

# GENETIC DIVERSITY OF PACIFIC OYSTER IN JAPAN



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## Background

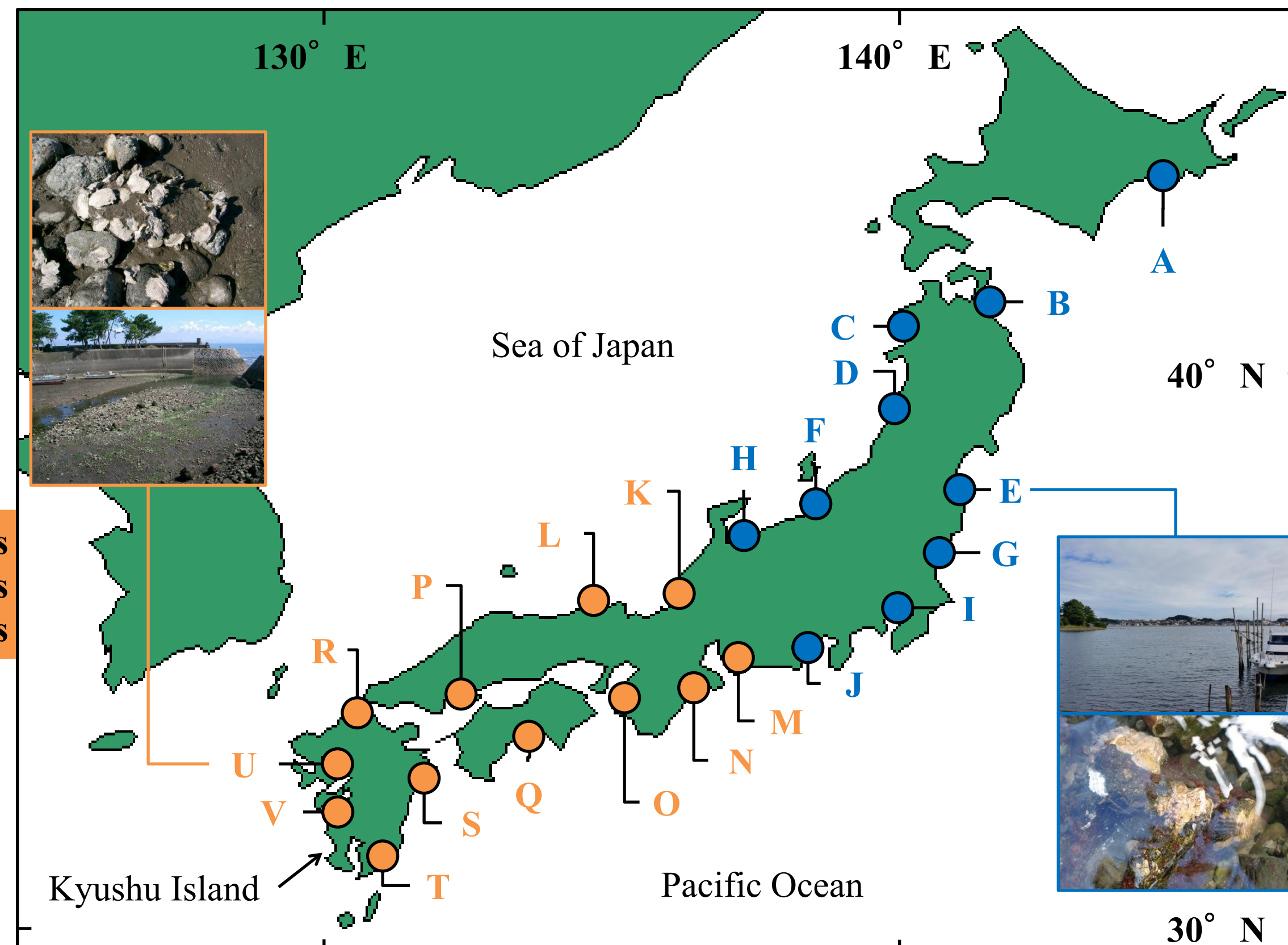
- Pacific oyster has so far been introduced worldwide from Japan.
- Genetic conservation of Pacific oyster in Japan is a prerequisite for sustainable global production.

