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Polymorphisms in the *ABO* blood group gene in three populations in the New Georgia group of the Solomon Islands

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Abstract To examine genetic affinity among Oceanian populations, polymorphisms of exons six and seven of the *ABO* blood group gene (*ABO*) were investigated in three populations—Munda town, Paradise village, and Rawaki village—in the New Georgia group of the Solomon Islands. The Munda and Paradise populations consist of Austronesian (AN)-speaking Melanesians; the Rawaki population consists of AN-speaking Micronesians who migrated from the Gilbert Islands to the New Georgia Islands approximately 30 years ago. We recently described the polymorphisms of *ABO* in three other Oceanian populations—Balopa

Islanders (AN-speaking Melanesians), Gidra (non-AN-speaking Melanesians), and Tongans (AN-speaking Polynesians). The results from these six Oceanian populations suggest: (1) the main alleles in Oceanian populations are *ABO**A101, *ABO**A102, *ABO**B101, *ABO**O01, and *ABO**O02, among which the most predominant is *ABO**O01, and (2) there are marked differences in the *ABO* allele frequency spectrum among Oceanian populations. The different geographical distribution of *ABO* alleles provides insight into the migration history of AN-speaking populations in Oceania.

Keywords *ABO* blood-group gene · Austronesian · Solomon Islands · Melanesian · Micronesian · Molecular anthropology

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Introduction

The *ABO* blood group gene (*ABO*) has high polymorphism at the molecular level (see Yip (2002) for review), and the allele frequency distribution of *ABO* differs among populations (Ogasawara et al. 1996; Olsson et al. 1998; Kobayashi et al. 1999; Iwasaki et al. 2000; Roubinet et al. 2001; Ohashi et al. 2004). Because of these characteristics, the *ABO* gene can serve as a genetic marker suitable for studying genetic affinity among populations.

We recently described the polymorphisms of *ABO* in three Oceanian populations:

- 1 Austronesian (AN)-speaking Melanesians in the Balopa islands of Manus Province of Papua New Guinea, located at the northwestern end of the Bismarck Archipelago;
- 2 non-Austronesian (NAN)-speaking Melanesians, known as Gidra, in the southwestern lowlands of Papua New Guinea; and
- 3 AN-speaking Polynesians living in Tonga.

It has been suggested that the AN-speaking groups who are ancestors of the Polynesian appeared at the main island of New Guinea approximately 5,000 years ago and moved eastward along the northern coast to the Bismarck Archipelago. Before the appearance of the AN-speaking groups, many islands of Melanesia, for example the Bismarck Archipelago and the Solomon islands had been occupied by NAN-speaking Melanesians. The AN-speaking groups are, therefore, believed to have come into contact with NAN-speaking Melanesians in Near Oceania. The extent of admixture between the AN-speaking newcomers and indigenous Melanesians is not fully understood, however. From *ABO* allele frequency data we concluded that Balopa Islanders, who are thought to be descendants of the indigenous Melanesians, were genetically more similar to the Polynesian Tongans than to the NAN-speaking Melanesian Gidra (Ohashi et al. 2004). Another finding of our previous study was that *ABO***A102* is useful for distinguishing AN-speaking groups from NAN-speaking groups in Melanesia, because this allele was found in Balopa Islanders and Tongans (AN-speaking Melanesians and Polynesians) but not in Gidra (NAN-speaking Melanesians) (Ohashi et al. 2004). *ABO***A102* has been reported to be a predominant *ABO***A* allele in East Asian populations—the allele frequencies of *ABO***A101* and *ABO***A102* are 2.3 and 18.6% in Han and 4.4 and 23.5% in Japanese populations (Ogasawara et al. 1996; Iwasaki et al. 2000). Because the AN-speaking groups are believed to have come from Asia/Taiwan, this allele may have been brought to island Melanesia by them.

