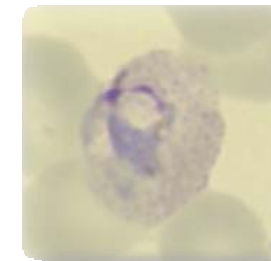


Origin of *Plasmodium vivax* in the Republic of Korea (South Korea): An approach using haplotype Network analysis based on mitochondrial DNA sequences of the parasite



Moritoshi Iwagami^a, Megumi Fukumoto^{a, b},
Weon-Gyu Kho^c, Shigeyuki Kano^{a, b}

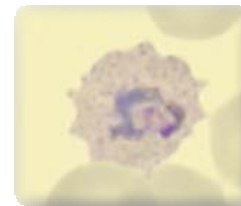


^aResearch Institute, International Medical Center of Japan

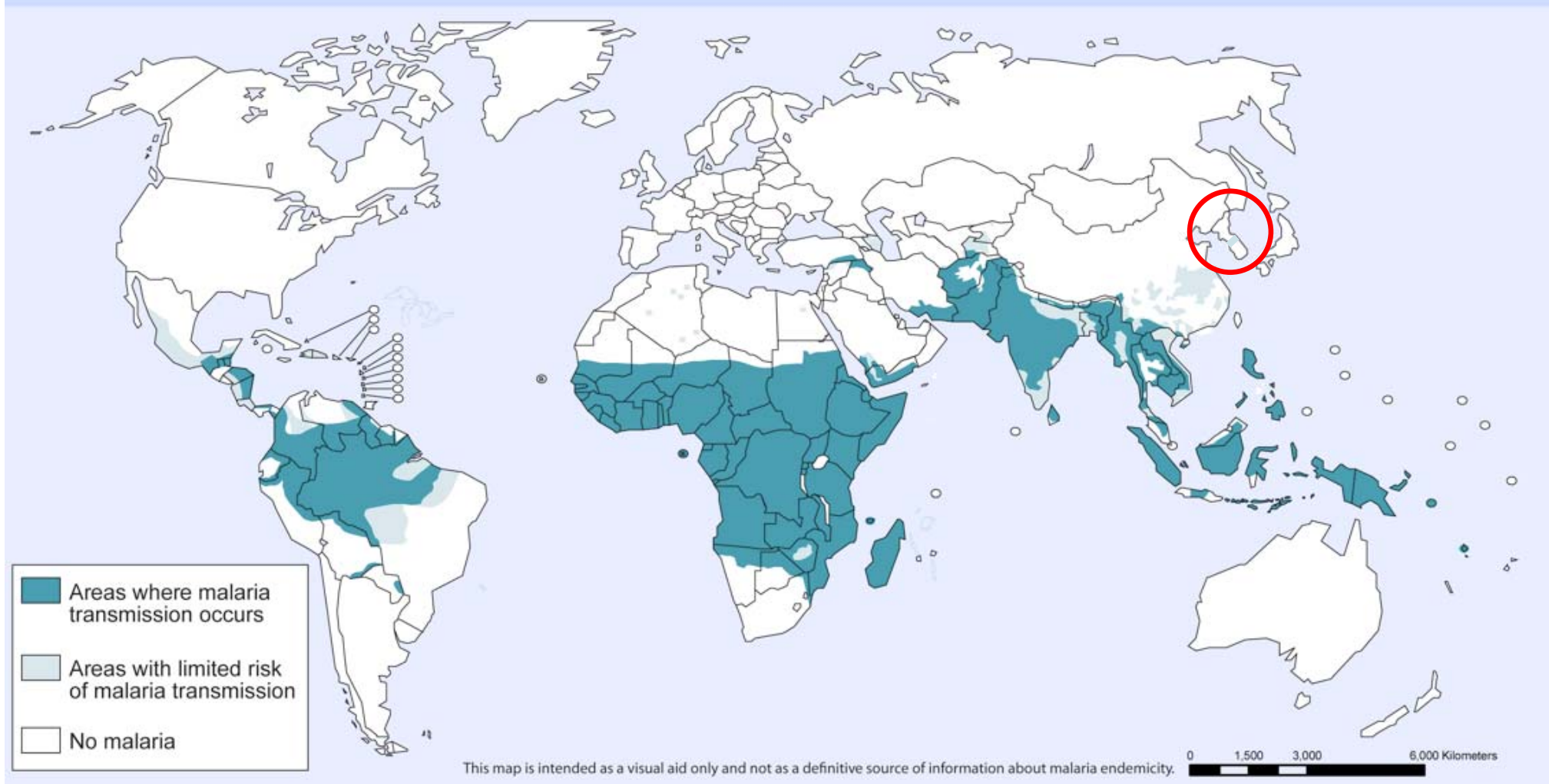
^bGraduate School of Comprehensive Human Sciences,
University of Tsukuba, Japan

