

# Preface to the special issue on the Yaponesia Genome Project

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We started the five-year ‘Yaponesia Genome Project’ in 2018. This project is one of those funded by a MEXT Grant-in-Aid for Scientific Research on Innovative Areas. The project home page is at [http://www.yaponesian.jp/index\\_e.php](http://www.yaponesian.jp/index_e.php). I am leader of this project. Please also see the introduction of this project reported by the Yaponesian Genome Project Managing Group (2020) in the new journal *iDarwin*.

There are six research groups in this project as follows (\* indicates the principal investigator of each group). Group A01—study modern human genomes. Members: Naruya Saitou\*, Ituro Inoue, Koichiro Yoshiura, Timothy A. Jinam, and Masatoshi Matsunami. Group A02—study ancient human genomes. Members: Ken-ichi Shinoda\*, Noboru Adachi, Tsuneo Kakuda, Takehiro Sato, and Hideaki Kanzawa-Kiriyama. Group A03—study animal and plant genomes. Members: Hitoshi Suzuki\*, Ryuichi Masuda, Takeshi Itoh, and Toshinori Endo. Group B01—study archaeological data. Members: Shin’ichiro Fujio\*, Naoko Kinoshita, Akira Seike, Yasuhiro Yamada, and Tatsuhiko Hamada. Group B02—study linguistic data. Members: Mitsuaki Endo, Nobuko Kibe, Shigehisa Karimata, Hiroshi Nakagawa, and Shinjiro Kazama. Group B03—study new genome data. Members: Naoki Osada\*, Yosuke Kawai, Akihiko Fujimoto, and Jun Gojobori.

There are also two-year limited research groups A04 and B04 as follows. Group A04 members: Kosuke Hanada, Kazuyoshi Hosomichi, Tadashi Imanishi, Ryosuke Kimura, Ken Naito, Kazuhiro Nakayama, Jun Ohashi, Hiroki Oota, Yoichi Sato, Kazuhiro Satomura, and Yohey Terai. Group B04 members: Reiko Aso, Kyoko Funahashi, Yuka Hayashi, Masakado Kawata, Takumi Nishiuchi, and Masami Takenaka.

Professor Hiroki Oota of The University of Tokyo, who is a member of Group A04, is also editor-in-chief of *Anthropological Science*. He kindly offered to publish a special issue of *Anthropological Science* on the Yaponesia Genome Project. I thus asked the principal investigators of the six research groups to contribute either a review or an original investigation of their research area to *Anthropological Science*. Group B01 declined to contribute an article; however, Professor Oota himself contributed one review article to this issue. Thus, there are six articles, four original investigations

and two reviews, in this special issue as follows.

Two review articles were contributed by Group B03 (Osada and Kawai) and by Group A04 (Koganebuchi and Oota). Osada and Kawai (2021) reviewed usage of genome-wide SNP data for estimating human migrations to Yaponesia. Koganebuchi and Oota (2021) reviewed human paleogenomic studies in East Asia including Yaponesia. Although it is a review article, Osada and Kawai (2021) found a weak but significant genetic tie of Jomon people to ancient North Siberians through meta-analysis of publicly available datasets.

Four original articles were contributed by Groups A01 and B03 (Jinam, Kawai, and Saitou), Group A02 (Adachi, Kanzawa-Kiriyama, Nara, Kakuda, Nishida, and Shinoda), Group A03 (Suzuki), and Group B02 (Endo).

Jinam et al. (2021b) analyzed three datasets of modern Yaponesian genomes, and showed that the ‘inner dual-structure’ model of Yaponesia proposed and discussed by Saitou (2015, 2017), Saitou and Jinam (2017), and Jinam et al. (2021a) is compatible with these datasets.

Adachi et al. (2021) reported the first Jomon genome data from the Higashimyo shell midden site, Kyushu, dated c. 8000 years ago. Their principal-components analysis shows that the genome of Hokkaido Jomon people reported by Kanzawa-Kiriyama et al. (2019) and that of Kyushu Jomon reported by Adachi et al. (2021) are very similar, suggesting striking homogeneity of the Jomon people over a long time.

Suzuki (2021) examined the substitution rates of rodent mitochondrial DNA (mtDNA), and showed the existence of a time dependence of those evolutionary rates. Based on this finding and using mtDNA data reported by Li et al. (2020), he suggested there were two waves of mice migration to Yaponesia: one by the subspecies *M. m. castaneus* 3500–3000 years ago and the other by the subspecies *M. m. musculus* around 2700 years ago. These two migrations fit pretty well with the second and third migrations of humans to Yaponesia proposed by Saitou (2017).

Endo (2021) examined four kinds of toponyms from a literature on the history of three kingdoms in the southern part of the Korean peninsula by Busik et al. (1145). He concluded that Japonic-speaking people still dwelled in the central area of the peninsula and in the northern area of the Yalu River during the three-kingdom period up to the 7th century A.D.

I hope these six articles are useful for researchers studying the origin and developments of Yaponesians.

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