As far as we are aware, however, *ABO* polymorphisms have not been analyzed in other Oceanian populations. Thus, more Oceanian populations should be examined to enable comprehensive understanding of *ABO* polymorphism and genetic admixture in Oceania. To achieve this goal, we investigated polymorphisms of *ABO* exons six and seven in three populations (Fig. 1)—Munda town, Paradise village, and Rawaki village in the New Georgia group of the Solomon Islands. The Munda and Paradise populations are AN-speaking Melanesians and the Rawaki population are AN-speaking Micronesians who migrated from the Gilbert Islands, Kiribati, to the New Georgia Islands, Solomon, approximately 30 years ago. These results also have implications in the study of migration history, especially of AN-speaking groups.

Materials and methods

Subjects

The polymorphisms of the *ABO* blood group gene were investigated for 39 individuals living in Munda town, 46 in Paradise village, and 46 in Rawaki village. These locations are shown in Fig. 1. Munda is the main town on New Georgia Island in the western Solomon Islands. Paradise is a coastal village, 32 km north of Munda. The

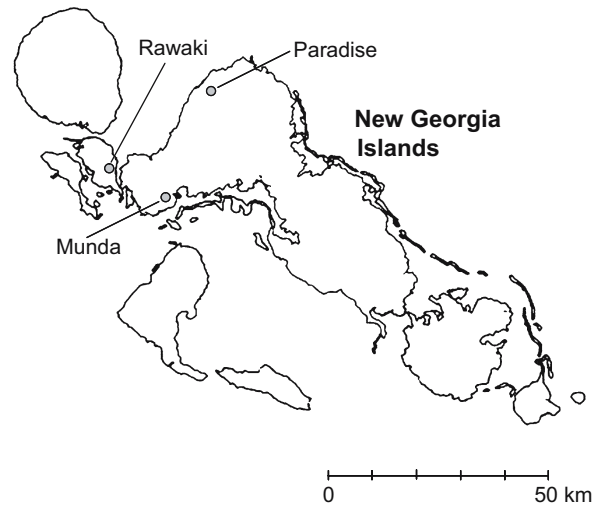


Fig. 1 Map of the New Georgia Islands showing the locations of the three populations studied

Paradise villagers are thought to have originally lived in a mountainous area and moved to the northern coast of New Georgia Island. Rawaki village is located on the New Georgia Islands, but Rawaki villagers are AN-speaking Micronesians who migrated from the Gilbert Islands, Kiribati, to the New Georgia Islands approximately 30 years ago. Thus, in this study, two AN-speaking Melanesian populations and one AN-speaking Micronesian population were investigated. Blood was sampled after obtaining informed written consent from each participant. This study was approved by the Health Ethics Committee, Ministry of Health, Solomon Islands, the Ministry of Education and Training, Solomon Islands, and the Research Ethics Committee of the Faculty of Medicine, The University of Tokyo.

Molecular typing of *ABO* gene

Genomic DNA was extracted from peripheral blood using a QIAamp Blood Kit (Qiagen, Hilden, Germany). Genotyping for exons six and seven of the *ABO* gene was performed as described previously (Ohashi et al. 2004). As in our previous study, we performed both gel electrophoresis-based typing and direct sequencing for all the subjects to determine the genotypes.

Statistical analysis

Allele frequencies of the *ABO* gene were estimated by direct counting. The *ABO* allele frequency data for Balopa Islanders, Gidra, and Tongans were obtained from our previous study (Ohashi et al. 2004). To examine genetic affinities based on *ABO* allele frequencies, Arlequin software (Schneider et al. 2000) was used for calculation of population pairwise fixation indices (F_{ST} values), which were subsequently tested for signif-

ificance. The neighbor-joining (NJ) tree was constructed for six populations based on the pairwise F_{ST} values. Principal components (PC) analysis was also performed to examine genetic affinities among the six Oceanian populations.

