

# Genetic diversity and phylogenetic analysis of Asian soybean rust within the U.S.A. and abroad

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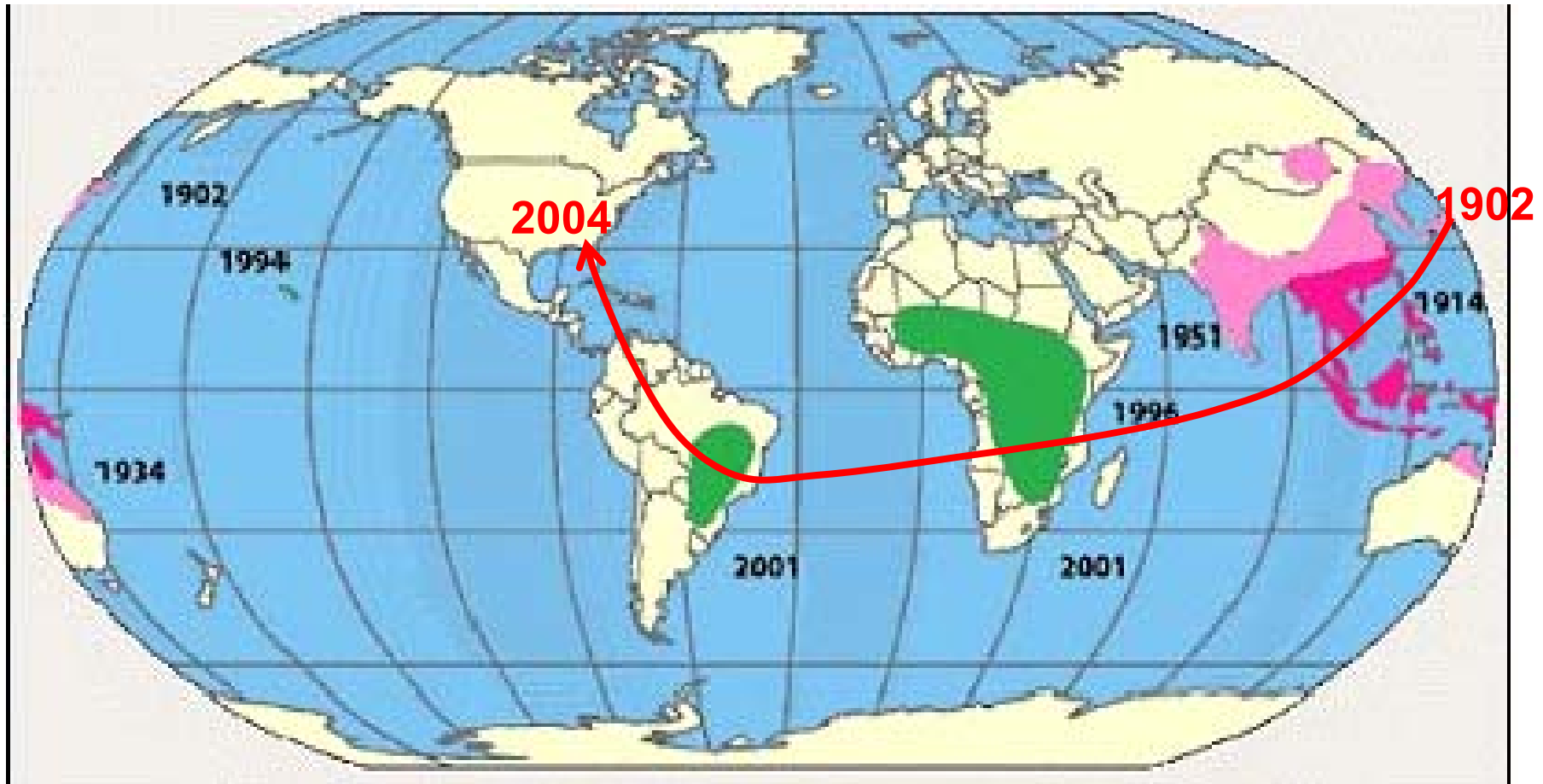
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MONSANTO



