 66%

オキナワ人へ： 27%

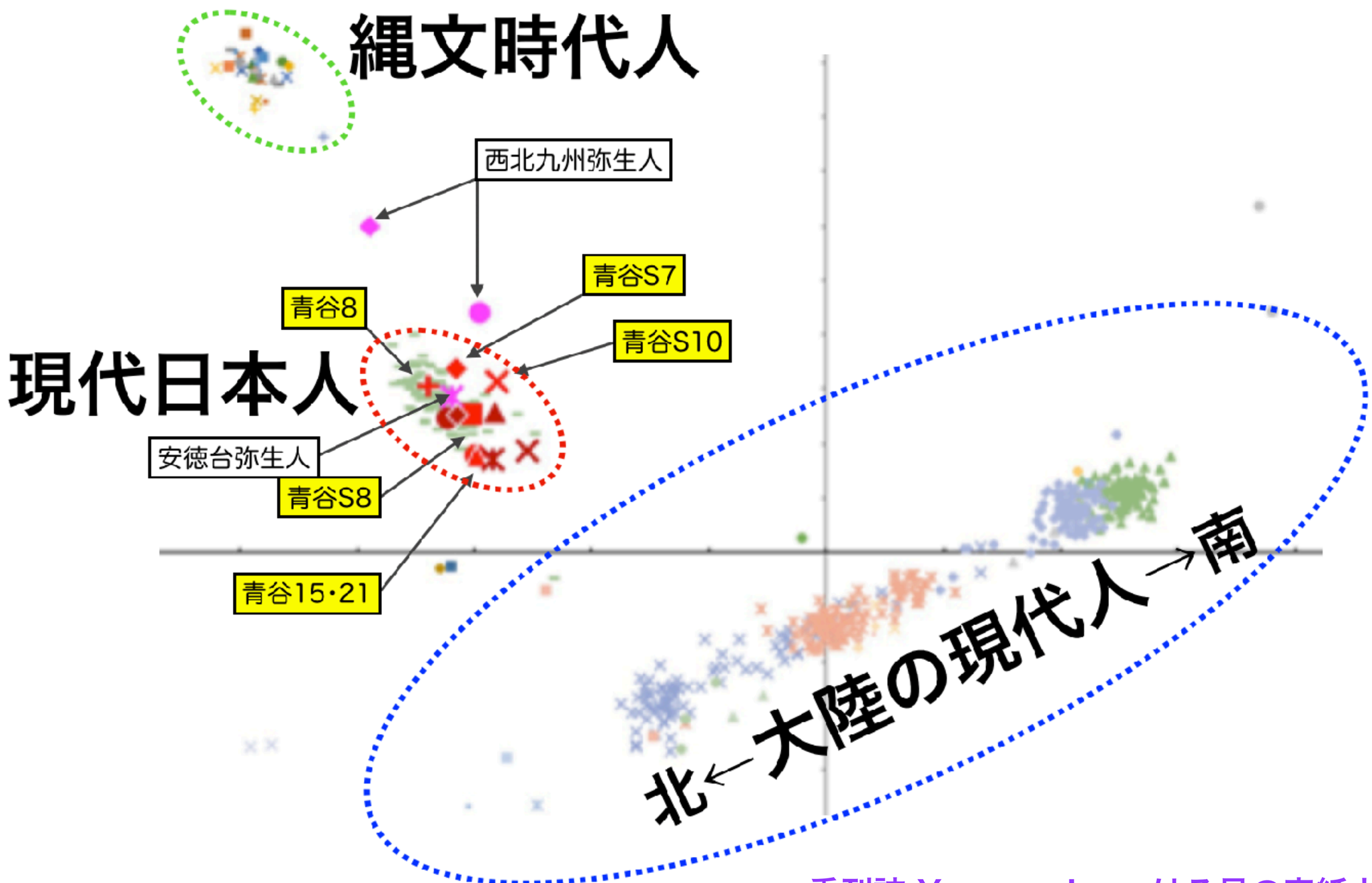
船泊縄文人女性F23との近縁関係



オーストロネシア語族

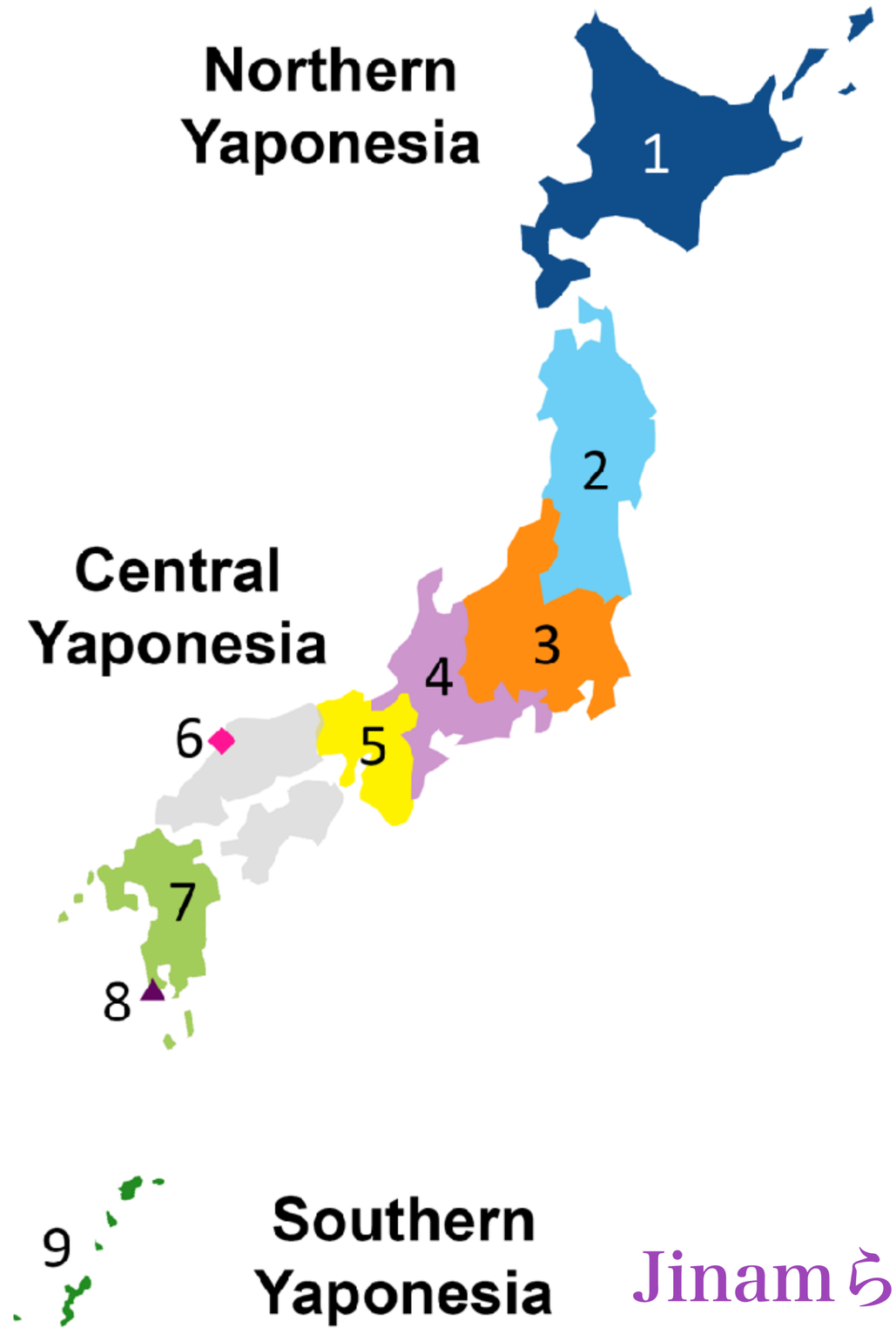
神澤秀明ら (2019) より

縄文時代人、弥生時代人、現代人のゲノムの関係



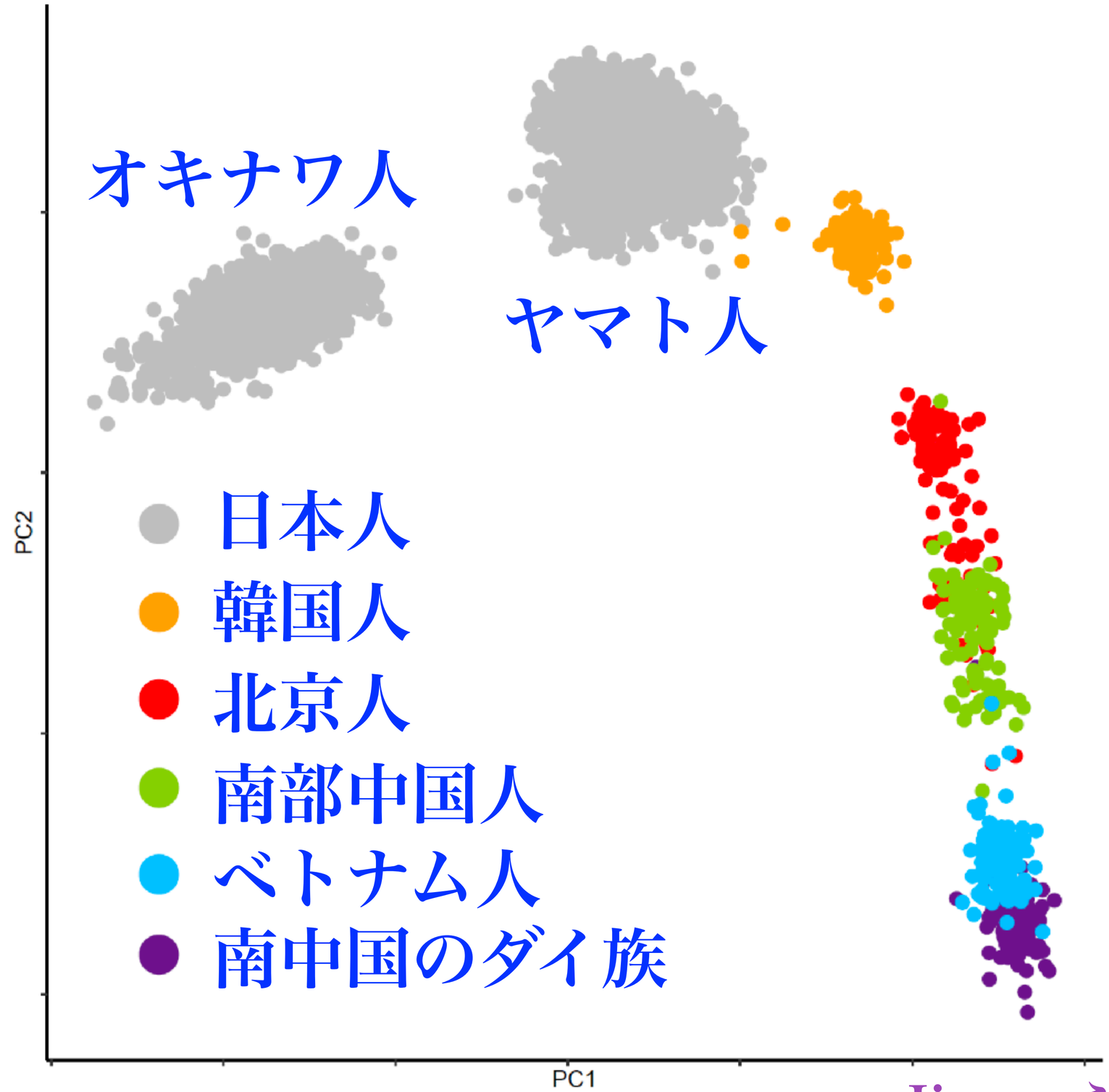