Results

The *ABO* allele frequencies for the Munda, Paradise, and Rawaki populations are presented in Table 1. As in our previous study of Oceanian populations (Ohashi et al. 2004), five *ABO* alleles (*ABO**A101, *ABO**A102, *ABO**B101, *ABO**O01, and *ABO**O02) were observed (Fig. 2), although the frequency distribution differed among populations. Interestingly, approximately 95% of *ABO* alleles in Paradise village were *ABO**O01 or *ABO**O02. The Paradise population is believed to have been both small and isolated. Thus, the observed high frequency of *ABO**O alleles in Paradise may have been caused by random genetic drift or a founder effect.

Figure 3 shows the geographic distribution of the *ABO* alleles in Oceanian populations, with data for Gidra, Balopa Islanders, and Tongans from our previous study (Ohashi et al. 2004). The *ABO* allele frequencies in the Munda population were similar to those in the Balopa population, which was expected because

both groups are AN-speaking Melanesians. The allele frequency of *ABO**B101 was found to be high in the Rawaki population. It would be interesting to study the polymorphisms of *ABO* in other Micronesian populations to examine whether the high frequency of *ABO**B101 is a general characteristic of Micronesians.

Pairwise F_{ST} values were calculated as a measure of genetic distance (Table 2). The highest F_{ST} value of 0.221 ($P < 10^{-5}$) was observed between Rawaki and Paradise villagers. For Munda villagers small pairwise F_{ST} values of 0.014, 0.012, and 0.017 were obtained for Gidra, Balopa Islanders, and Tongans, respectively. Nevertheless, a relatively large F_{ST} value of 0.081 ($P < 10^{-5}$) was obtained between Munda and Paradise villagers, although they are AN-speaking Melanesians and they live close to each other. This may suggest that significant migration or admixture has not occurred for Munda and Paradise villagers. An NJ tree based on pairwise F_{ST} values is shown in Fig. 4a. In the tree, Munda was located between Gidra and Tongan populations whereas the Paradise and Rawaki populations were situated apart from the other populations.

Figure 4b shows results from PC analysis of *ABO* allele frequencies. Each population is plotted in two dimensions based on the coordinates of the two PCs. The contributions of the first and second components were 0.686 and 0.229, respectively (the cumulative contribution was 0.915). As in the NJ tree, Munda was genetically placed between the Gidra and Tongan populations.

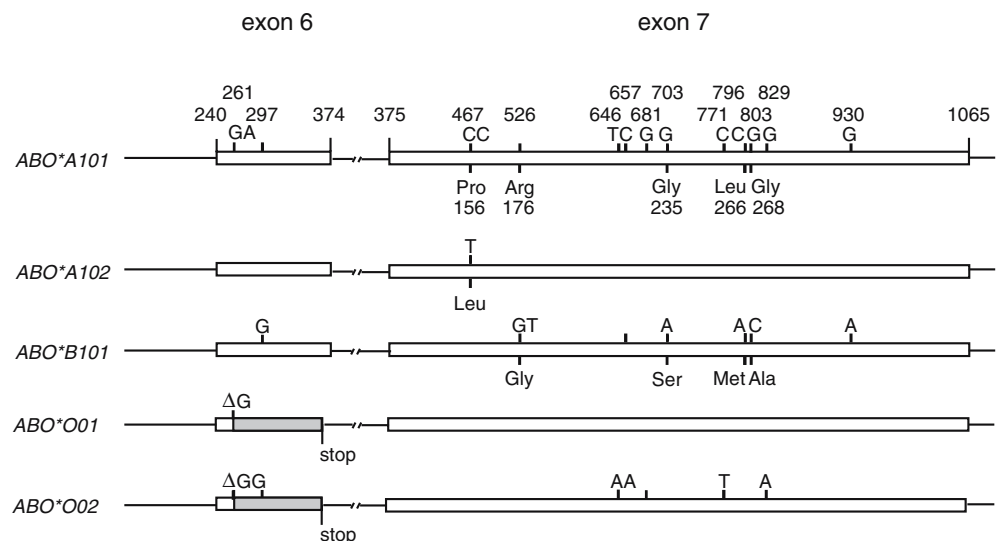
Table 1 Allele frequencies of the *ABO* gene in three populations in the New Georgia group of the Solomon Islands