## Method

- Nucleotide sequence analysis of mtDNA region (507 bp) encoding COI gene to elucidate genetic structure of Pacific oyster throughout Japan

## West Japan

12 sites  
545 individuals  
91 haplotypes



10 sites  
488 individuals  
59 haplotypes

## East Japan

- Small genetic differentiation
- 3 topographically local groups

- Non-significant genetic differentiation
- High gene flow

Fig. 1. Map of Japan, showing 12 sites in west Japan and 10 sites in east Japan at which a total of 1,033 individuals of Pacific oysters were collected.

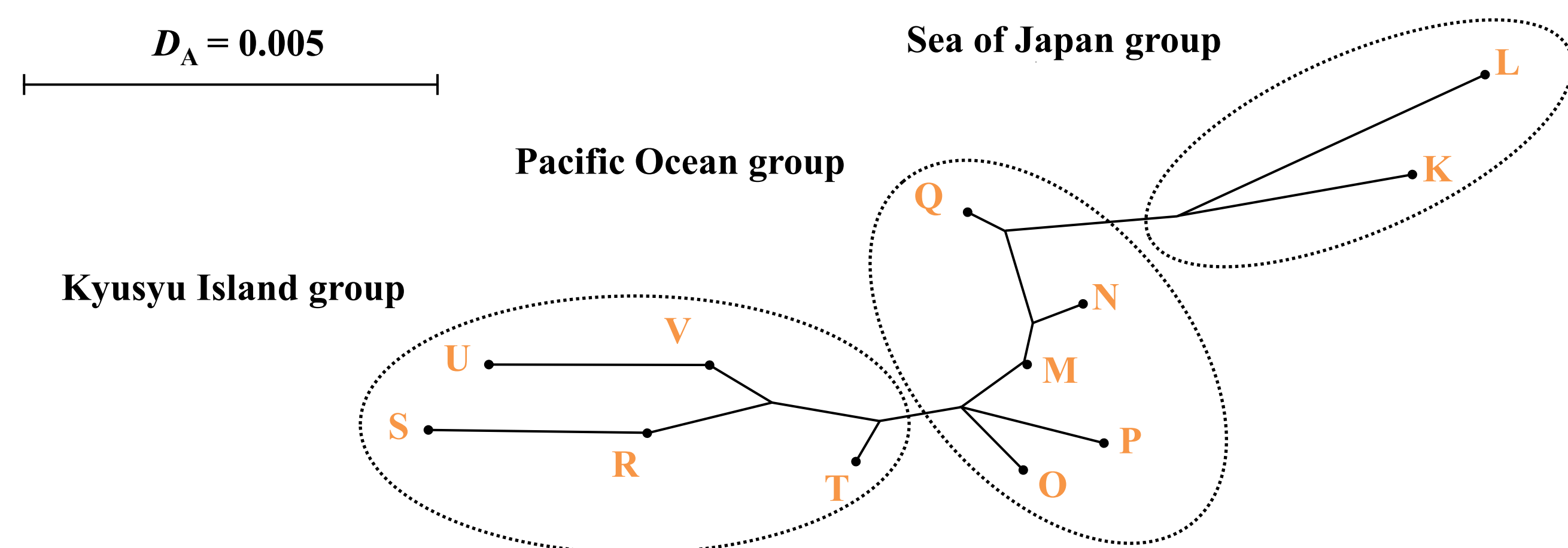


Fig. 2. Neighbor-joining tree summarizing the genetic relationships of pairwise genetic distance ( $D_A$ ) between 12 sites in west Japan.

Table 1 The degree of genetic differentiation in pairwise  $F_{ST}$  values (below diagonal) and the probability of genetic differentiation in  $P$  values (above diagonal) between 10 sites in east Japan

	A	B	C	D	E	F	G	H	I	J
A		0.425	0.421	0.741	0.508	0.398	0.360	0.266	0.904	0.919
B	0.004		0.529	0.549	0.440	0.453	0.747	0.375	0.730	0.913
C	0.003	0.004		0.931	0.918	0.582	0.981	0.669	0.731	0.974
D	0.007	0.005	0.010		0.737	0.512	0.632	0.446	1.000	0.808
E	0.004	0.003	0.011	0.008		1.000	0.784	0.939	0.868	0.924
F	0.003	0.003	0.007	0.004	0.013		0.603	1.000	0.725	0.775
G	0.001	0.008	0.011	0.006	0.009	0.007		0.591	0.541	0.921
H	0.001	0.000	0.006	0.003	0.012	0.014	0.005		0.647	0.747
I	0.009	0.008	0.008	0.011	0.010	0.009	0.005	0.007		0.970
J	0.009	0.010	0.011	0.008	0.010	0.009	0.010	0.008	0.012	