^cDepartment of Malariology,
Paik Institute of Clinical Research and Department of Parasitology,
Inje University, College of Medicine, Korea

World Distribution of Malaria

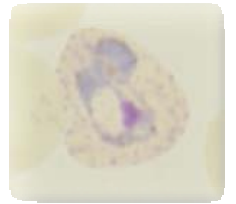


Malaria, 2008

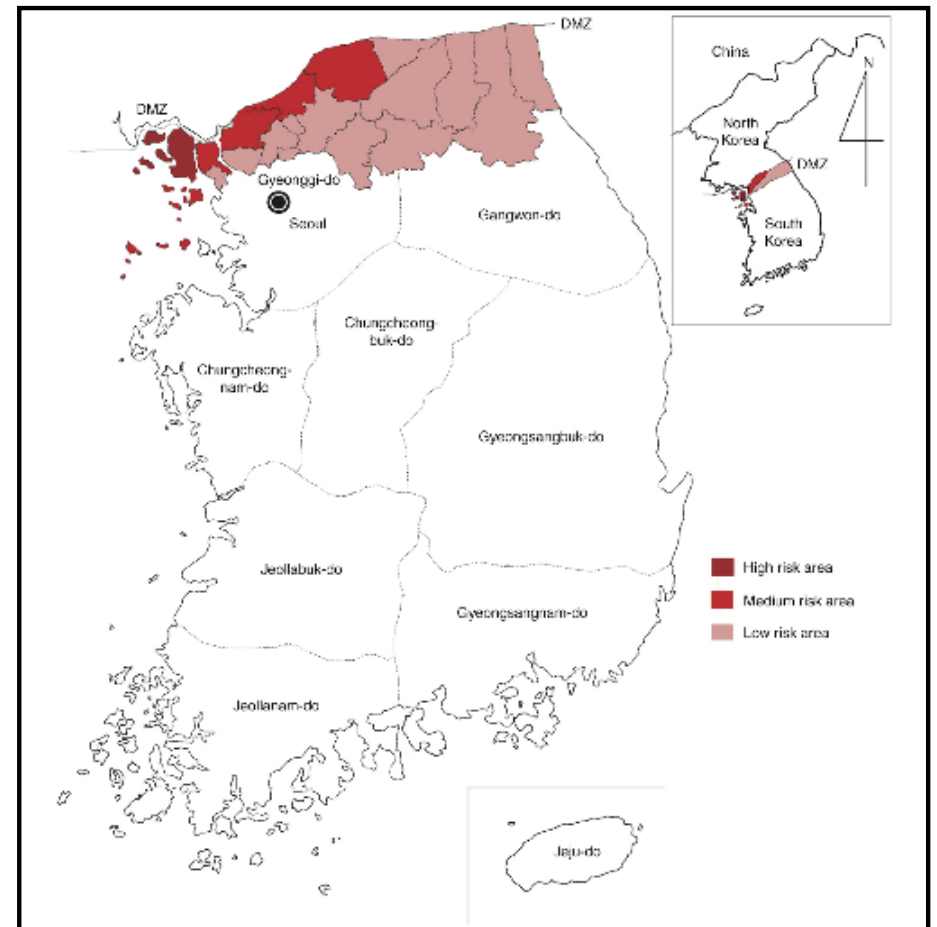


World Health Organization 2008

Malaria endemic area in South Korea

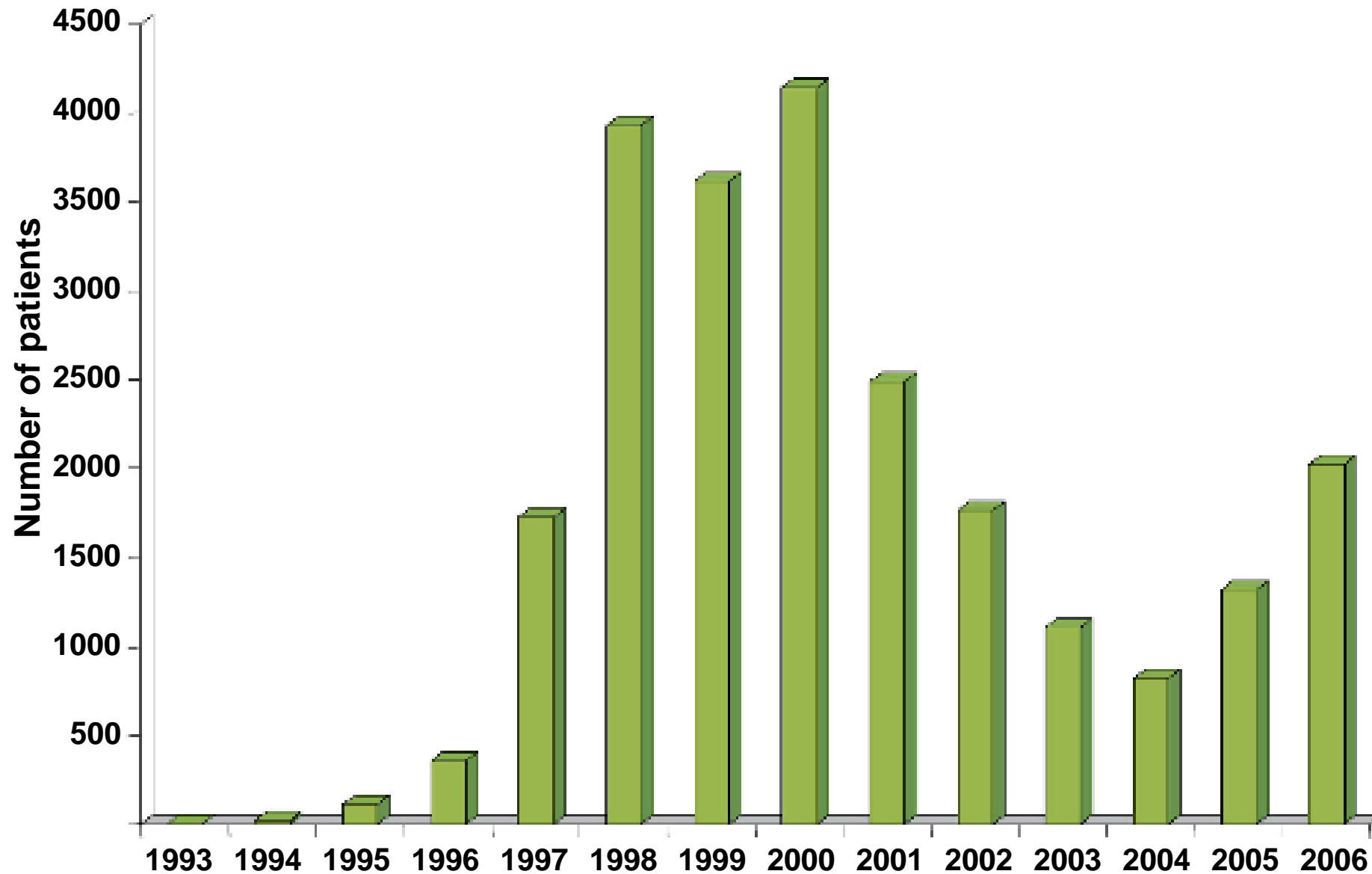
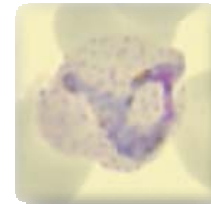


