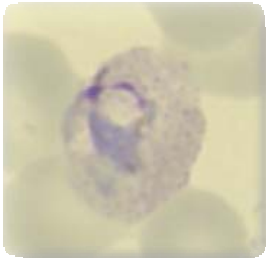
Origin of *Plasmodium vivax* in the Republic of Korea (South Korea): An approach using haplotype Network analysis based on mitochondrial DNA sequences of the parasite



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[a]*Research Institute, International Medical Center of Japan*

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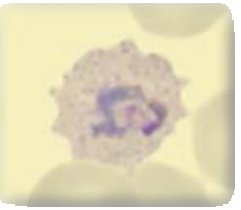
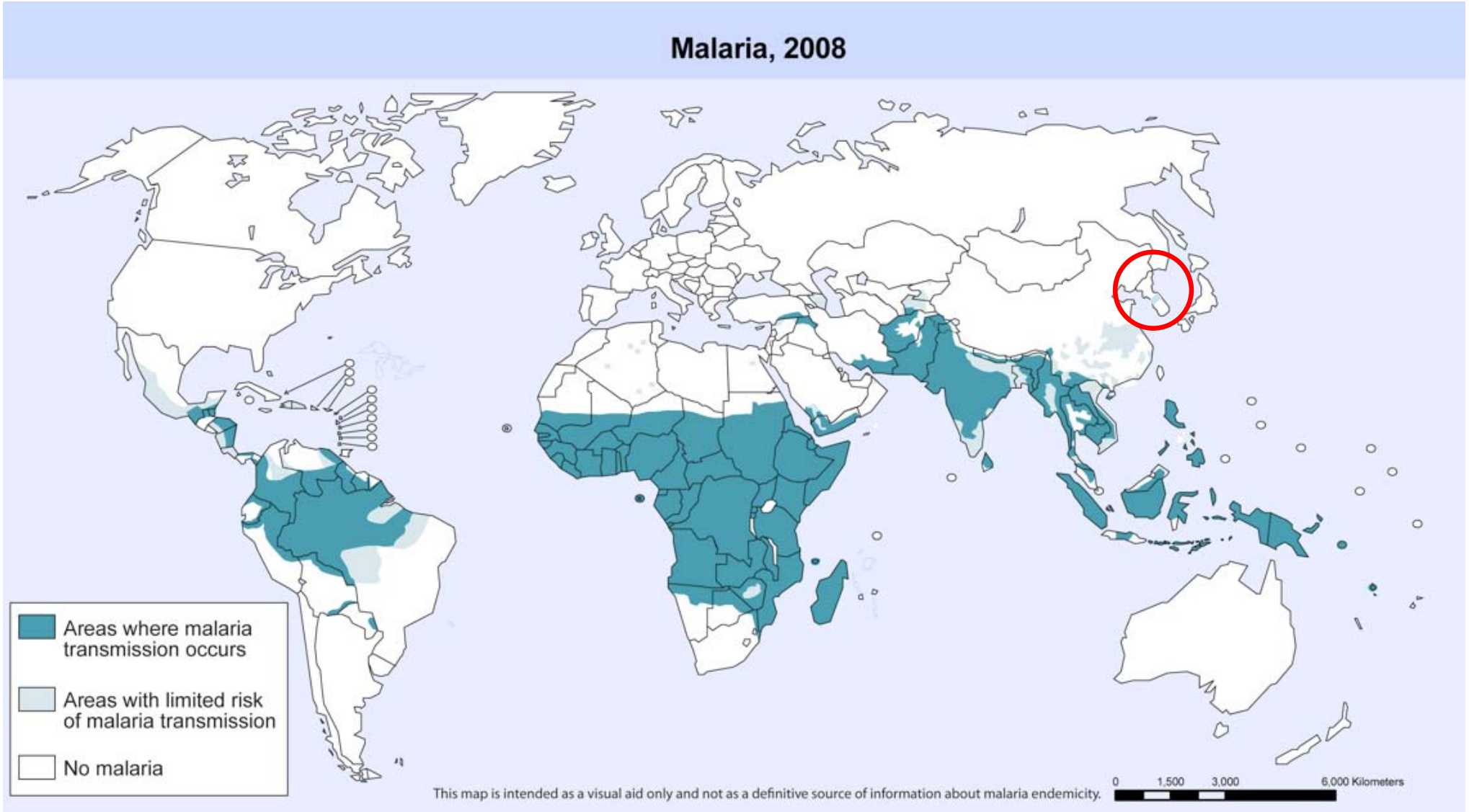
JITMM 2009, Bangkok, 3-4, Dec, 2009