# ASR global movement: a century-old tale



**Many prevalent hypotheses.....  
Make sense time wise, but lack direct evidence.**

Adapted from source of USDA-ARS

# **Origins and genetic diversity of ASR**

**The population structure of ASR isolates, especially U. S. Isolates, has not been determined.**

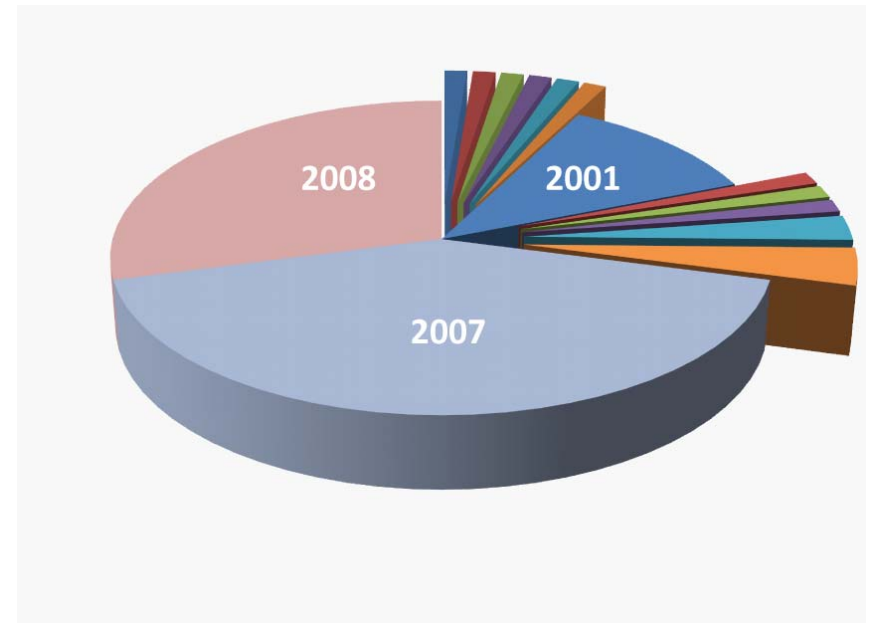
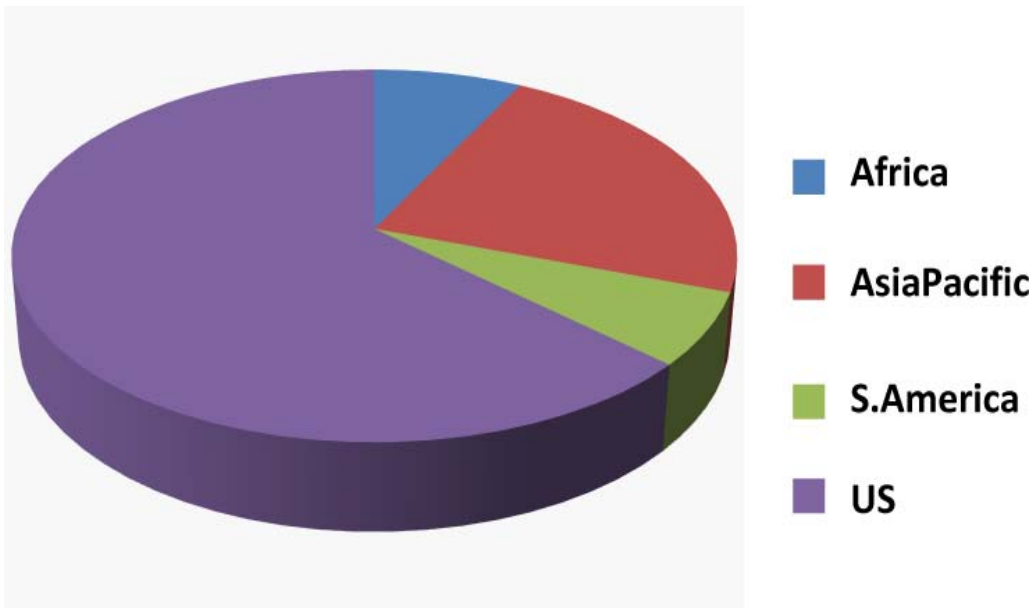
**Germplasm screening suggests the presence of significant genetic diversity.**