Allele	Munda (2n = 78)	Paradise (2n = 92)	Rawaki (2n = 92)
<i>ABO</i> *A101	14 (18.0%)	1 (1.1%)	19 (20.6%)
<i>ABO</i> *A102	10 (12.8%)	2 (2.2%)	15 (16.3%)
<i>ABO</i> *O01	45 (57.7%)	72 (78.2%)	26 (28.3%)
<i>ABO</i> *O02	4 (5.1%)	15 (16.3%)	13 (14.1%)
<i>ABO</i> *B101	5 (6.4%)	2 (2.2%)	19 (20.7%)

Discussion

Polymorphisms of *ABO* were studied for three populations living in the New Georgia group of the Solomon Islands. Taking these results together with those from our previous study (Ohashi et al. 2004), we conclude that:

Fig. 2 Nucleotide and amino acid sequence differences among the five *ABO* alleles detected in this study. Only differences from the nucleotide and amino acid sequences of *ABO**A101 are indicated



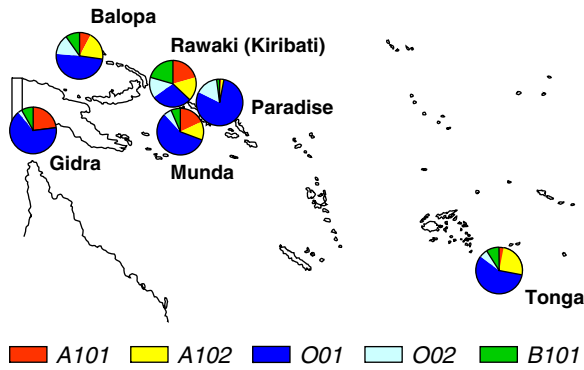


Fig. 3 Map displaying the geographic distribution of *ABO* alleles in Oceania. It should be noted that Rawaki villagers migrated from the Gilbert Islands, Kiribati, to the New Georgia Islands 30 years ago. They should, therefore, be genetically regarded as Micronesians. The data for Gidra, Balopa Islanders, and Tongans were obtained from our previous study (Ohashi et al. 2004)

Table 2 Pairwise F_{ST} values among six Oceanian populations

	Munda	Paradise	Rawaki	Gidra	Balopa
Paradise	0.0811				
Rawaki	0.0653	0.2214			
Gidra	0.0141	0.0793	0.1302		
Balopa	0.0121	0.0947	0.0379	0.0722	
Tonga	0.0169	0.0964	0.0809	0.0847	0.0028

- 1 the main alleles in Oceanian populations are *ABO***A101*, *ABO***A102*, *ABO***B101*, *ABO***O01*, and *ABO***O02*, among which the predominant *ABO* allele in Oceanian populations is *ABO***O01*; and
- 2 there is marked difference in the *ABO* allele frequency spectrum among Oceanian populations. The variety of *ABO* alleles in Oceanian populations enables us to use it as a genetic marker for studying the history of Oceanian populations.

Melanesians can be divided into two groups—AN-speaking and NAN-speaking—on the basis of their languages. It has been suggested that AN-speaking groups are derived from Southeast Asians who reached the main island of New Guinea approximately 5,000 years ago and, by approximately 3,000 years ago, spread into island Melanesia including the Solomon Islands, New Hebrides Islands, and Fiji Islands, and further into western Polynesian islands, for example Tonga and Samoa. Before the AN-speaking populations appeared, the Bismarck Archipelago and the Solomon Islands had already been occupied by NAN-speaking populations whose ancestors had come to Papua New Guinea approximately 50,000 years ago. In studies on the history of Oceanian populations, much attention has been focused on the mixing between AN-speaking and NAN-speaking groups in Melanesia. Our previous studies on the *ABO* and mitochondrial DNA (mtDNA) polymorphisms suggested that extensive gene flow