World Distribution of Malaria

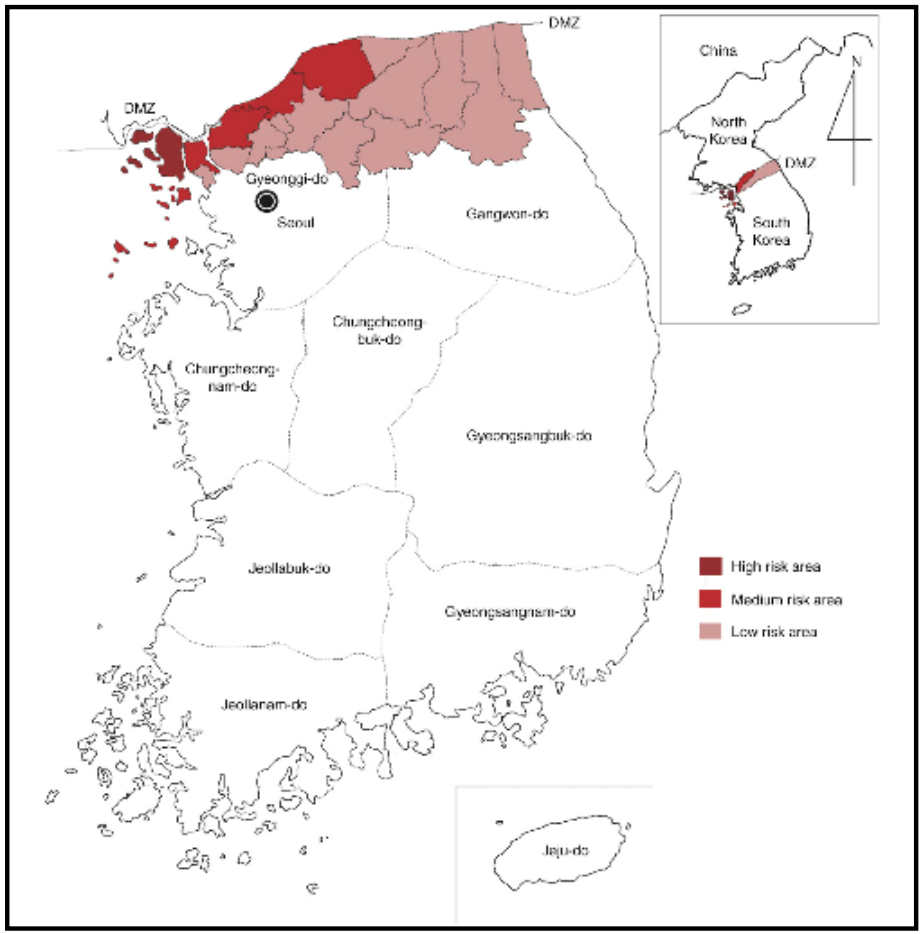




World Health Organization 2008

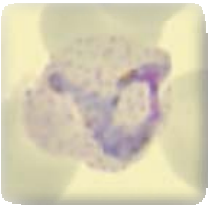
Malaria endemic area in South Korea

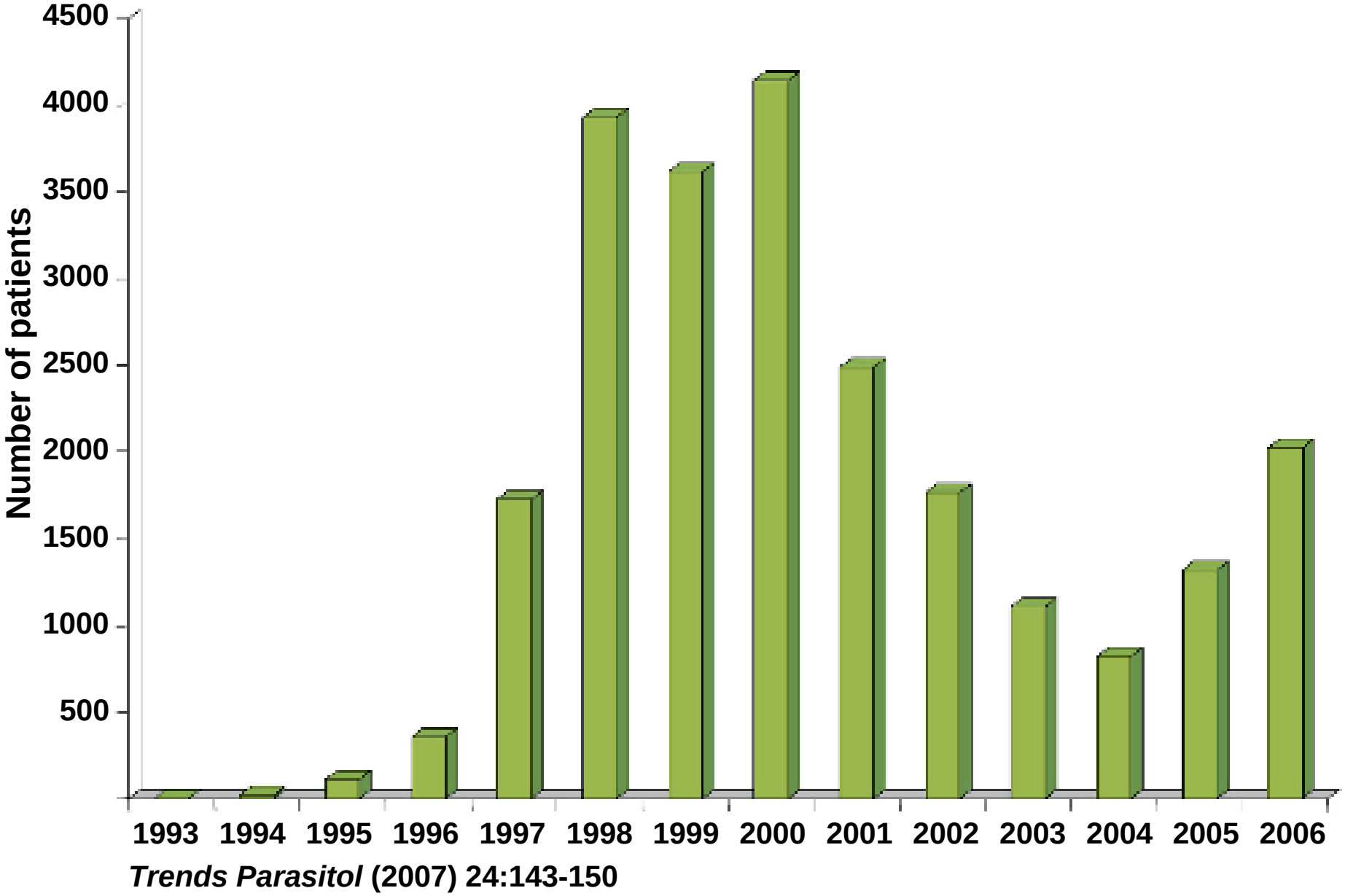
Demilitarized zone (DMZ) in South Korea



***Trends Parasitol* (2007) 24:143-150**

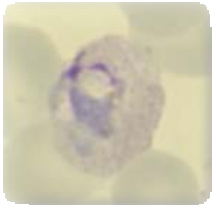
Annual number of vivax malaria patients reported in South Korea (1993–2006)