**Molecular diagnostic resources need to be developed.**

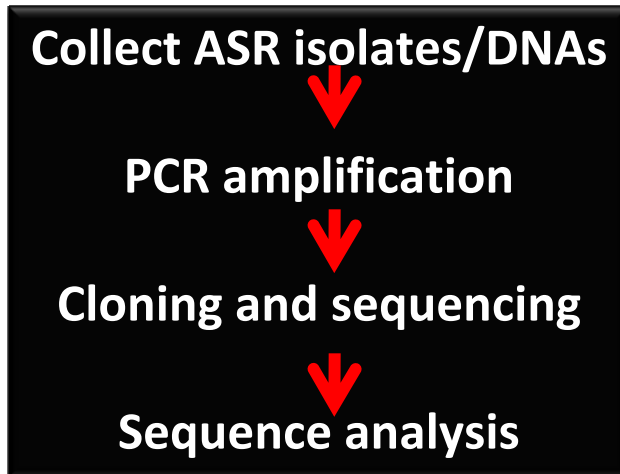
# Collection of ASR isolates/DNAs

A total of 80 isolates

- ✓ 3 are from Kudzu plant
- ✓ 35 are from pustule(s)
- ✓ 55 are environmental isolates



# Experimental Plan



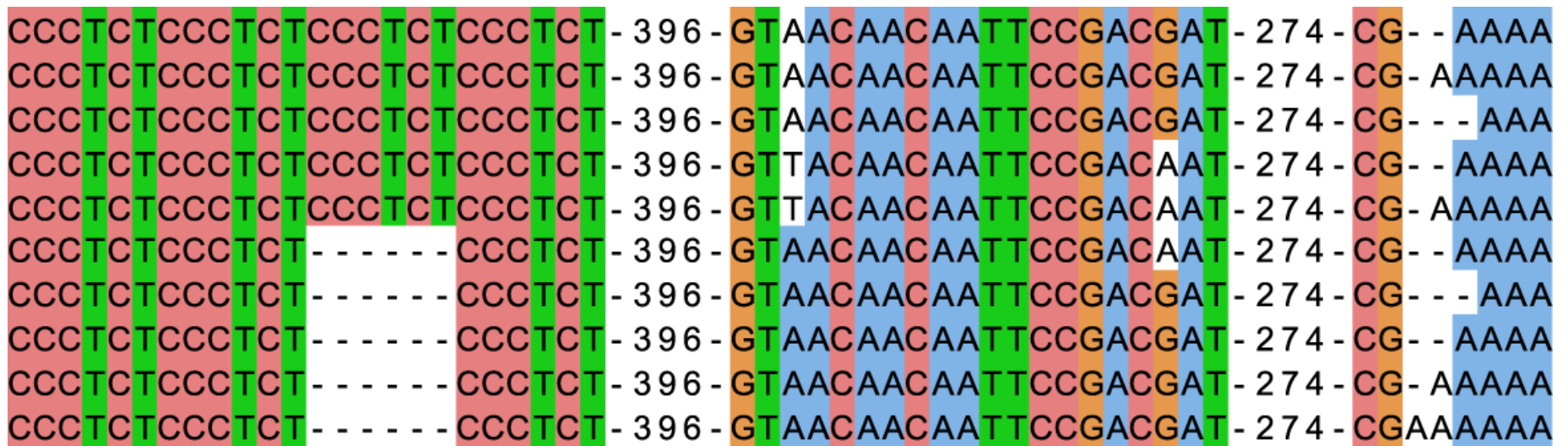
**ITS**  
Polyubiquitin5  
HistoneH4  
Aldehyde dehydrogenase  
  