Demilitarized zone (DMZ) in South Korea



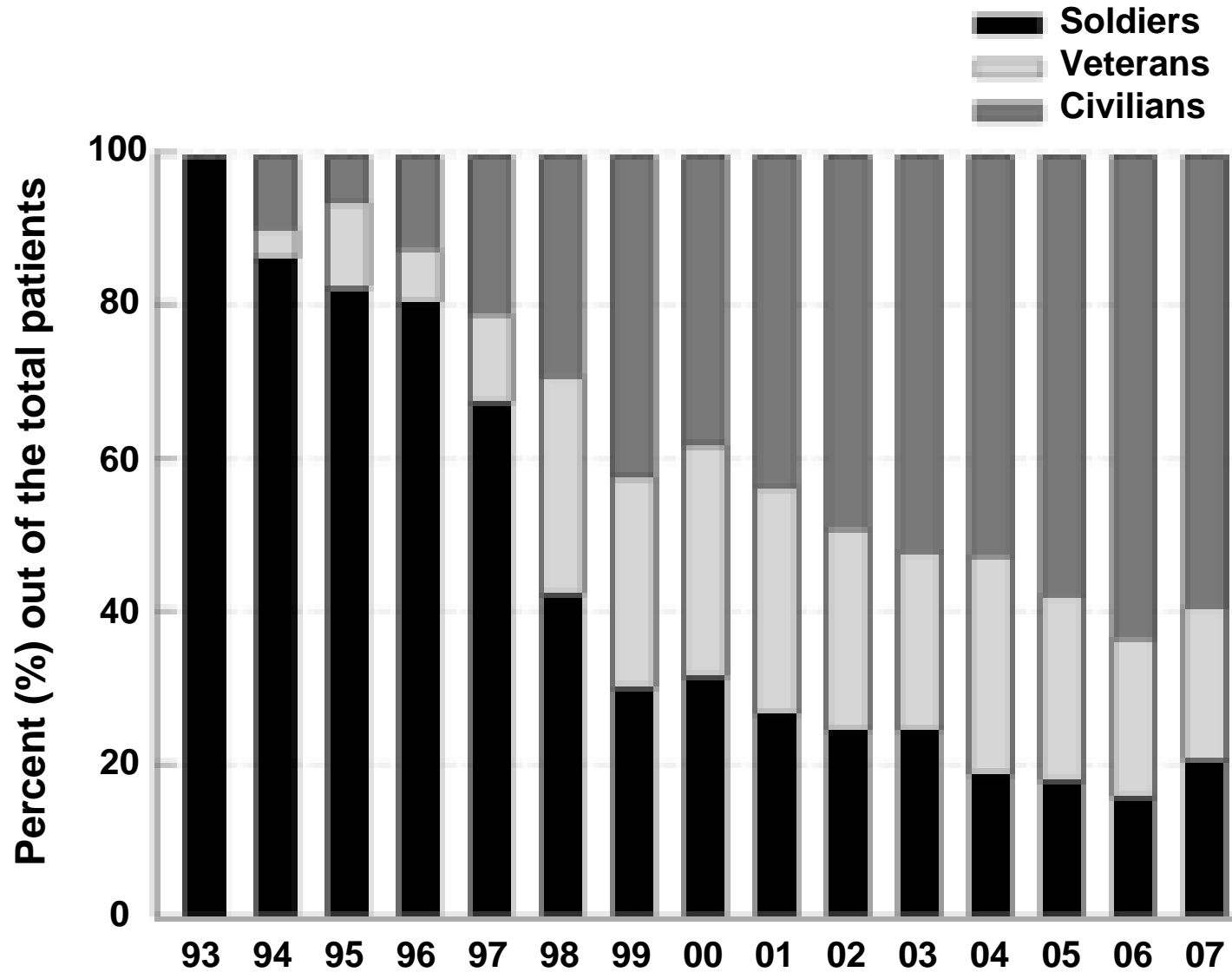
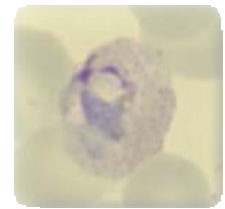
Trends Parasitol (2007) 24:143-150