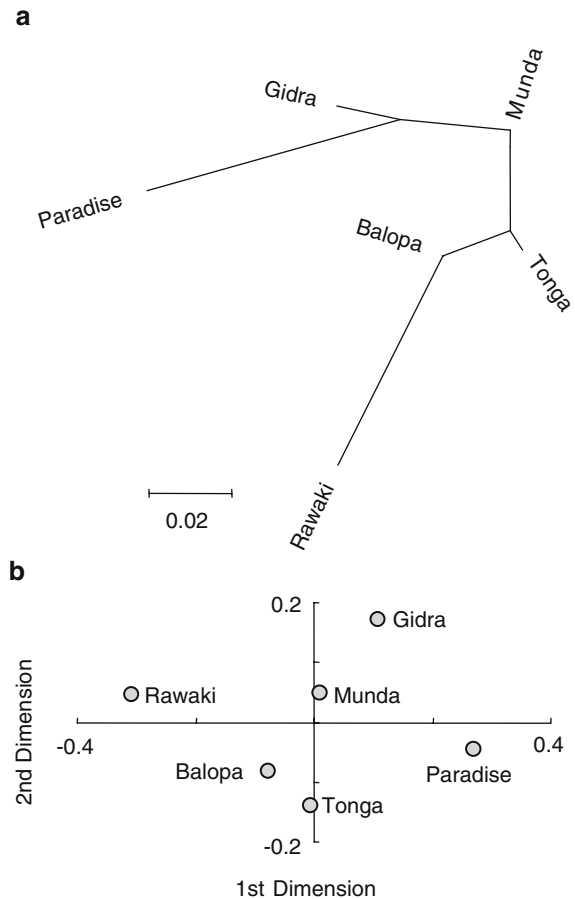


Fig. 4 a An NJ tree for the six populations based on pairwise F_{ST} . b Results from PC analysis for the six populations based on the *ABO* allele frequency distribution. The contributions of the first and second dimensions were 0.686 and 0.229, respectively. The data for Gidra, Balopa Islanders, and Tongans were obtained from our previous study (Ohashi et al. 2004)

occurred from Polynesian ancestors to indigenous Melanesians, because Balopa Islanders (AN-speaking Melanesians) were genetically similar to Tongans (AN-speaking Polynesians) rather than to Gidra (NAN-speaking Melanesians) (Ohashi et al. 2004; Ohashi et al. in press). Thus, the “express train” model, which supposes rapid expansion of Polynesian ancestors along the coast of New Guinea to Polynesia and negligible mixing with indigenous Melanesians (Diamond 1988; Bellwood 1989), is not compatible with our observation for Balopa Islanders of the Bismarck Archipelago. In this study, two AN-speaking populations, Munda and Paradise, in the Solomon Islands were examined, and the Munda population was genetically placed between the Gidra and Tongan populations (Fig. 4). This is also supported by mtDNA polymorphisms (our unpublished data). These results lead us to hypothesize that mixing between Polynesian ancestors and indigenous Melanesians occurred not only in the Bismarck Archipelago, but also in the Solomon Islands.

Among these six Oceanian populations, only the Gidra (NAN-speaking Melanesians) seem to lack the

*ABO**A102** allele (Fig. 3). Thus, *ABO**A102** might be a genetic marker distinguishing AN-speaking groups from NAN-speaking groups in Melanesia. The *ABO**A102** allele in AN-speaking groups in Oceania may have been derived mainly from Polynesian ancestors who presumably had migrated from Asia/Taiwan, although this allele may have been lost in Gidra only, after the ancestors of Gidra had come to Papua New Guinea. To examine this, *ABO* polymorphisms need to be investigated in more NAN-speaking Melanesian populations.

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