## All Japan

- Shallow haplotype genealogy (Fig. 3)
- Gene flow from west to east (Fig. 4)
- Unidirectional northeastward migration to subsequent population expansion from southwestern to other regions probably by the ocean currents (Fig. 5)

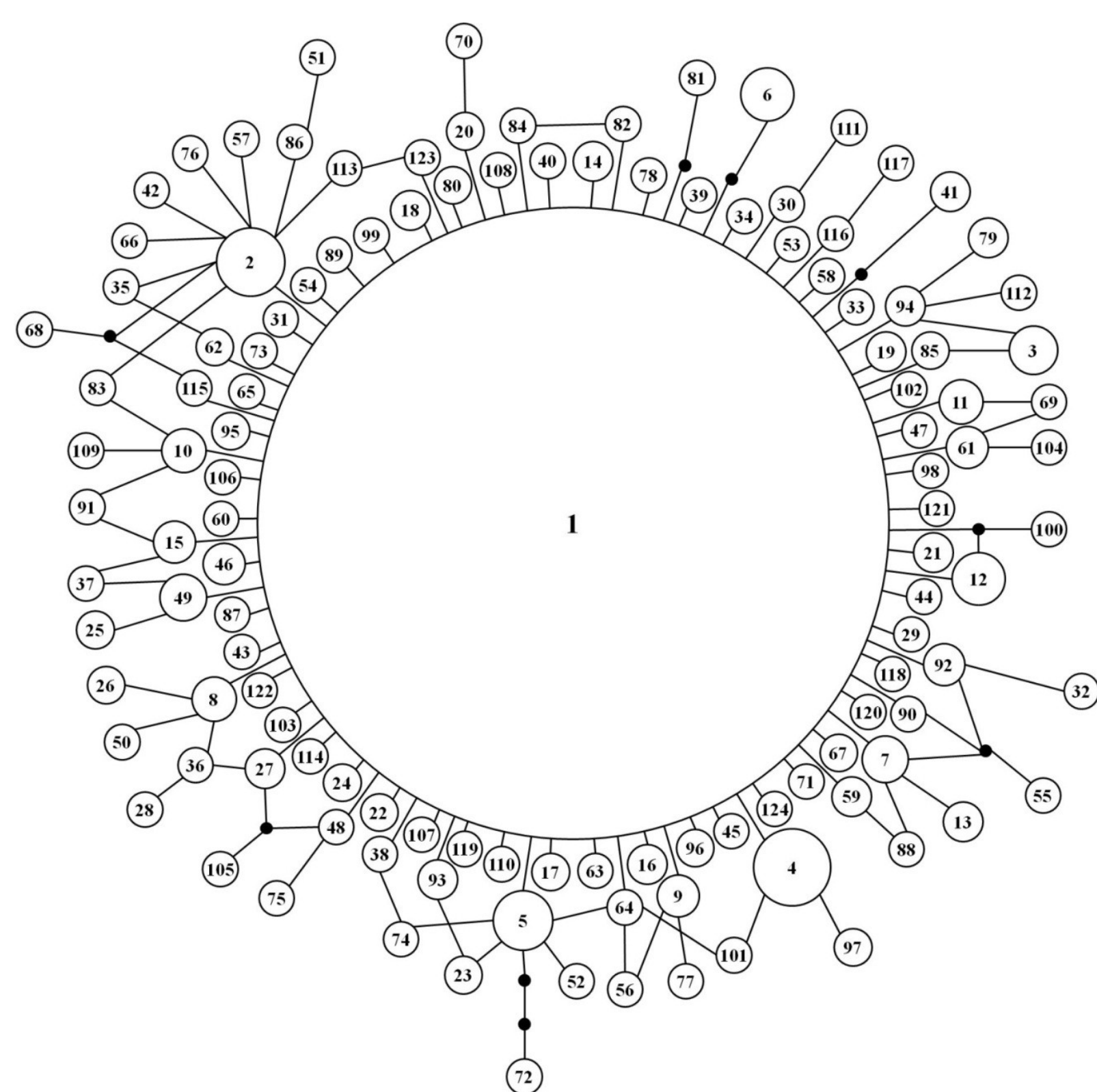


Fig. 3. Parsimony network tree of 124 haplotypes for 1,033 individuals from 22 sites in all Japan. Solid lines and black dots represent single base pair differences among haplotypes and putative mutational step between haplotypes, respectively. Size of circle is proportional to the number of individuals per haplotype.