Annual number of vivax malaria patients reported in South Korea (1993–2006)



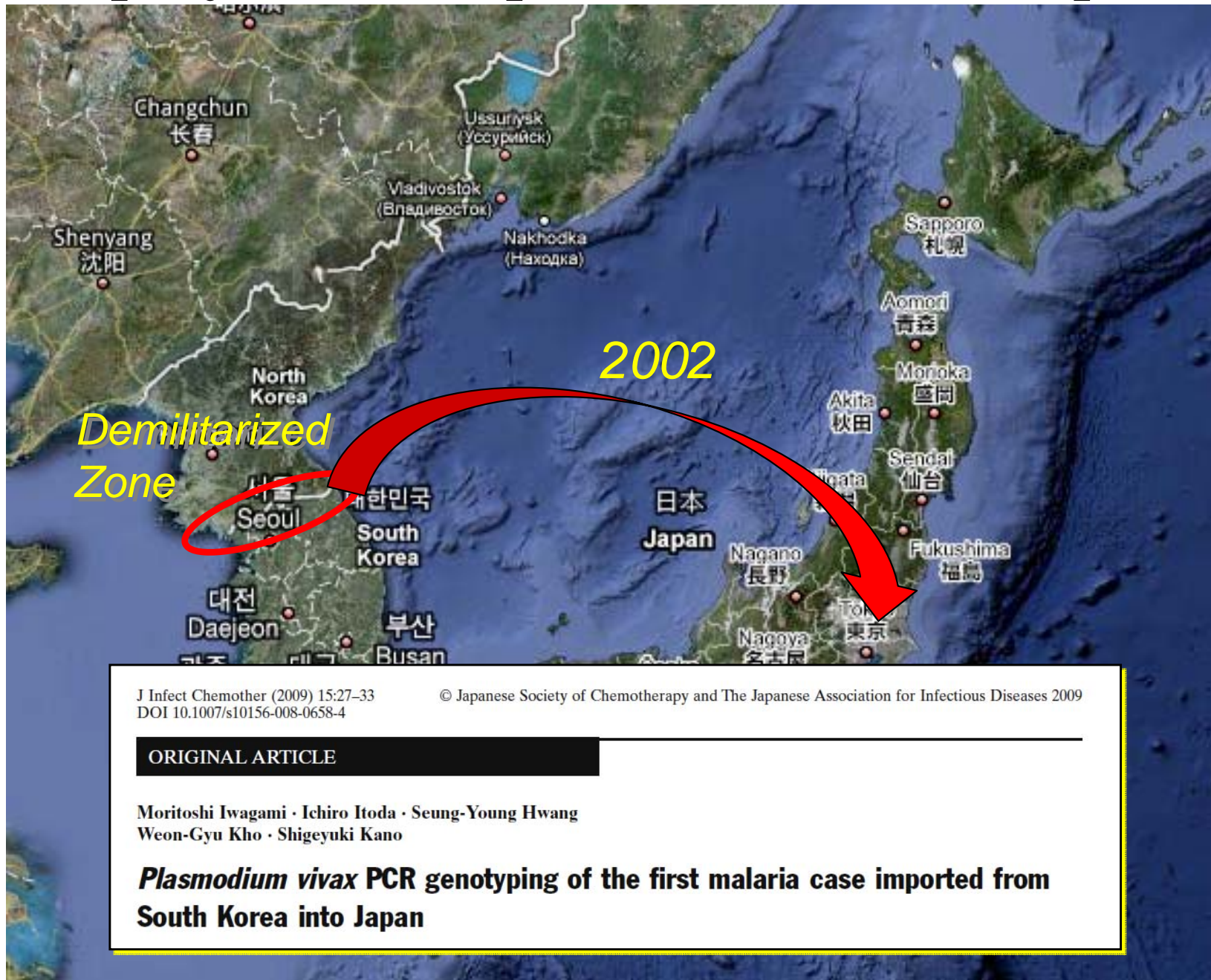
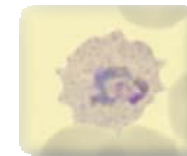
Trends Parasitol (2007) 24:143-150