季刊誌 Yaponesian　はる号の表紙より

DNAを比較した日本列島の9地域



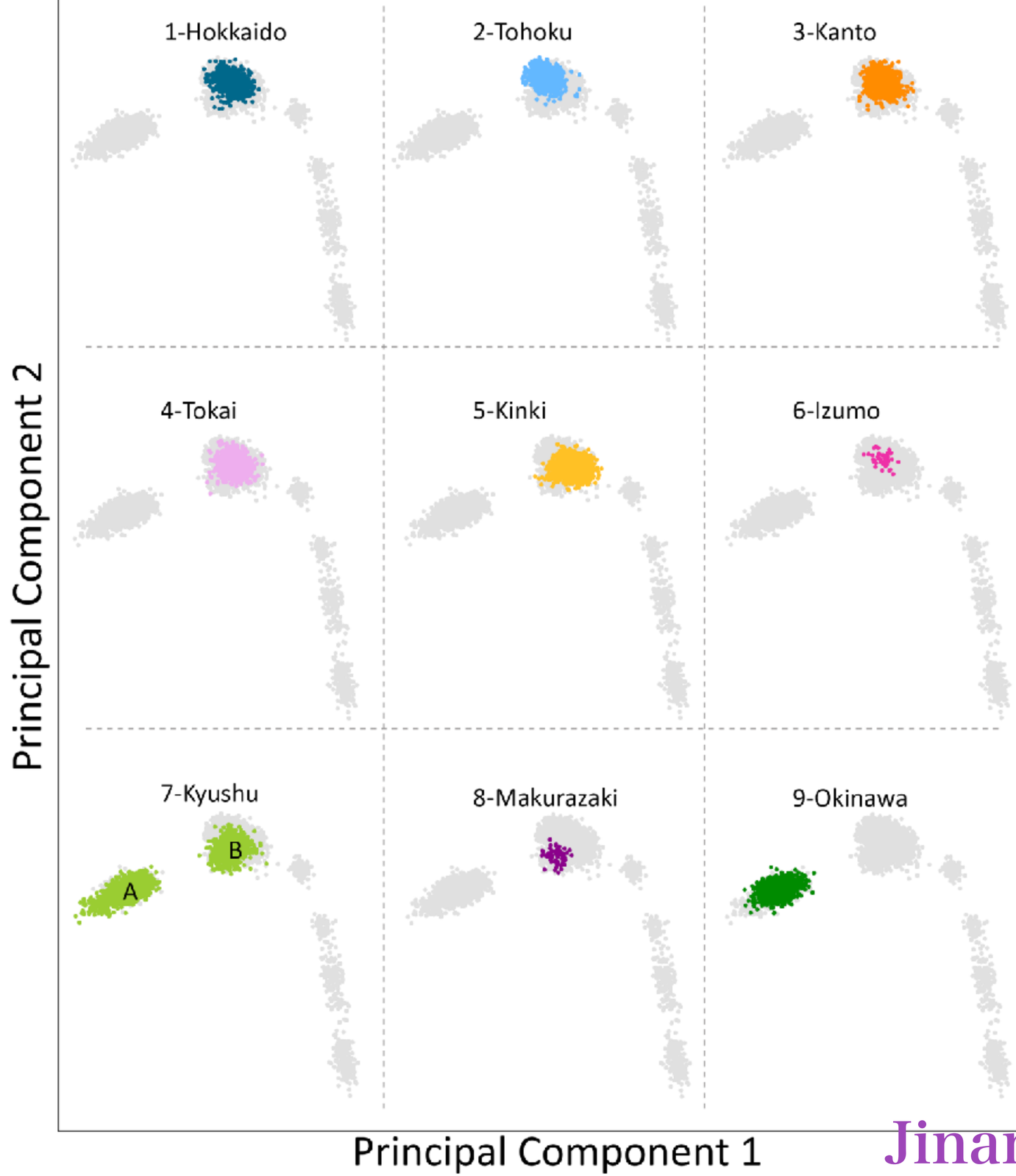
Jinamら(投稿中)より

東アジア６集団の関係



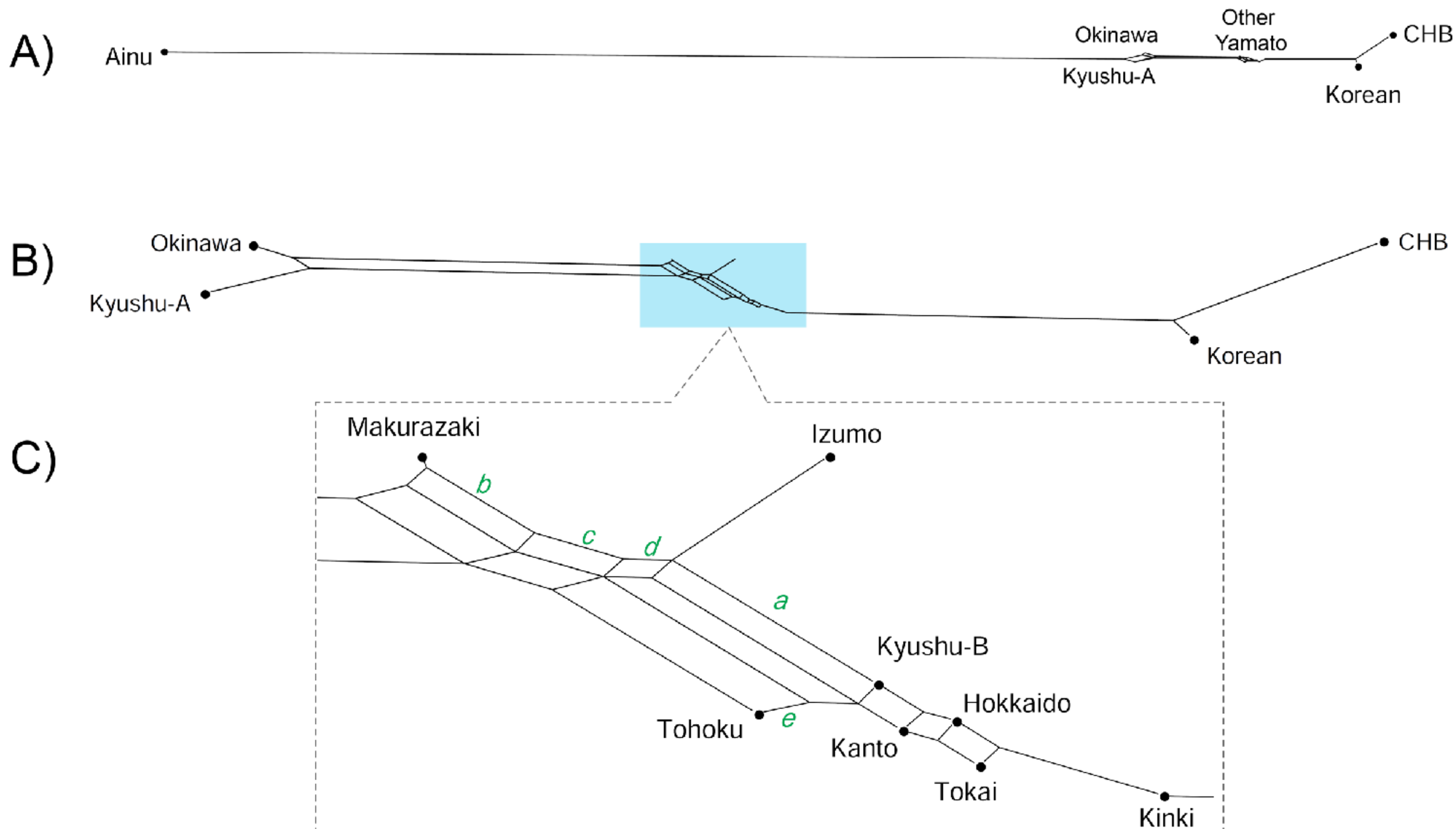
Jinamら(投稿中)より

日本列島9地域の関係



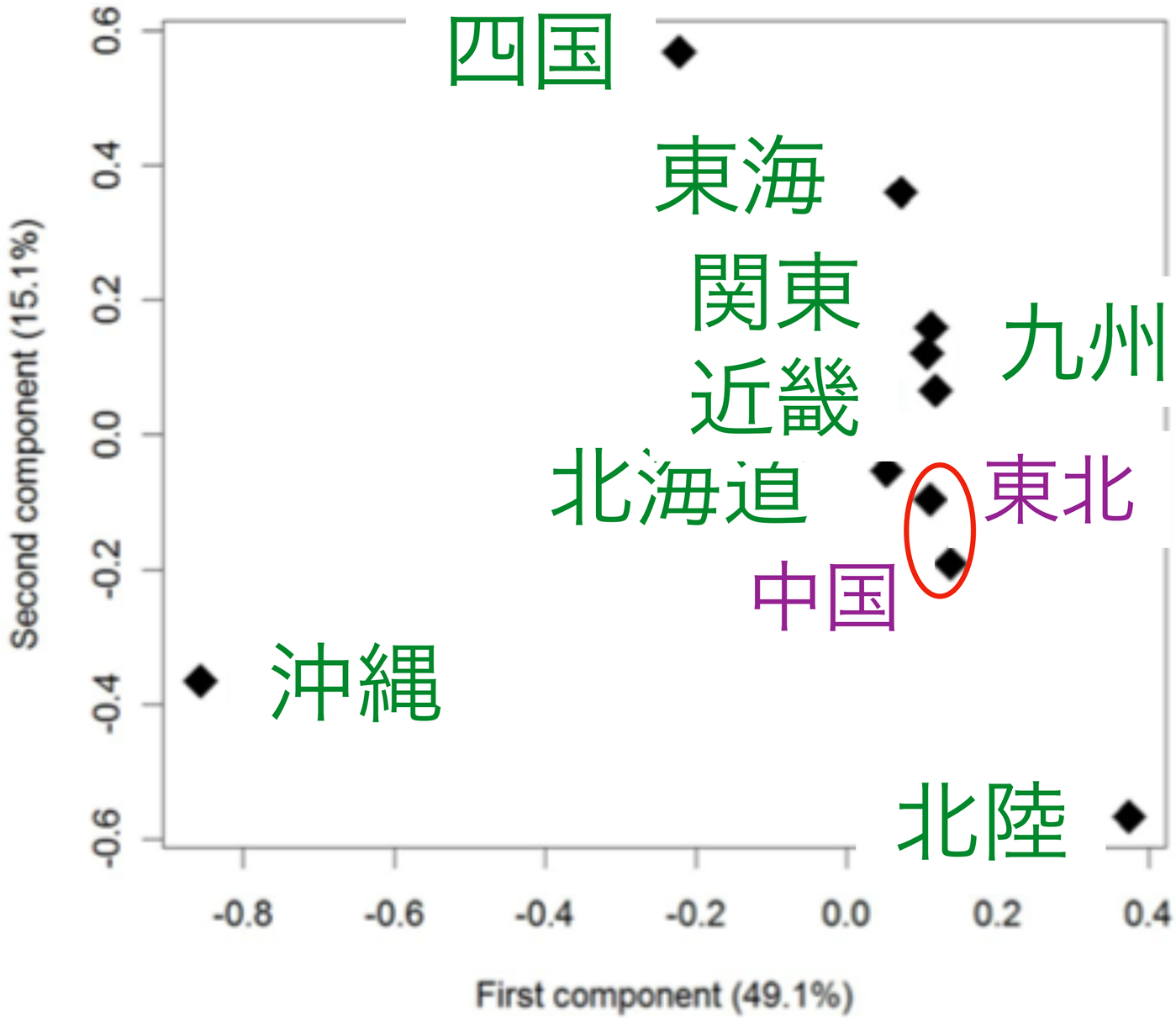