ADP ribosylation factor  
14-3-3  
B-D-galactosidase  
18s rRNA  
unknown  
  
Mt cytochrome B

## Why sequence-based Phylogenies?

- ✓ Reveal the exact genetic polymorphisms, especially SNPs
- ✓ Optimize the phylogenetic analysis
  - consider SNPs
  - consider transitions and transversions
  - consider gaps for indels
- ✓ Marker development for molecular diagnose

# Predominant ASR polymorphisms

A total of 29 polymorphisms identified from 5 genes,  
each amplicon is ~700 bp



Microsatellite

1 out of 29

In coding region

SNP

17 out of 29

6 in coding region  
11 in non-coding region

Indel

11 out of 29

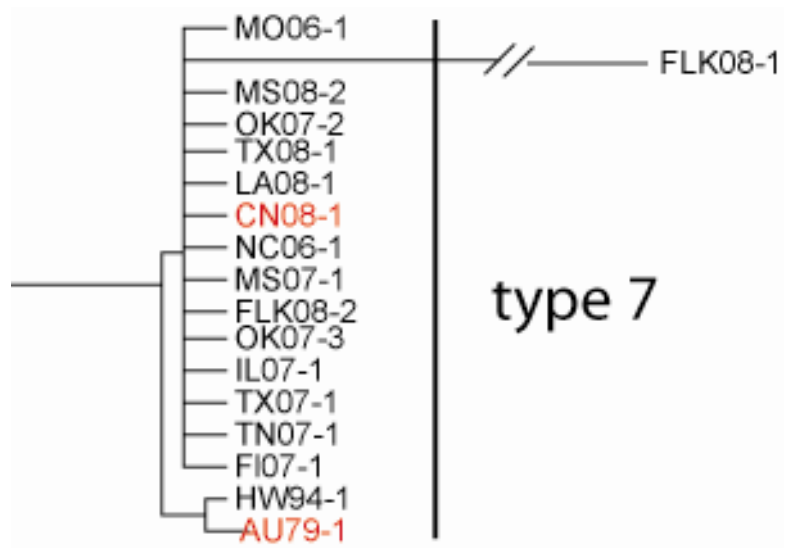
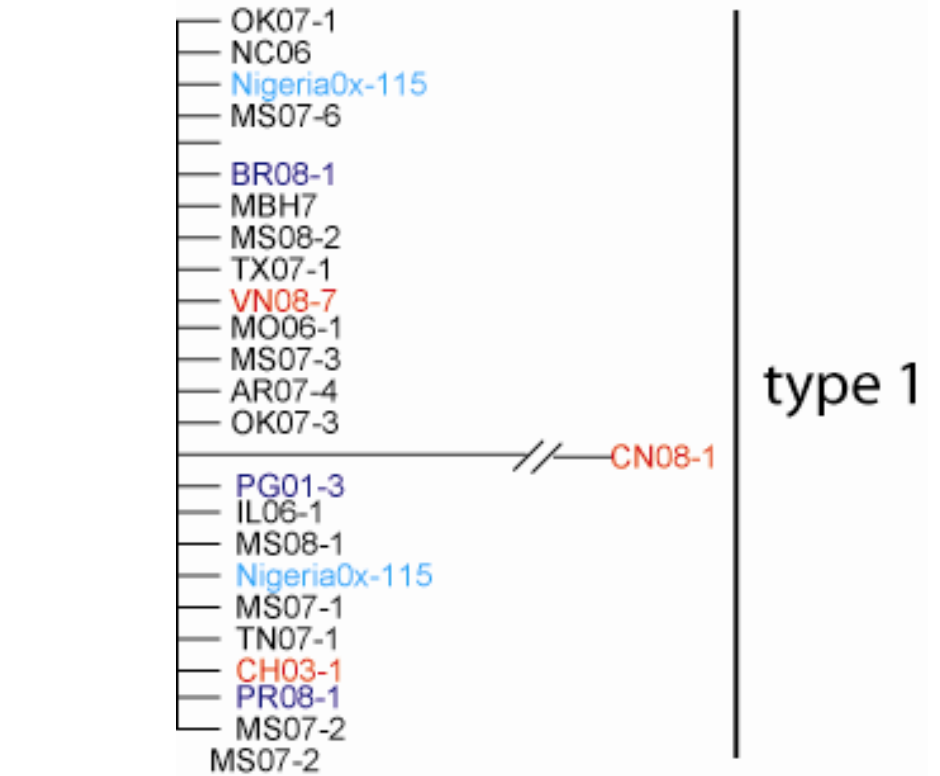
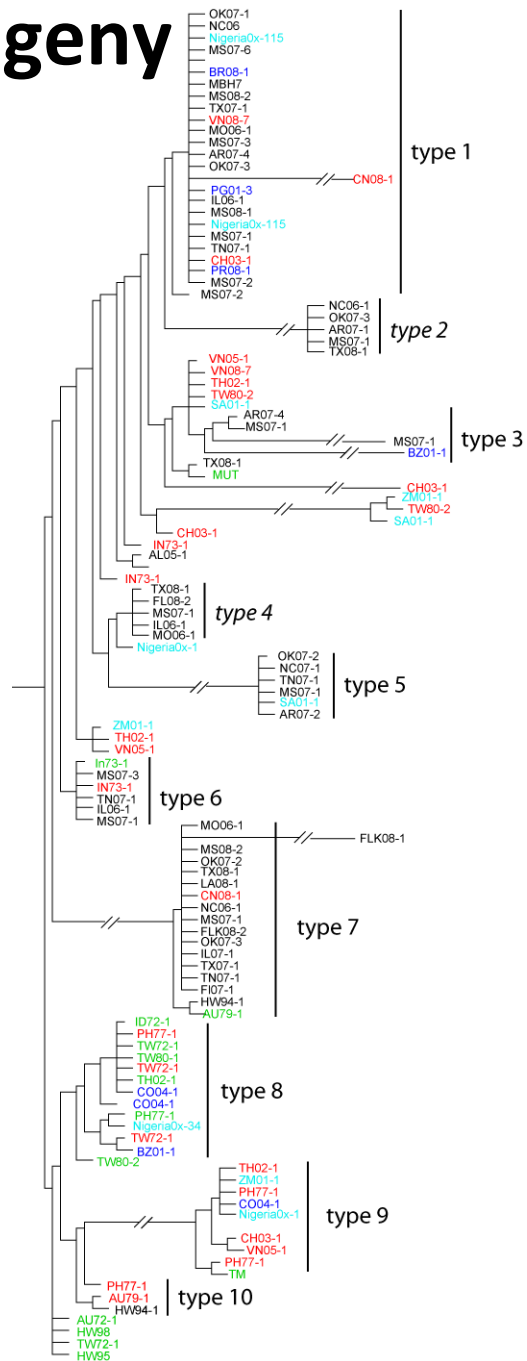
2 in coding region  
9 in non-coding region