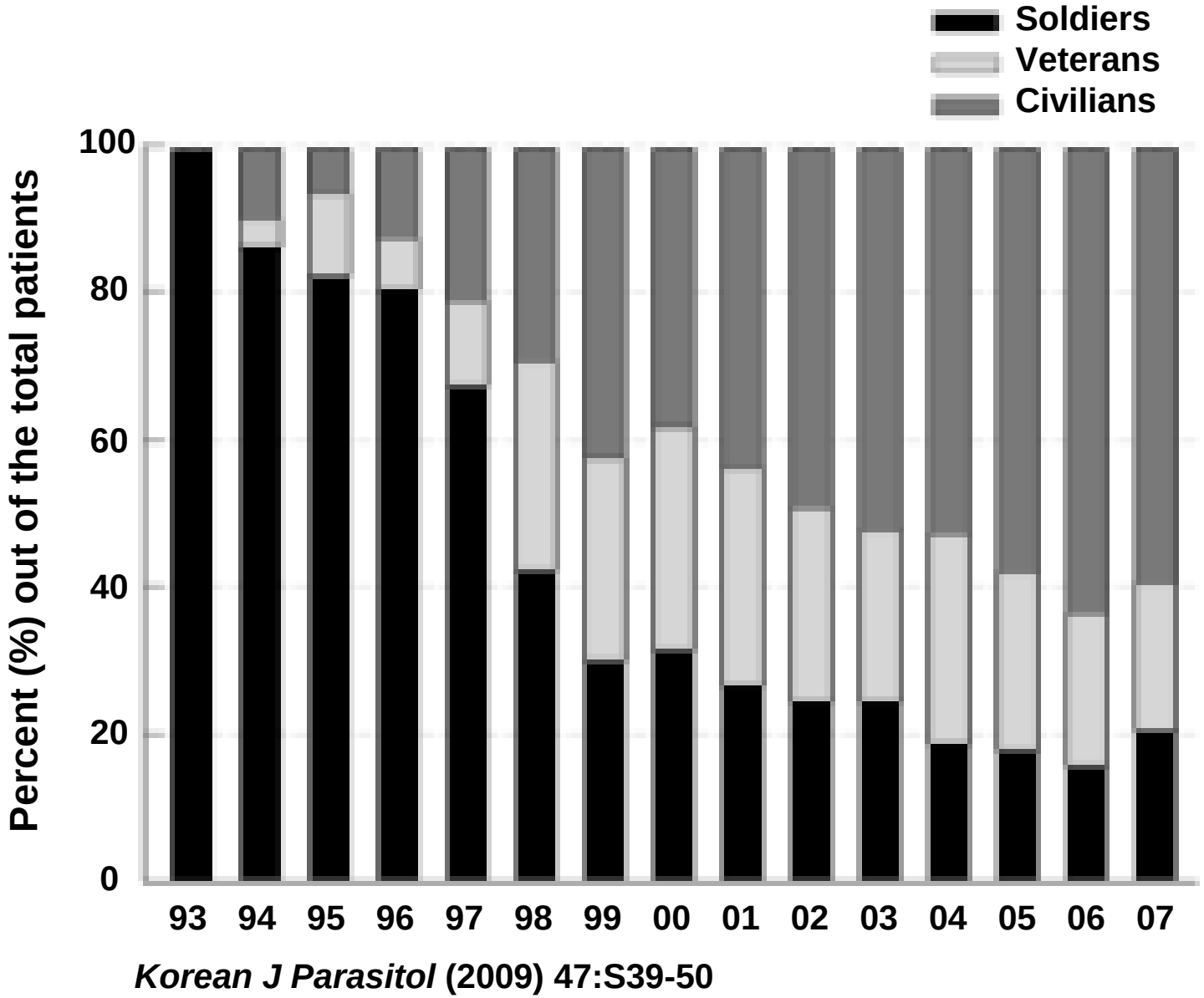




***Trends Parasitol* (2007) 24:143-150**

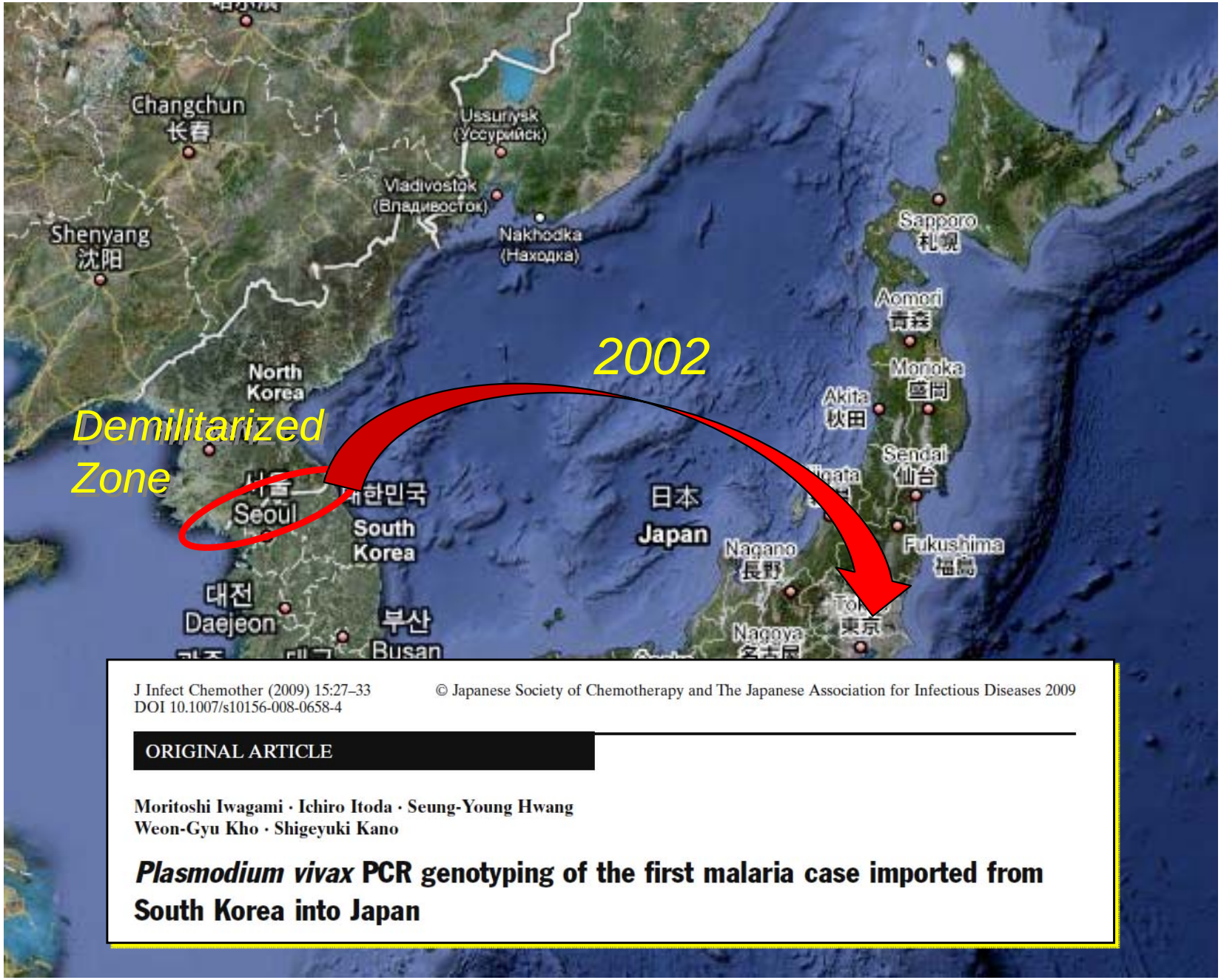
Proportion of P. vivax malaria patients in South Korea (1993–2007)





Korean J Parasitol (2009) 47:S39-50

Map of Korean peninsular and Japan



J Infect Chemother (2009) 15:27–33
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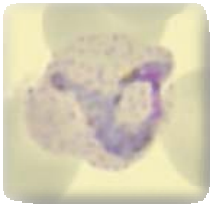
ORIGINAL ARTICLE

Moritoshi Iwagami · Ichiro Itoda · Seung-Young Hwang
Weon-Gyu Kho · Shigeyuki Kano