Jinamら(投稿中)より

ヤポネシアと東アジアの集団の関係



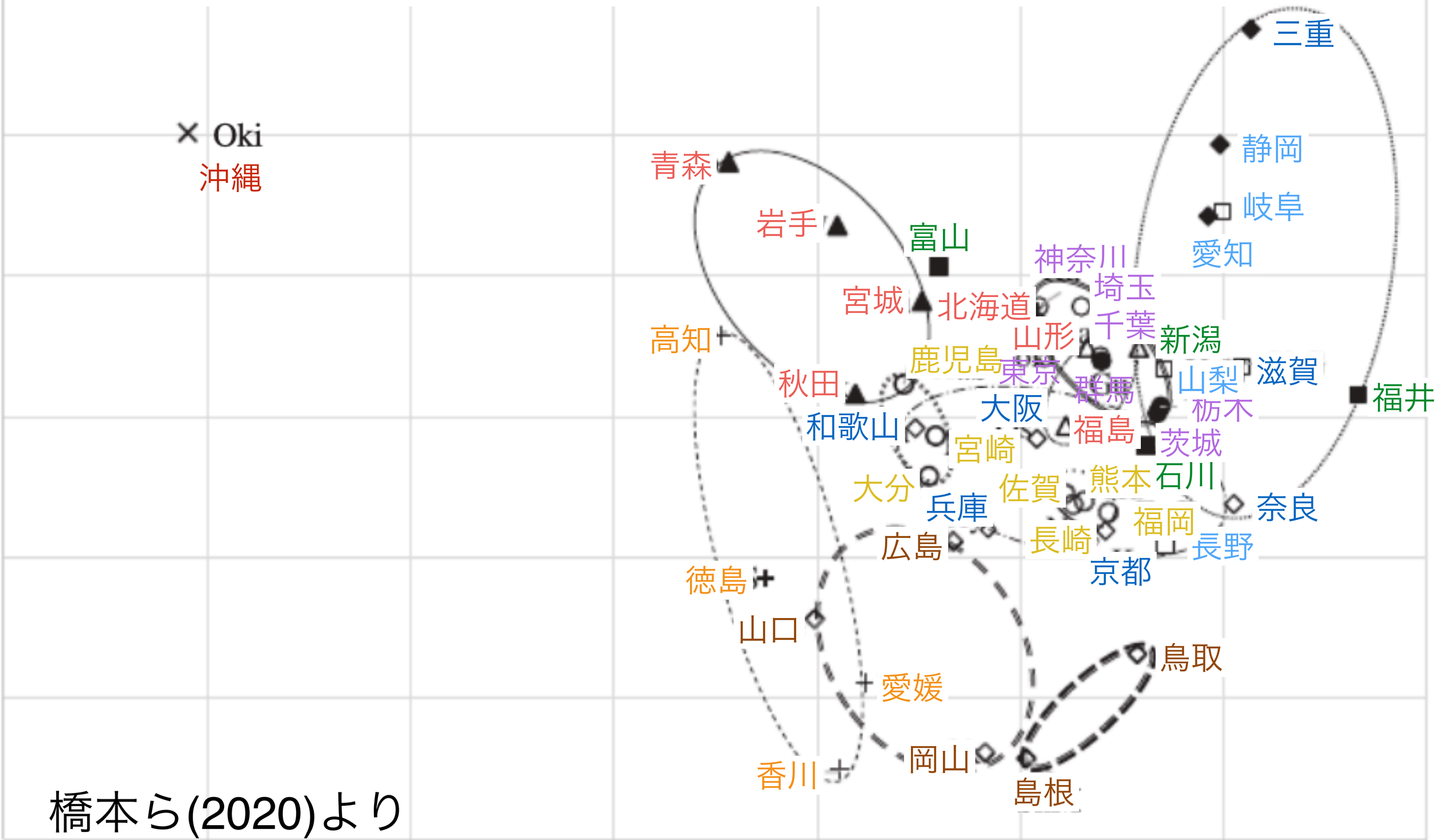
Jinamら(投稿中)より

HLA遺伝子のＤＮＡからみた日本列島人



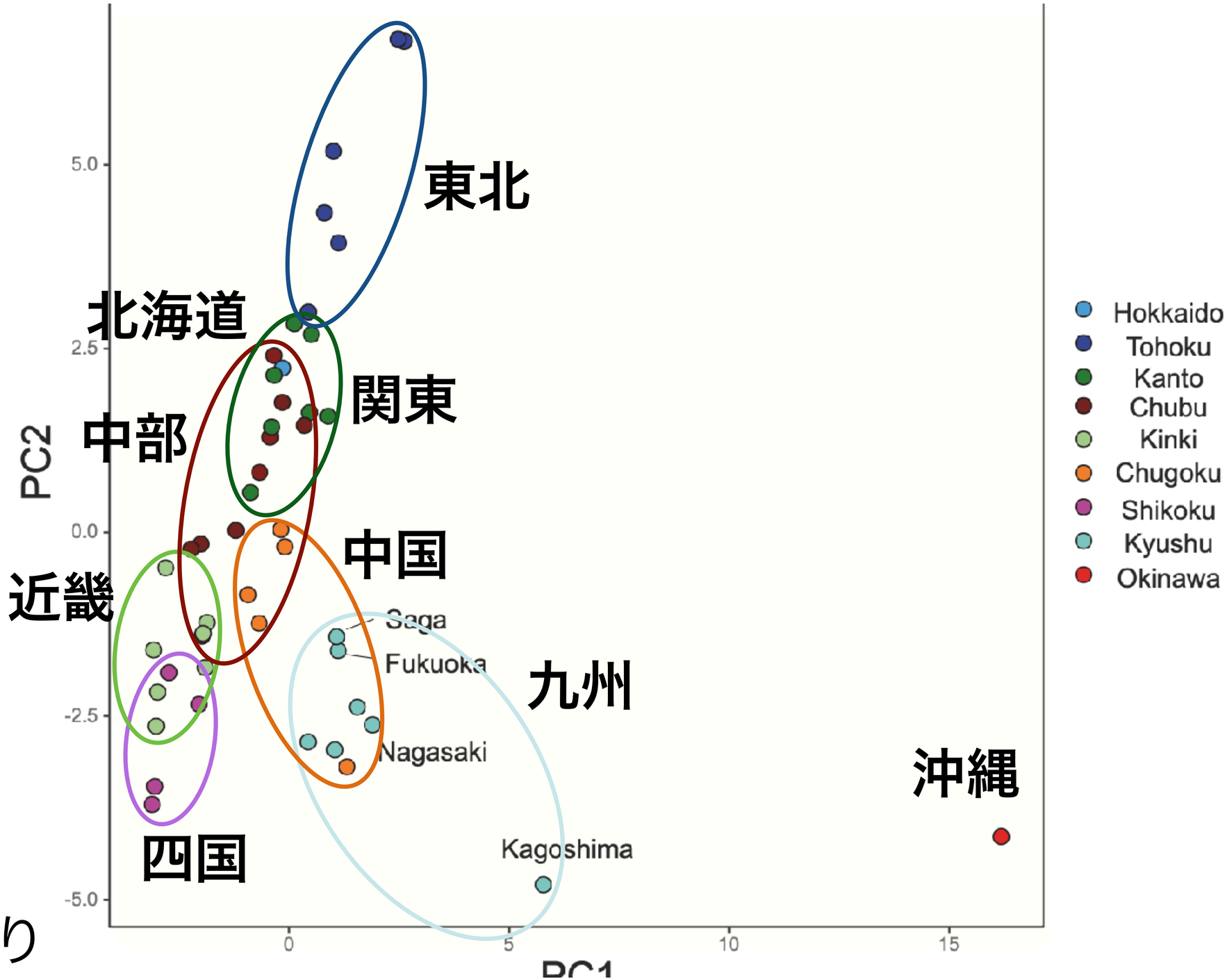
中岡・井ノ上ら (2013)より

骨髄バンク17,7000名のHLA遺伝子情報にもとづく47都道府県の関係



橋本ら(2020)より