# Most samples are a mixture of distinct isolates

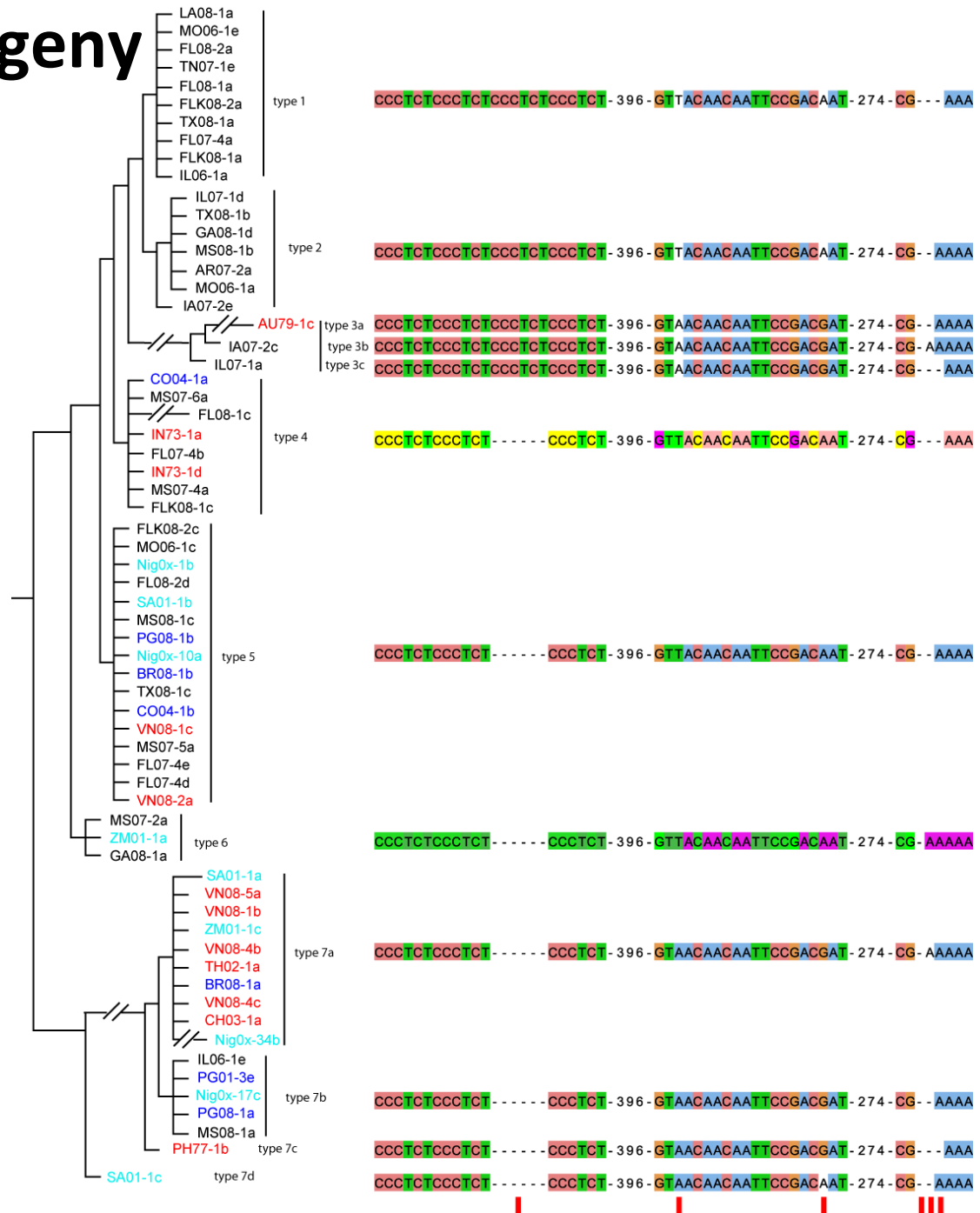
isolate	its	gene A	gene B	gene C
VN08-7	1	7	1*4	3
BZ08-1	1	5*7	3*4	3
PG08-1	1	5*7	1*4	
MS08-1	1	2*5*7		1*3
MO07-1	1	5*7	1*4	3
NG01-115	1			3
OK07-1	1	5*7	1*4	3
LA08-1	7	1	1	2*3
FLK08-1	7	1*4	1	1*3
FLK08-2	7	1*5		2*3
SA01-1	3*5	5*7	2*3*4	
IN73-1	3*6	4	2*3	
BZ01-1	3*8		2*4	