***Plasmodium vivax* PCR genotyping of the first malaria case imported from South Korea into Japan**

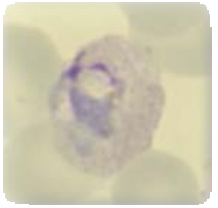
Google Map

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

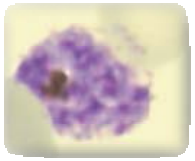
DNA Analysis

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

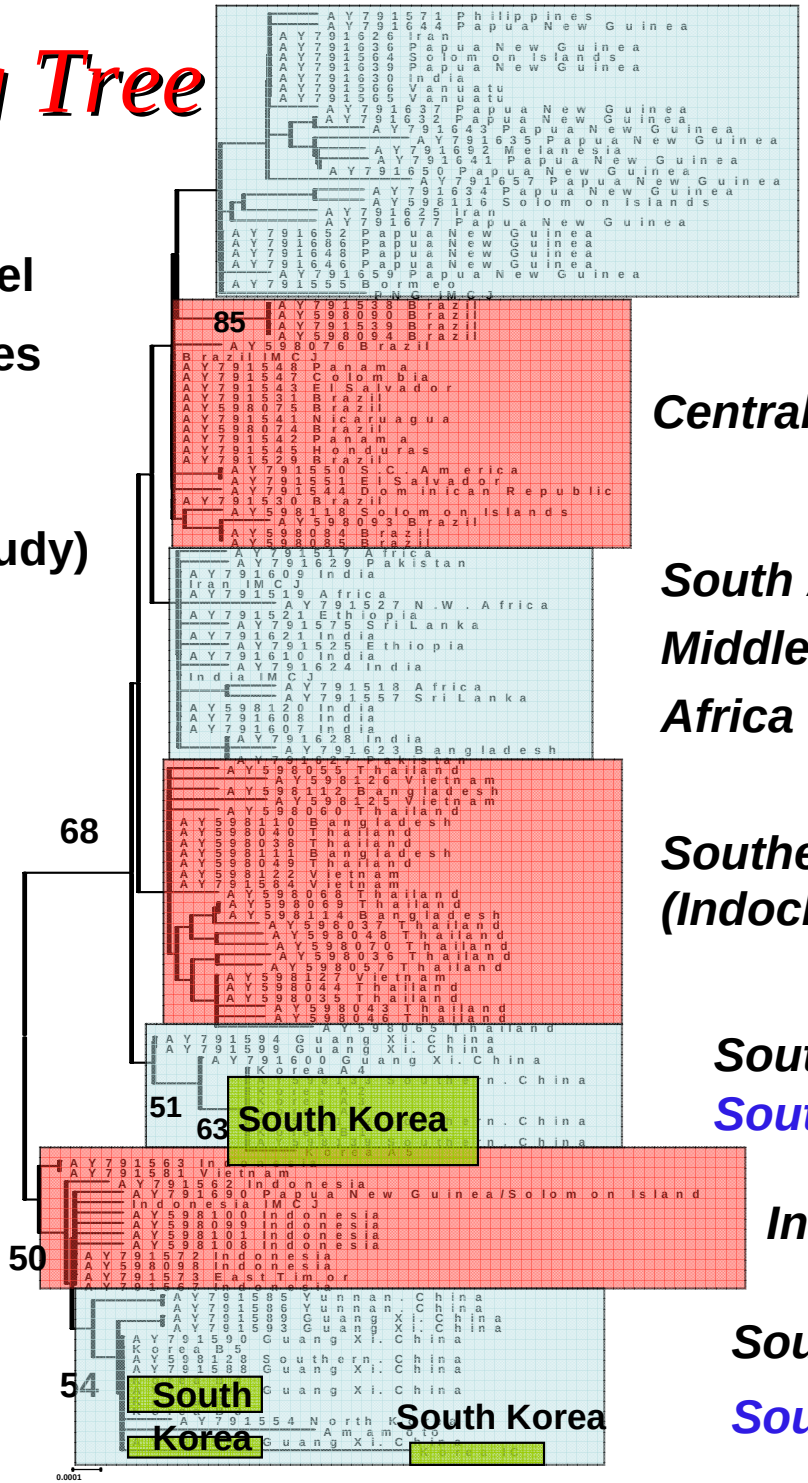
Phylogenetic Analyses

- **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

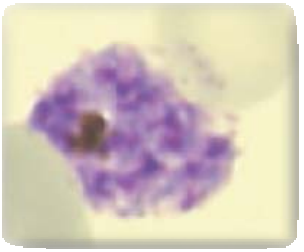
Southern China Group B

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 A complex

South Korea A

South Korea A

Southern China A

Group B complex

North Korea

Southern China B

Southern China B

Southern China B

South Korea B

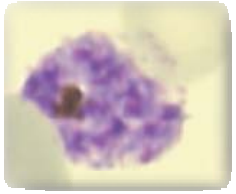
Southern China B

- 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

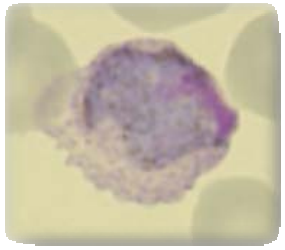


- **In South Korea, there were two groups (i.e. SK group A and B) in the *Pv* population.**
- **In Southern China, there were also two groups (i.e. SC group A and B).**
- **The North Korean isolate was included in the group B complex.**

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.**

Acknowledgements



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