計11,000名の核DNA多型情報にもとづく47都道府県の関係



渡辺ら(2020)より

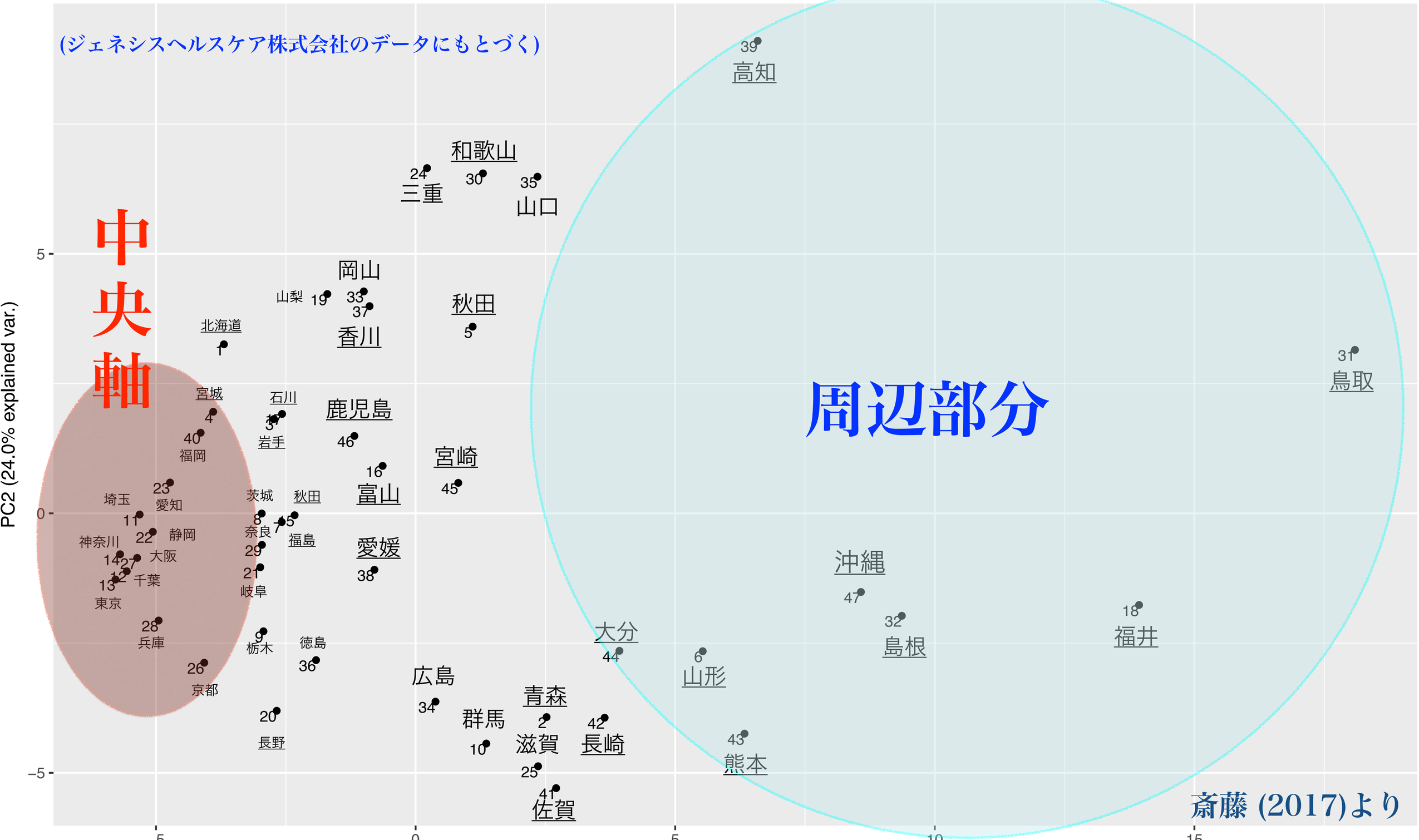
図48：日本列島中央部の中央軸と周辺部分

ヤマト人の「うちなる二重構造」

斎藤 (2017)より

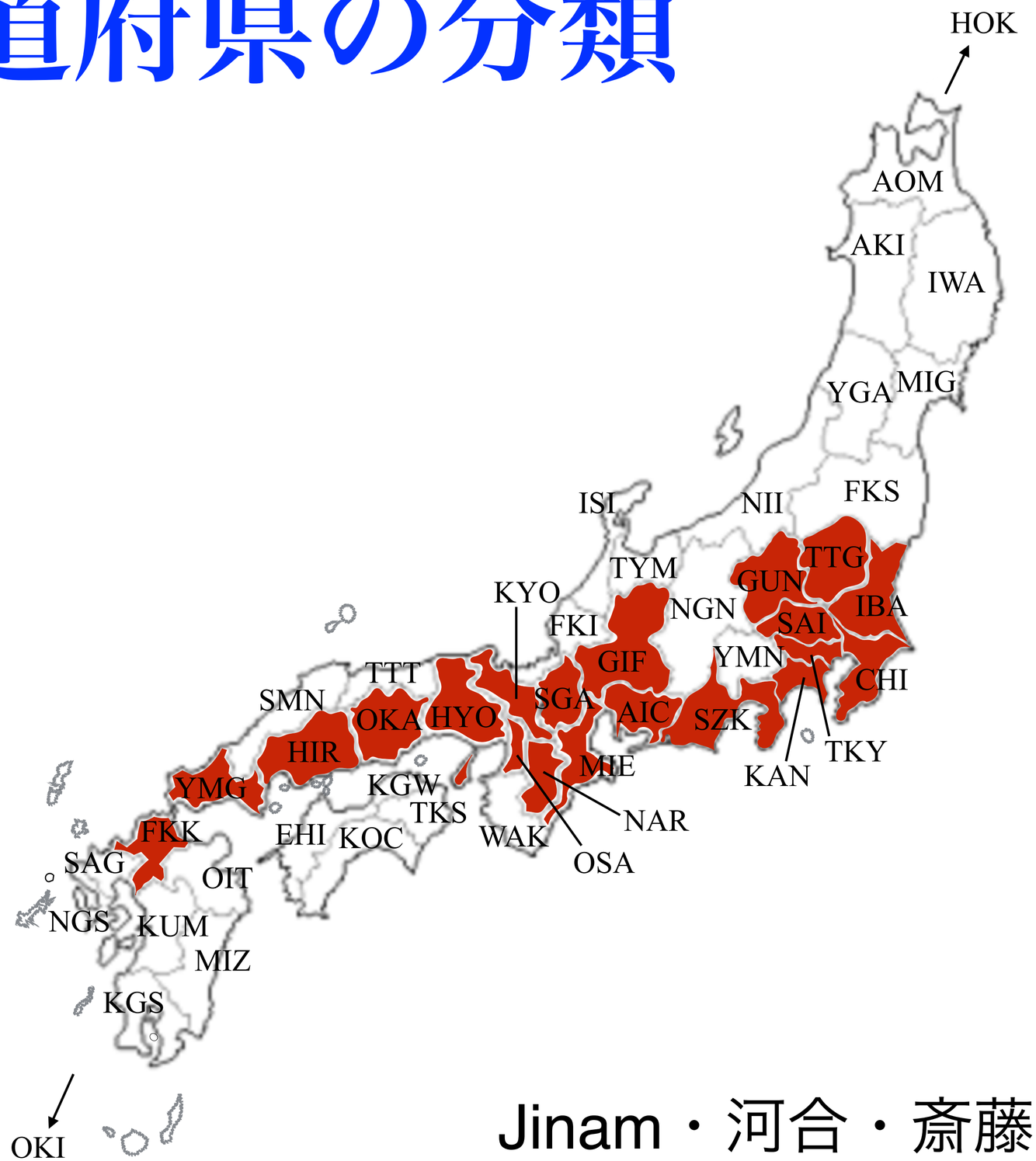
日本47都道府県15000名のミトコンドリアハプロタイプ頻度にもとづく主成分分析結果