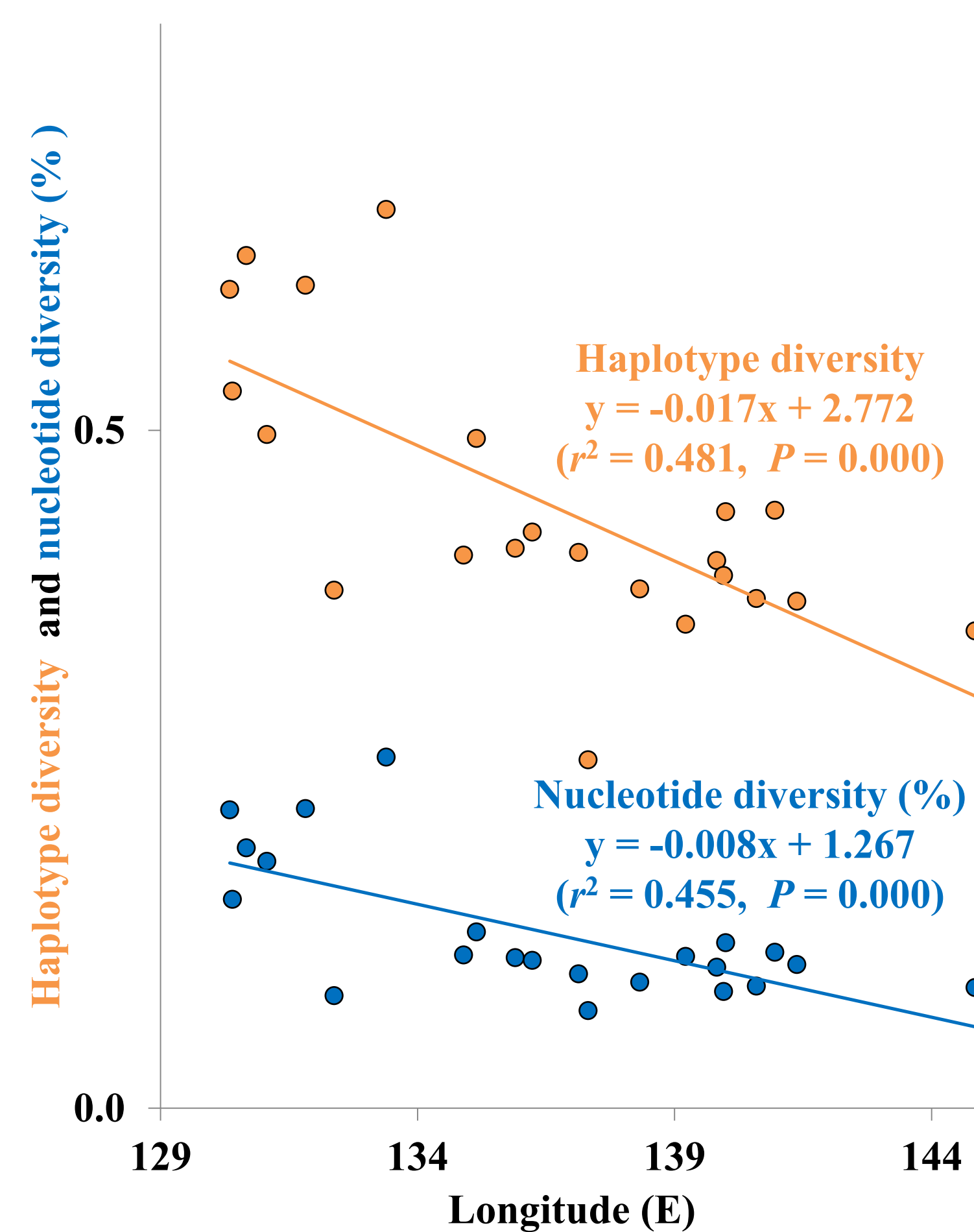


Fig. 4. Regression of haplotype diversity (●) and nucleotide diversity (%) (●) versus geographical longitude (E) of 22 sites in all Japan.