Proportion of P. vivax malaria patients in South Korea (1993–2007)



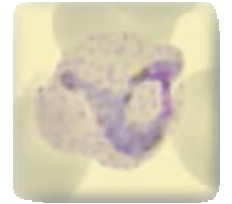
Korean J Parasitol (2009) 47:S39-50

Map of Korean peninsular and Japan



Google Map

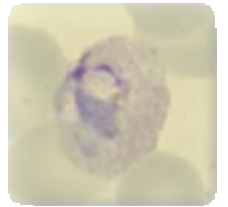
Objective



The objective of this study is to estimate **the origin of the *Plasmodium vivax* (*Pv*) population in South Korea** by phylogenetic analyses based on mitochondrial (mt) DNA sequences of *Pv* isolates from South Korea and other countries in the world.



Materials and Methods



Materials

- **11 South Korean *Pv* isolates**
- **10 other *Pv* isolates (Southeast Asia, South Asia, Western Pacific, Middle East, South America, Africa)**
- **282 *Pv* isolates (including 1 North Korean isolate) from GenBank database**

Methods

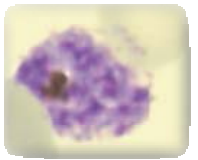
DNA Analysis

- **Mitochondrial (mt) DNA analysis (PCR & Sequencing)**

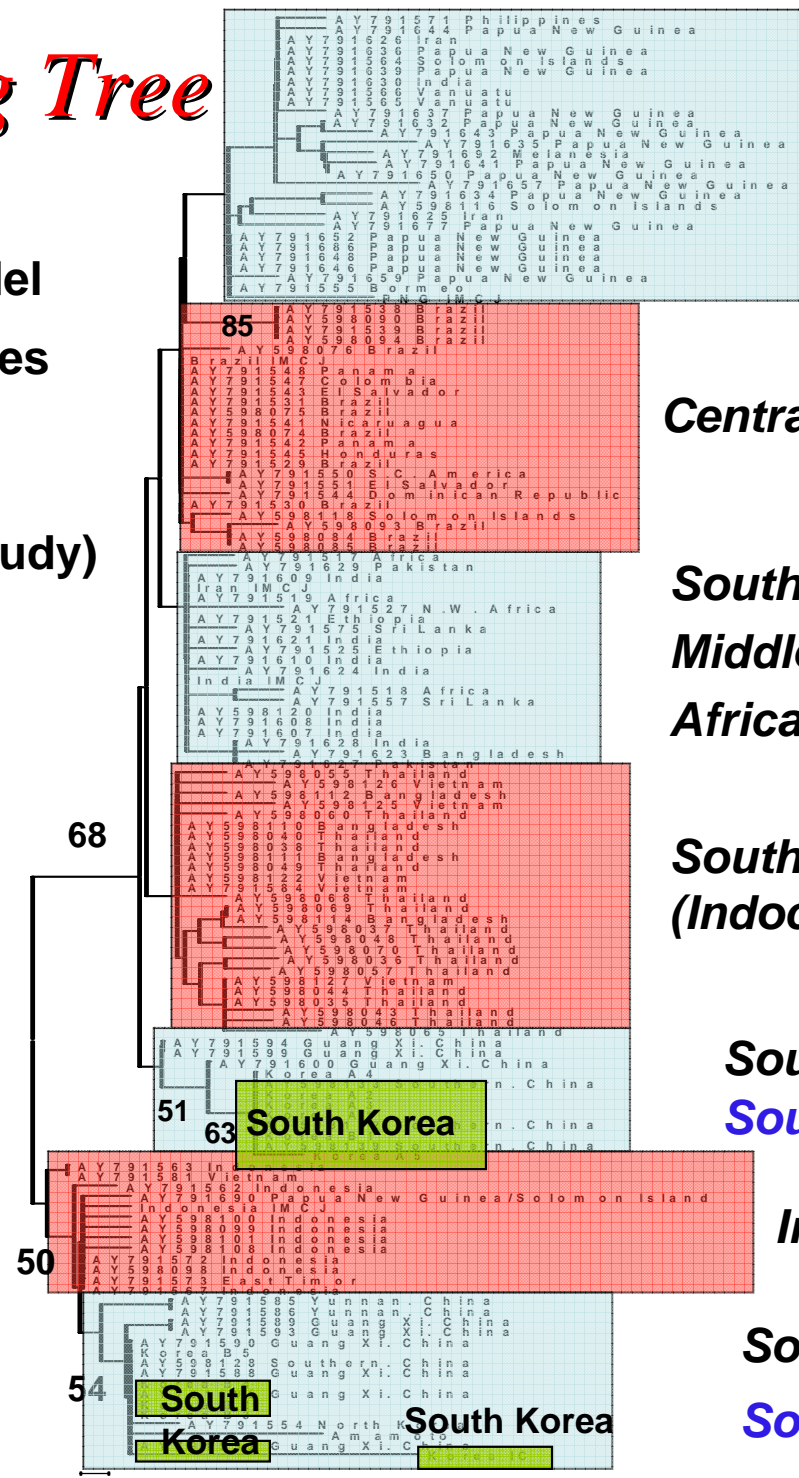
Phylogenetic Analyses

- **A neighbor-joining tree**
- **A haplotype network tree (Median-joining method)**

Neighbor-Joining Tree



- Kimura 2-parameter model
- *P. vivax* mtDNA sequences
- 145 isolates
(124 isolates: GenBank,
21 isolates: Present Study)



Papua New Guinea
Western Pacific

Central & South America

South Asia

Middle East

Africa

Southeast Asia
(Indochina peninsula)