(ジェネシスヘルスケア株式会社のデータにもとづく)



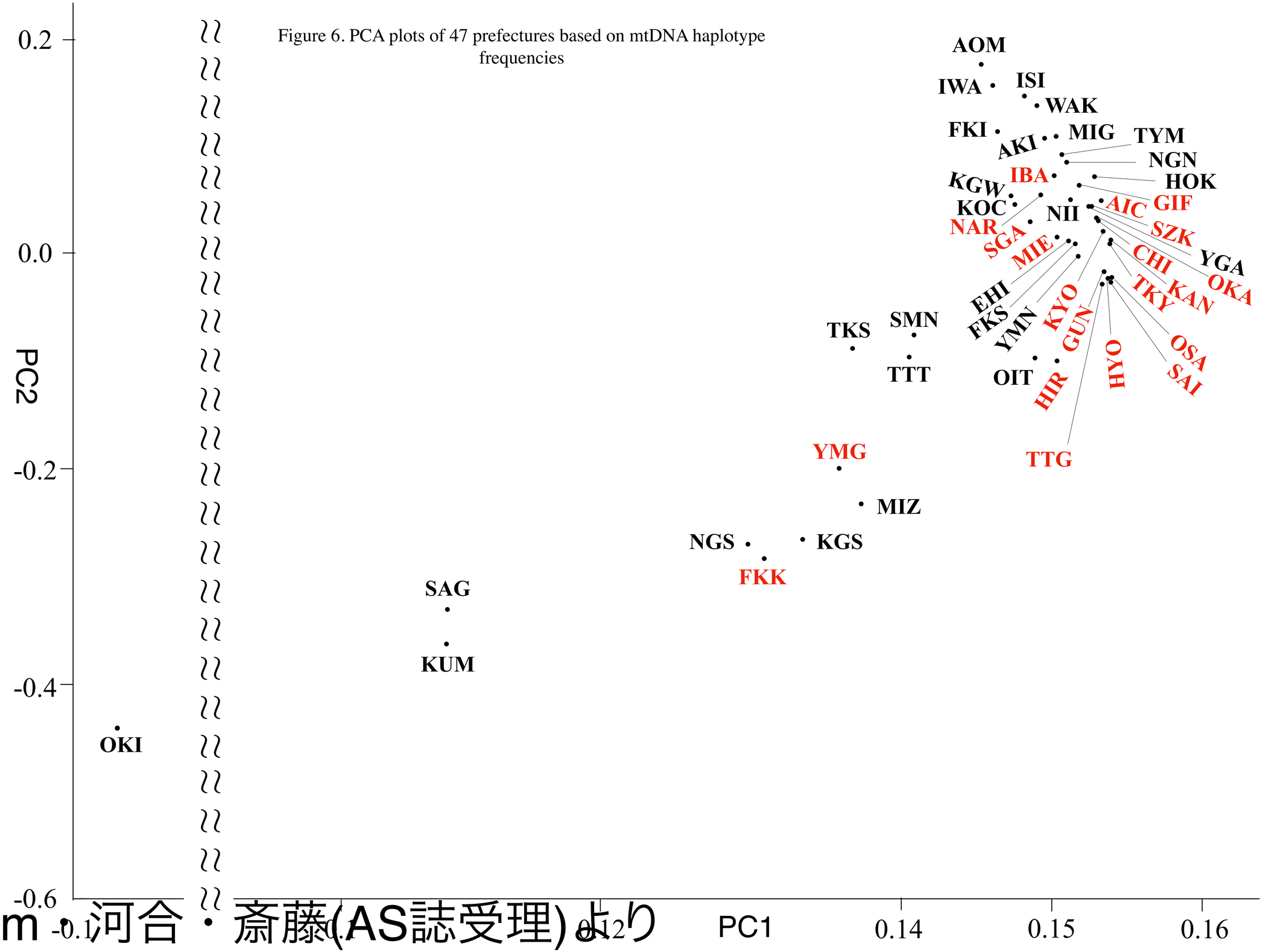
斎藤 (2017)より

47都道府県の分類



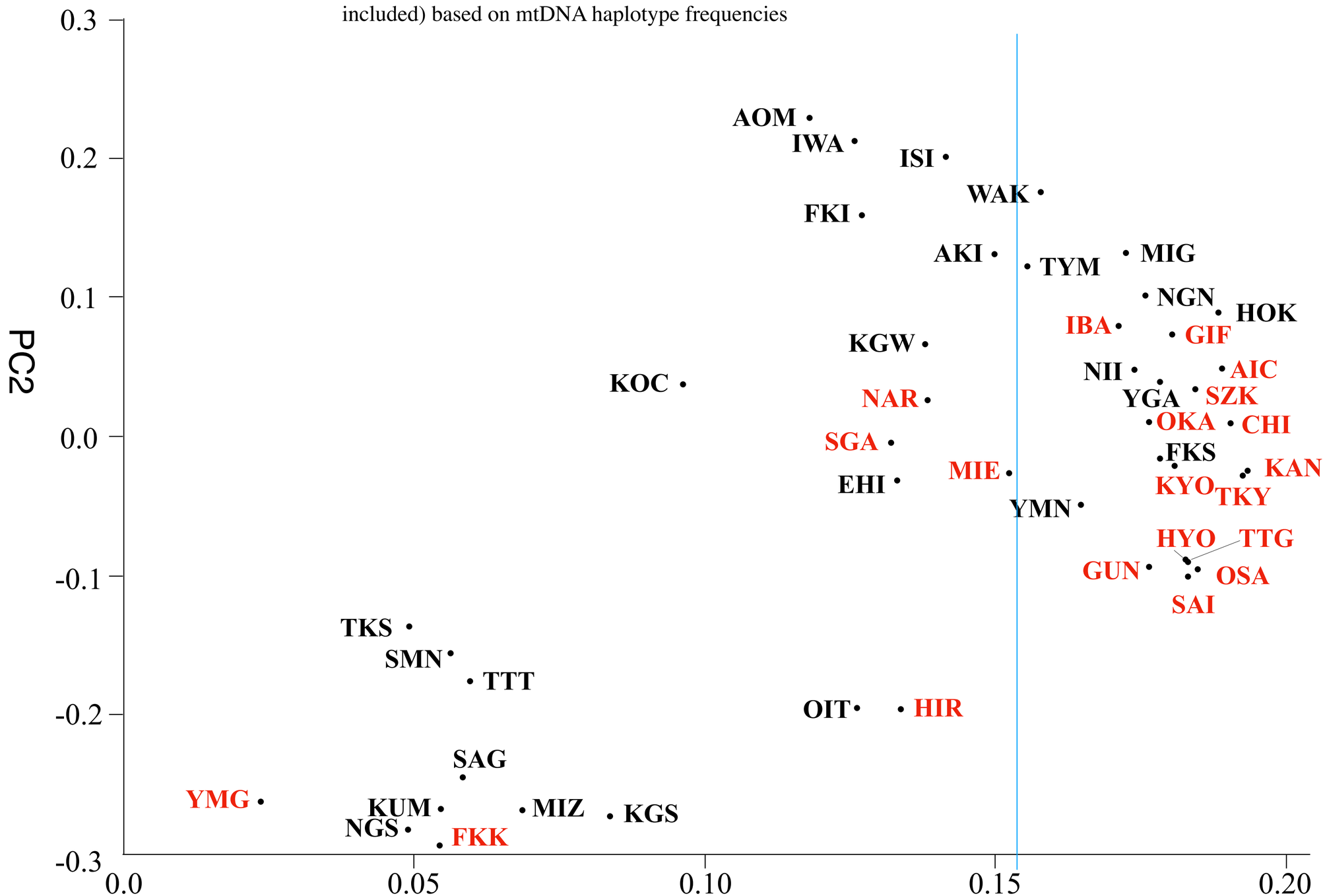
Jinam・河合・斎藤(AS誌受理)より

Figure 6. PCA plots of 47 prefectures based on mtDNA haplotype frequencies



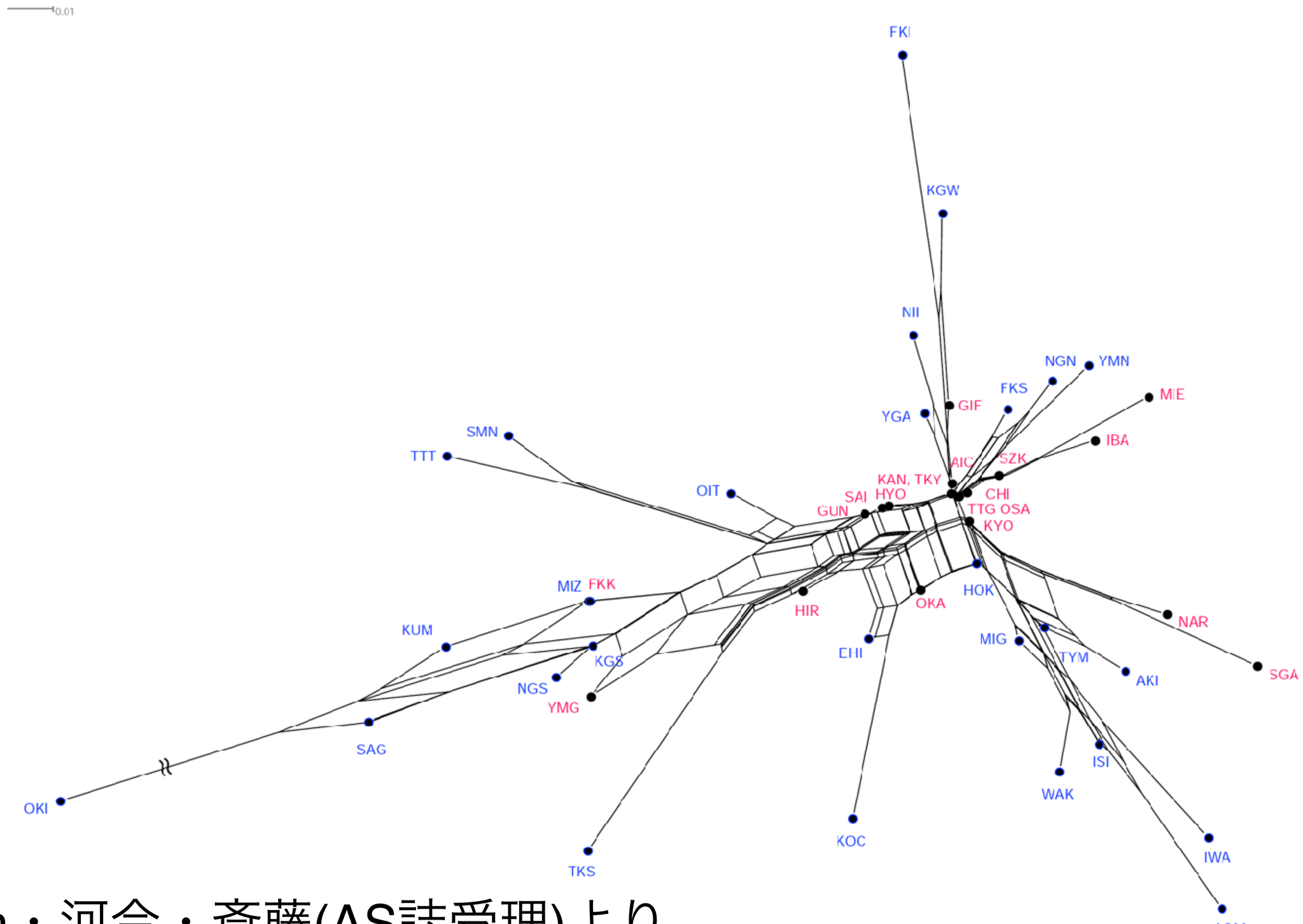
Jinam・河合・斎藤(AS誌受理)より