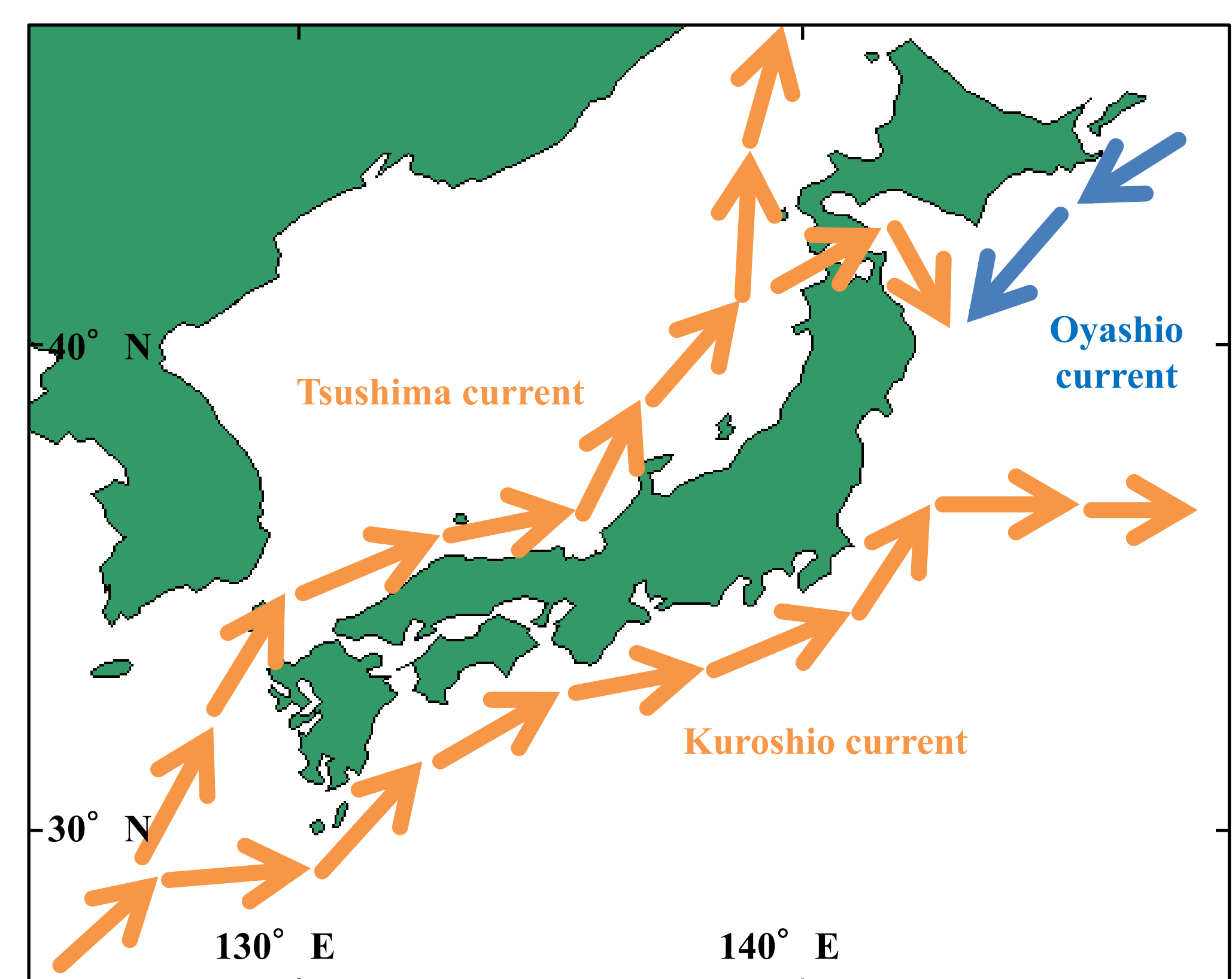


Fig. 5. Ocean currents around all Japan. Orange and blue arrows indicate the warm currents of Kuroshio and Tsushima flowing northeast and the cold current of Oyashio flowing southwest, respectively.