Southern China Group A
South Korea Group A

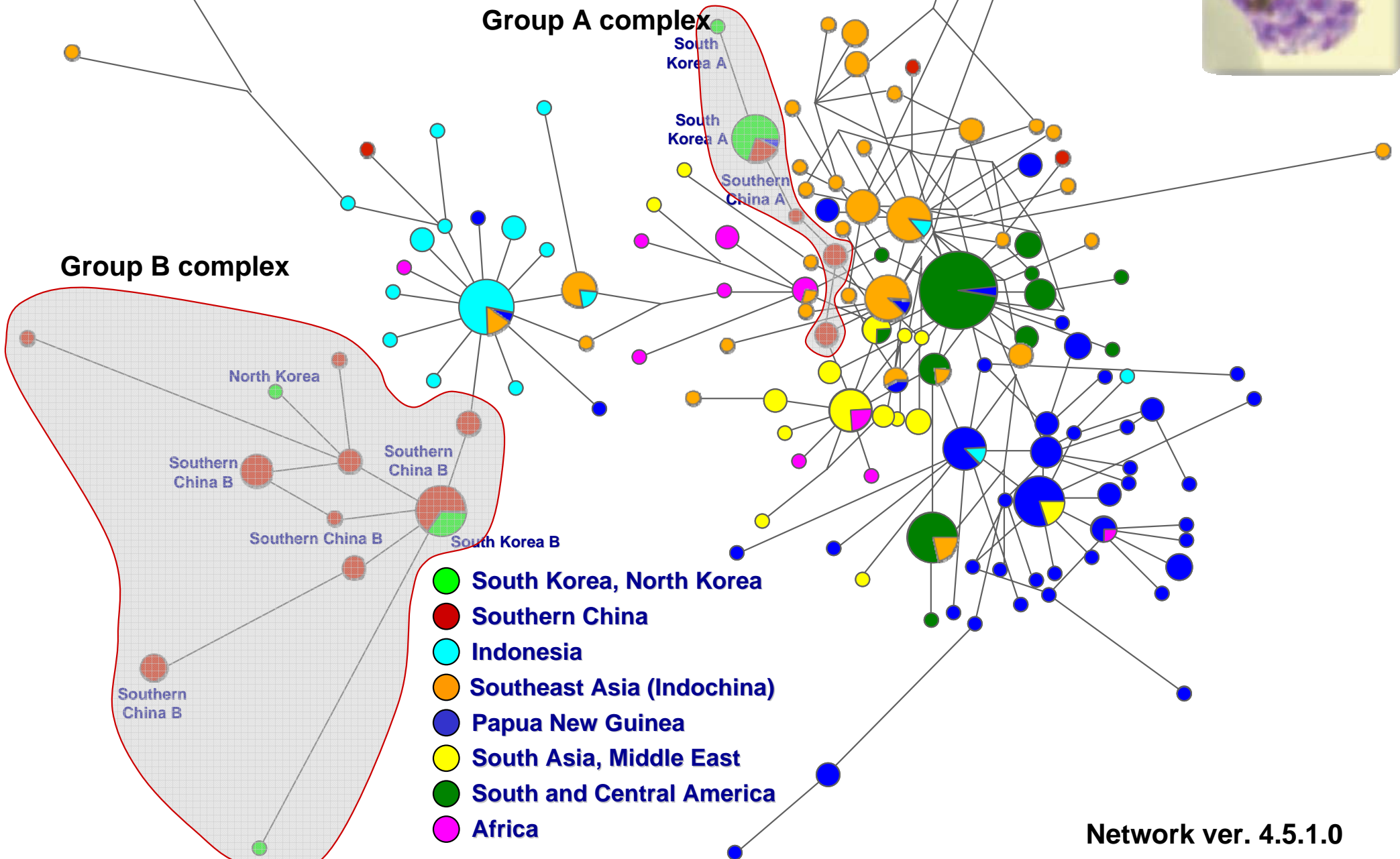
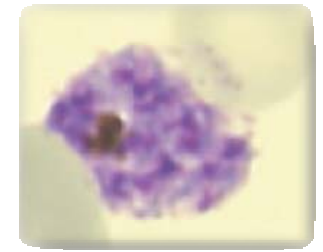
Indonesia

Southern China Group B
South Korea Group B

The numbers for interior branch represent the bootstrap values (%) of 500 replications (> 50)

MEGA ver. 3.1

Haplotype Network Tree



Group B complex

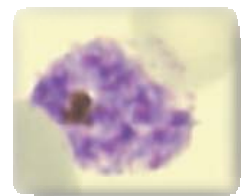
Group A complex

- South Korea, North Korea
- Southern China
- Indonesia
- Southeast Asia (Indochina)
- Papua New Guinea
- South Asia, Middle East
- South and Central America
- Africa

Network ver. 4.5.1.0

P. vivax mtDNA haplotype network tree (Median-joining method)
303 isolates (282 isolates: GenBank, 21 isolates: Present Study)

Results

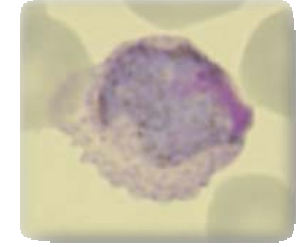


- In South Korea, there were two groups (i.e. SK group A and B) in the *Pv* population.
- In Southern China, there were also two groups (i.e. SC group A and B).
- The North Korean isolate was included in the group B complex.

Conclusion

- The direct origin of the *Pv* population in South Korea is thought to be from **North Korea** via the DMZ, but the true origin of *Pv* populations in Korean peninsular is now suggested to be from **Southern part of China**. The Chinese *Pv* populations have two different origins.

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