Figure 4. PCA plots of 46 prefectures (Okinawa is not included) based on mtDNA haplotype frequencies



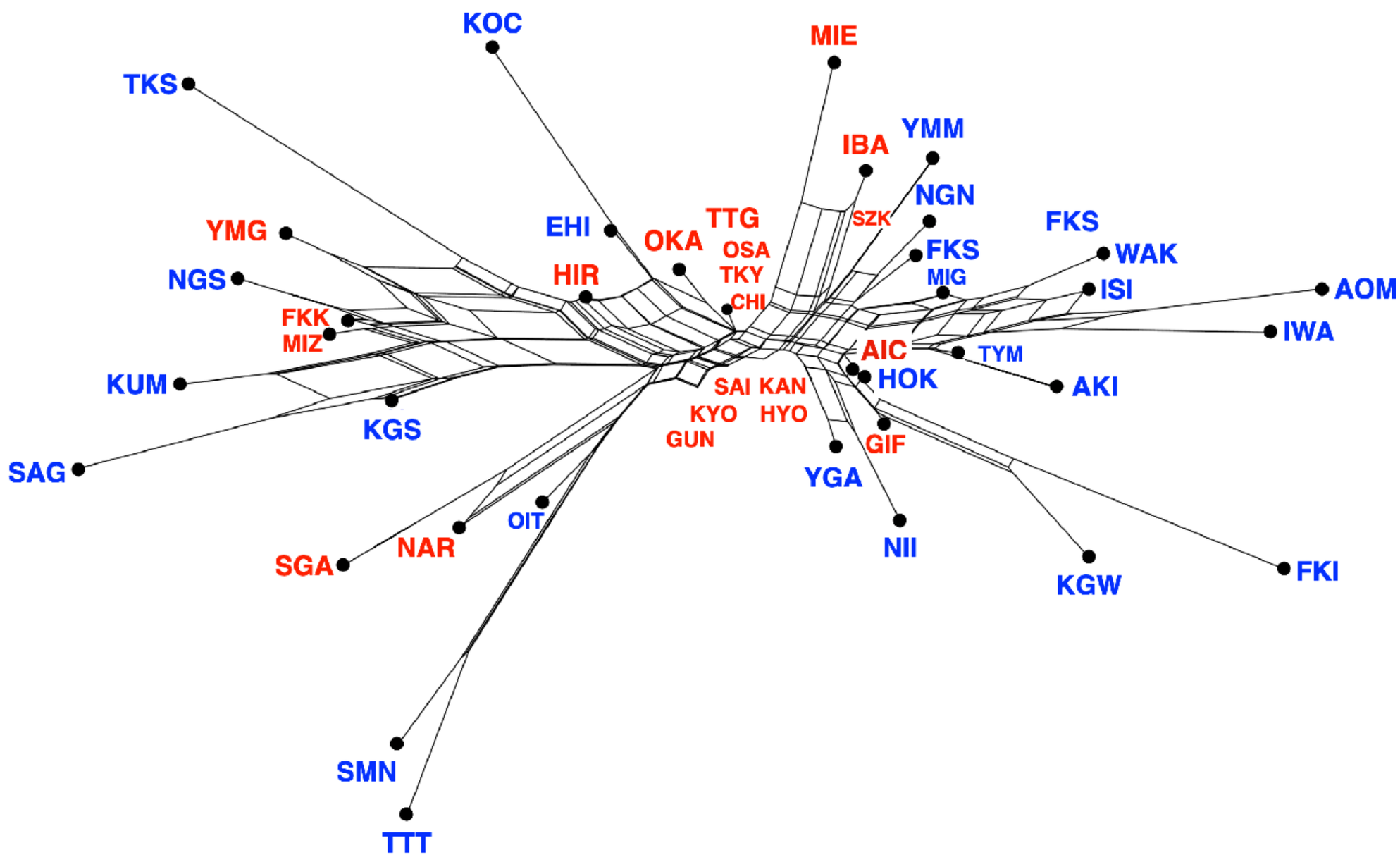
Jinam・河合・斎藤(AS誌受理)より

Figure 5. Phylogenetic network of 47 prefectures based on mtDNA haplotype frequencies



Jinam・河合・斎藤(AS誌受理)より

Figure 6. Phylogenetic network of 46 prefectures (Okinawa is not included) based on mtDNA haplotype frequencies



Jinam・河合・斎藤(AS誌受理)より

日本列島への三段階渡来モデル

斎藤成也(2015)『日本列島人の歴史』より

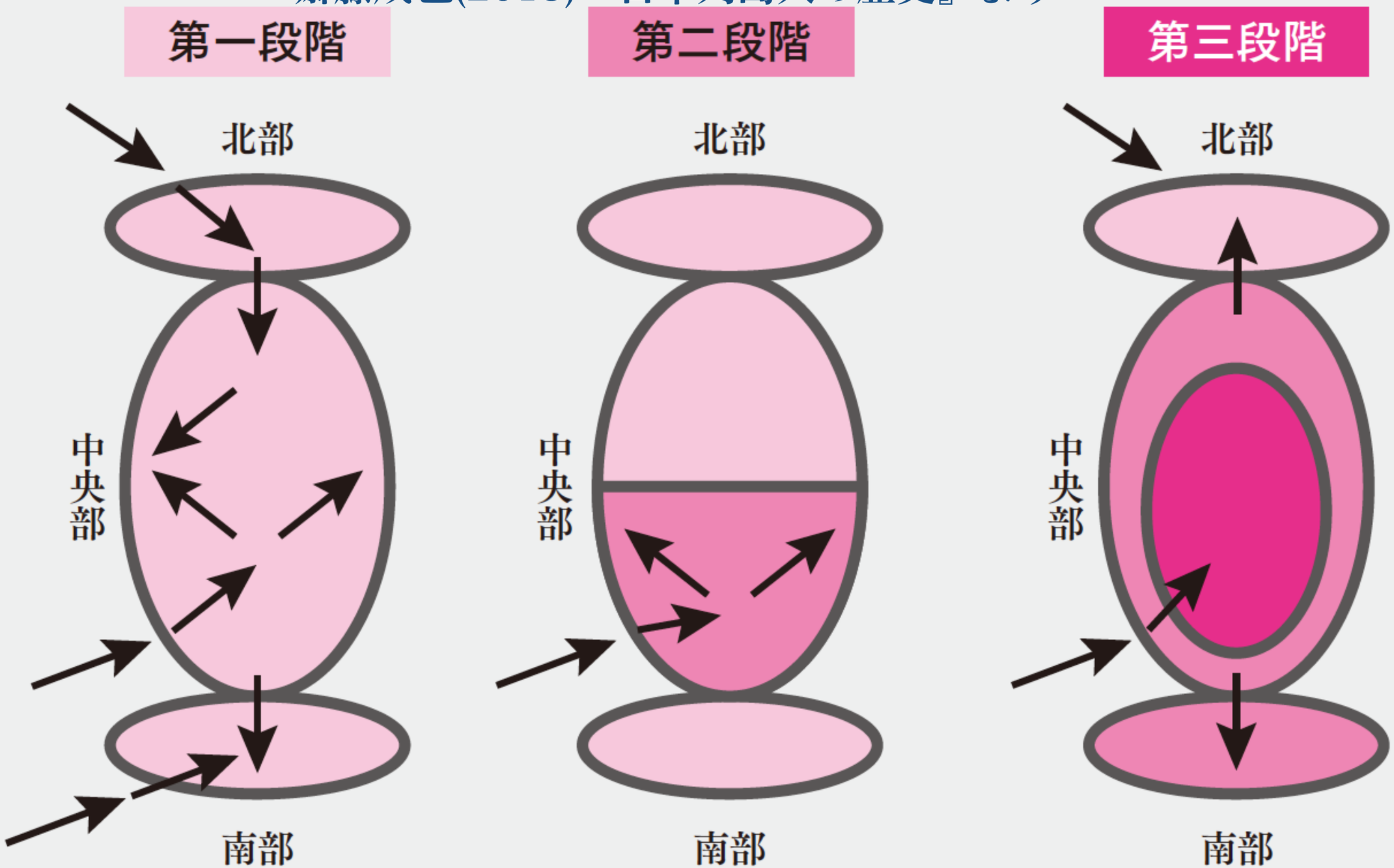


Figure 7: a) Admixture result from k=2 to k=4; b) Cross-validation error of admixture from k=2 to k=7

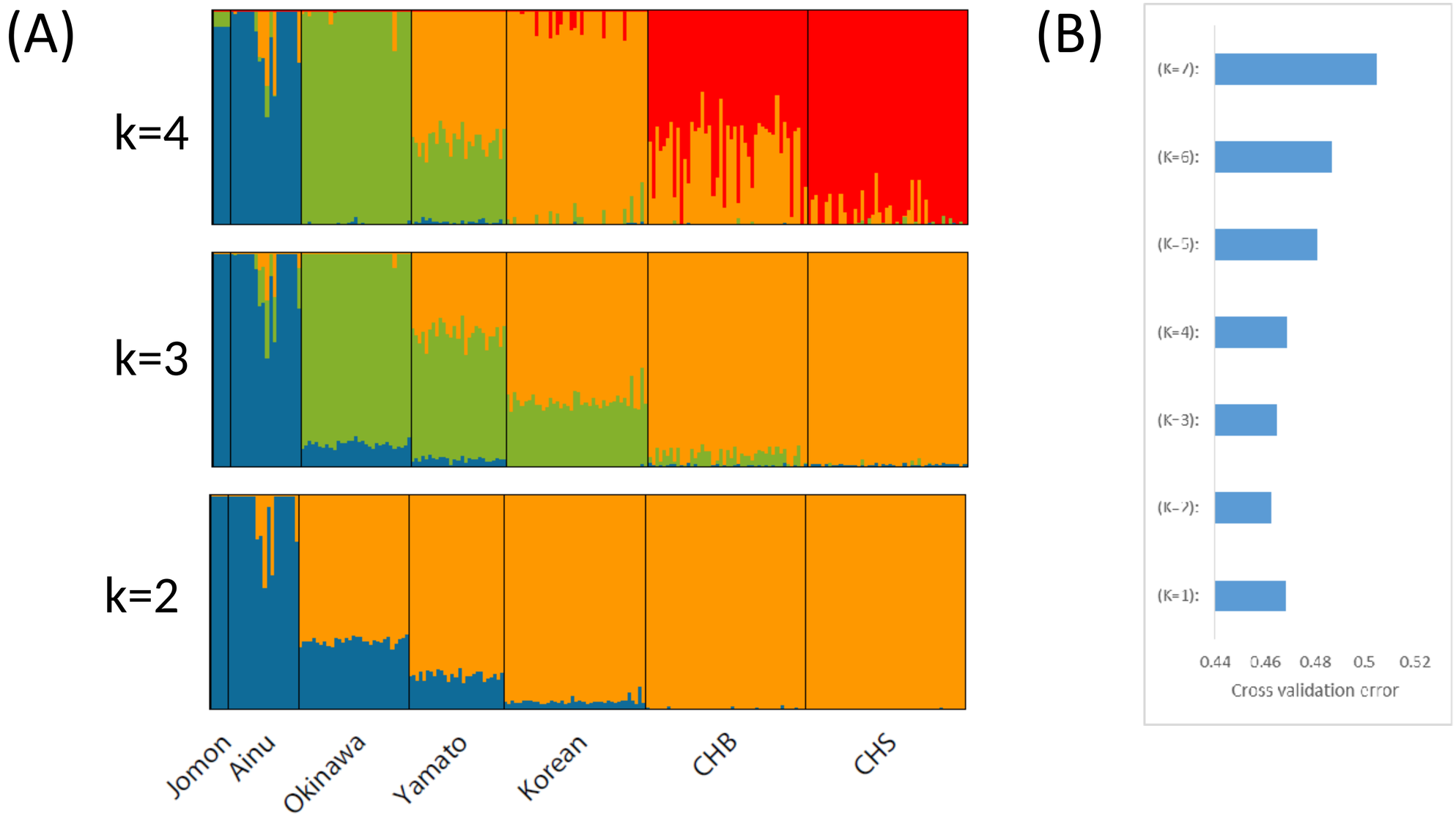


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Figure 2(A) Coding region

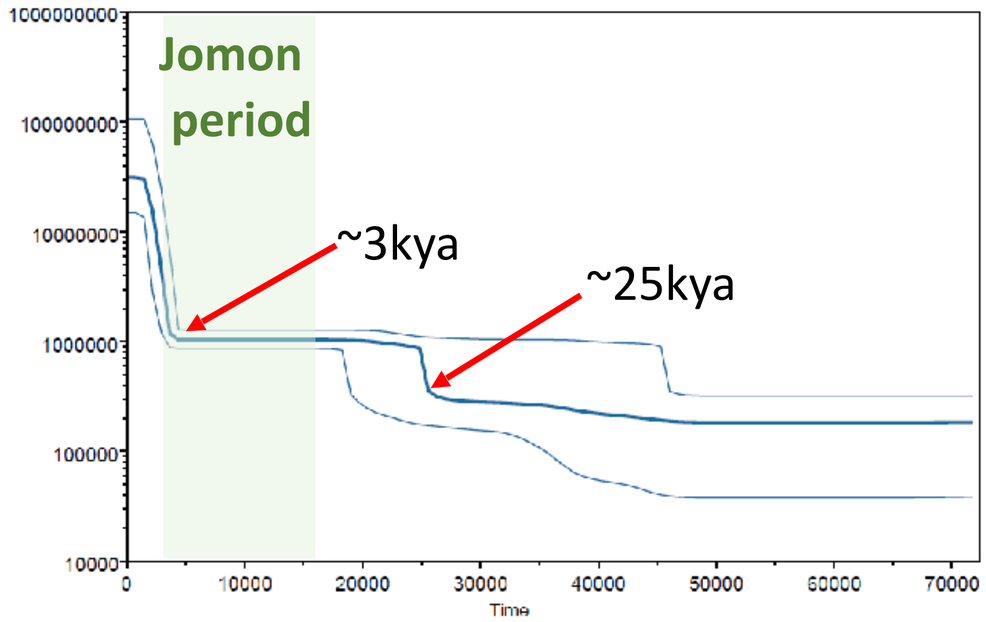
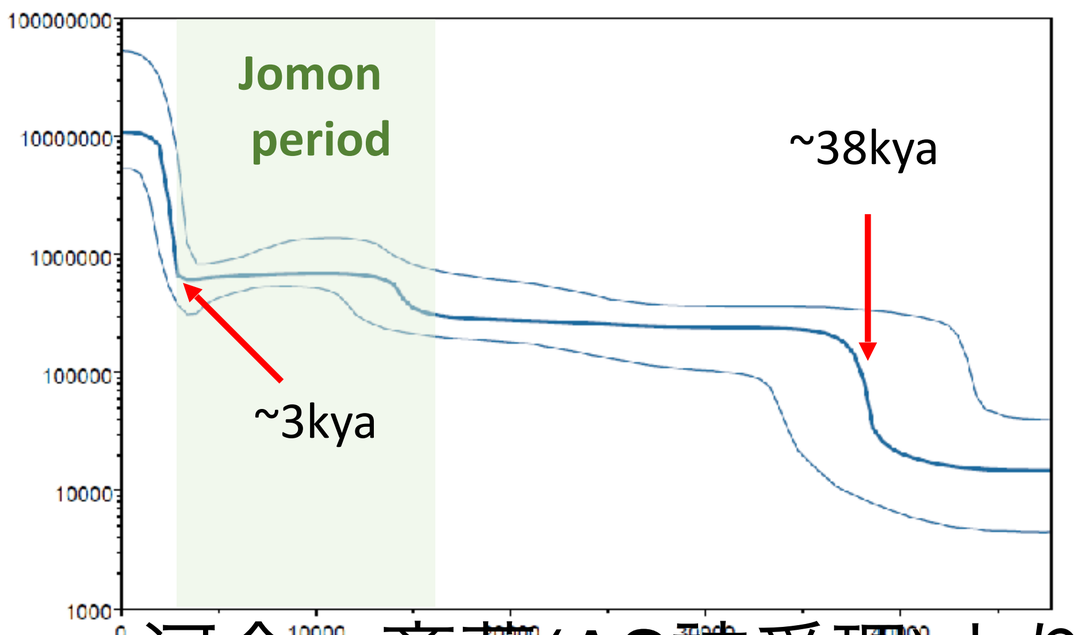


Figure 2 (B) Whole mtDNA



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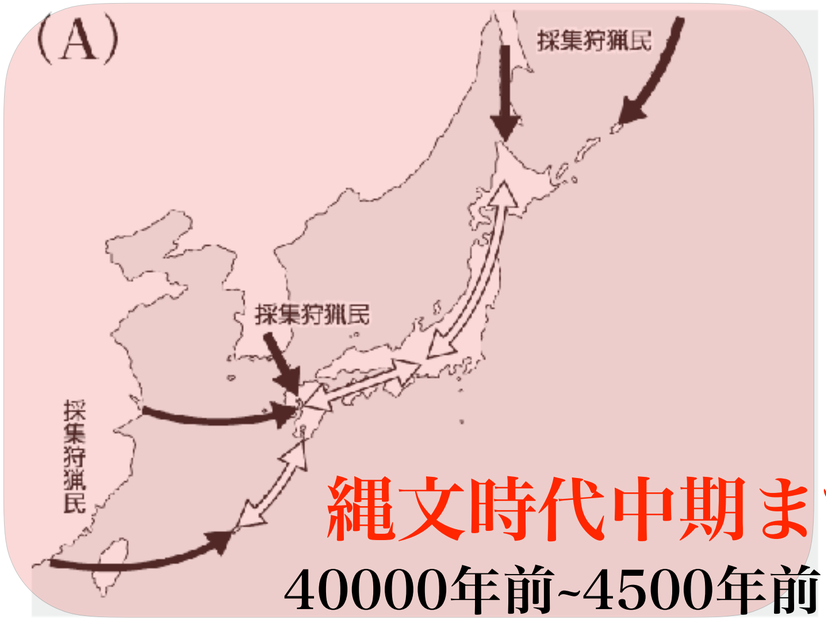
日本列島への三段階渡来モデルにもとづく渡来時期

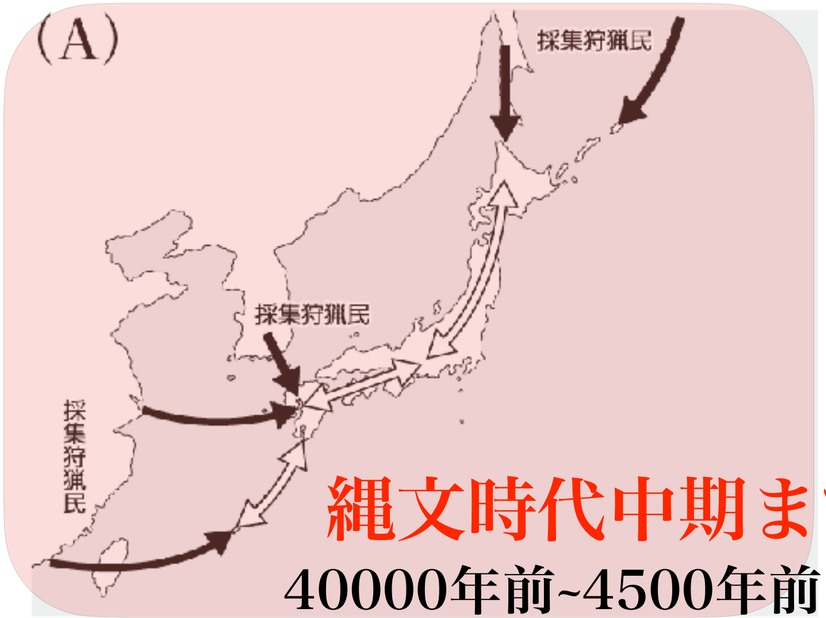
可能性1



斎藤成也(2017)より

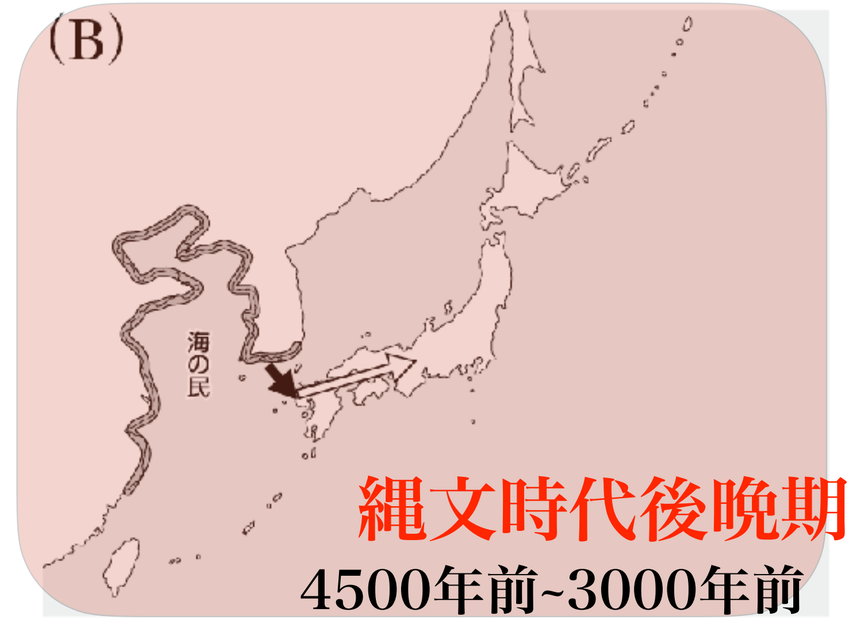
日本列島への三段階渡来モデルにもとづく渡来時期

可能性2



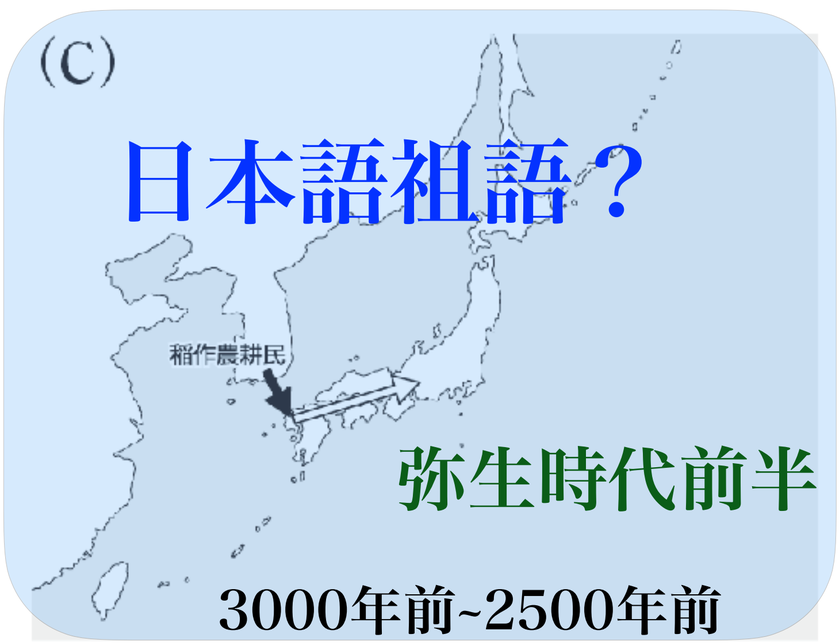
縄文時代中期まで

40000年前~4500年前



縄文時代後晩期

4500年前~3000年前



日本語祖語？

弥生時代前半

3000年前~2500年前

弥生時代後半以降

2500年前～現在