# ITS phylogeny



# Example phylogeny

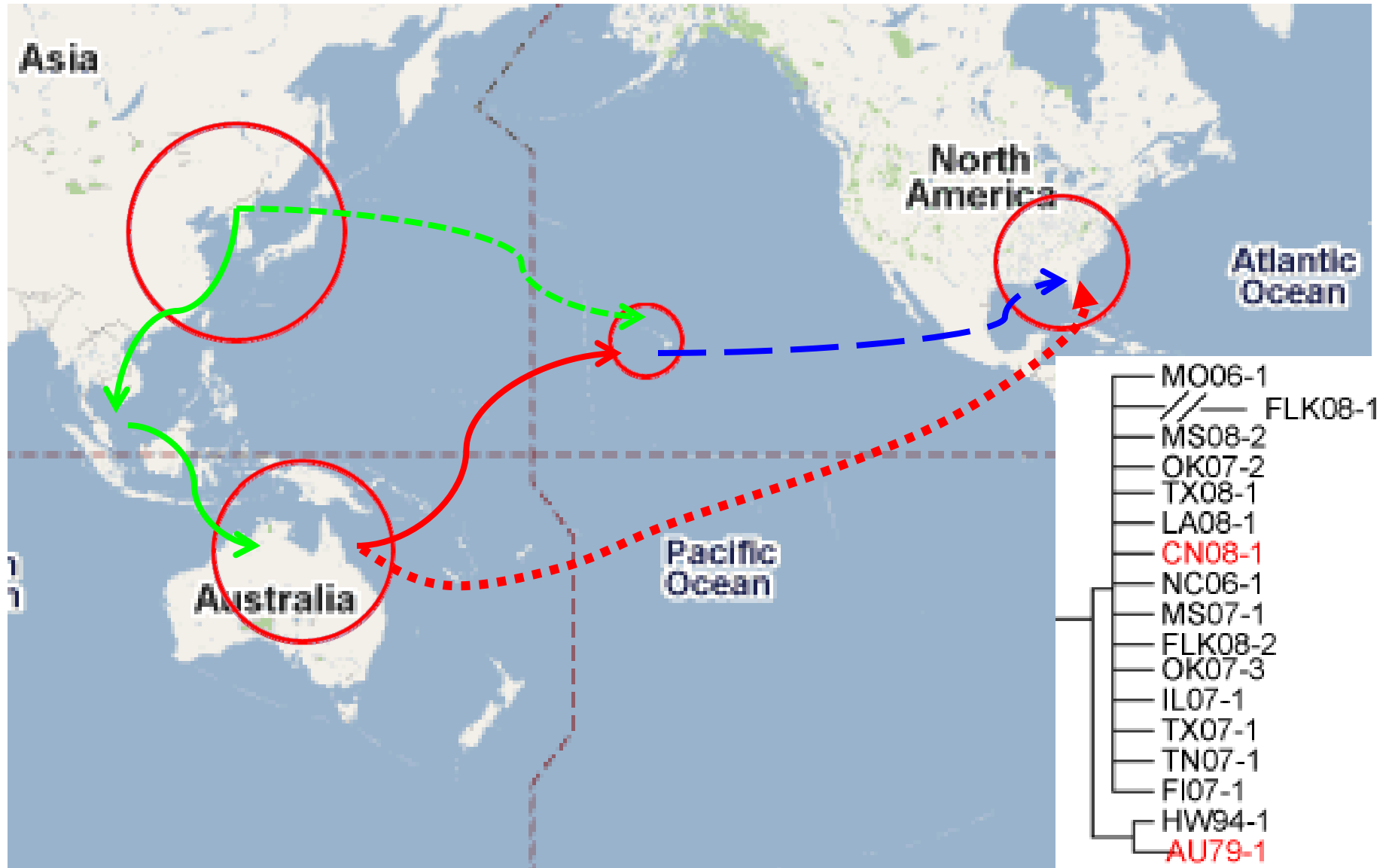


# The prevalent ASR migration hypothesis



# A path of ASR from East Asia to the USA

China--Australia—Hawaii---USA



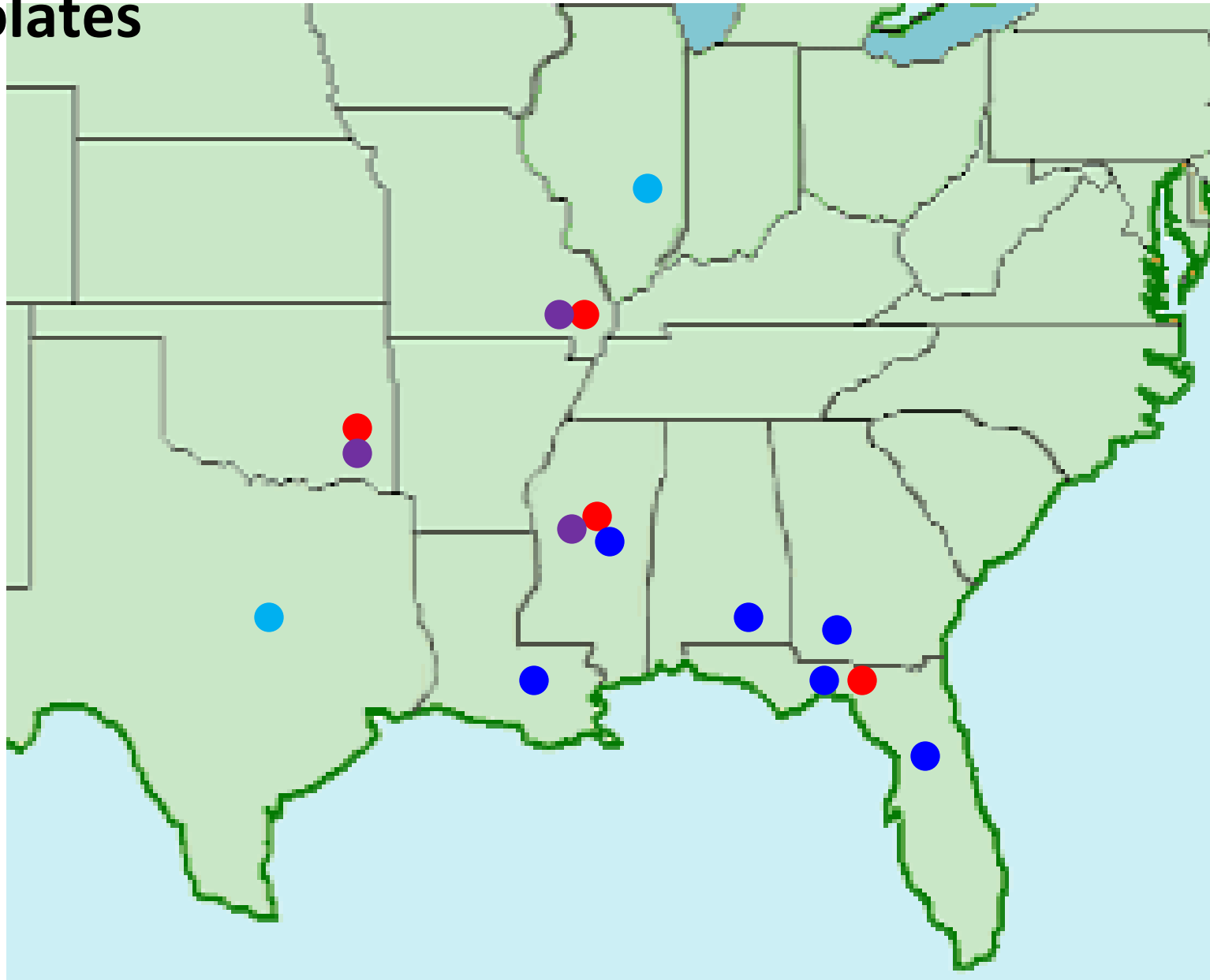
# Sessile ASR



# ASR population structure worldwide

isolate	its	gene A	gene B	gene C
VN08-7	1	7	1*4	3
BZ08-1	1	5*7	3*4	3
PG08-1	1	5*7	1*4	
MS08-1	1	2*5*7		1*3
MO07-1	1	5*7	1*4	3
NG01-115	1			3
OK07-1	1	5*7	1*4	3
LA08-1	7	1	1	2*3
FLK08-1	7	1*4	1	1*3
FLK08-2	7	1*5		2*3
SA01-1	3*5	5*7	2*3*4	
IN73-1	3*6	4	2*3	
BZ01-1	3*8		2*4	

# An example of geophylogenetic distribution of US isolates



# Summary

- ✓ ASR isolates are highly divergent and rich in genetic polymorphisms.
- ✓ Most ASR types are present worldwide; while some isolates are confined to a few geographic locations.
- ✓ ASR isolates likely migrated globally via several paths.
- ✓ Further research should be able to define the geographic distribution of ASR isolates within the U. S. and abroad.
- ✓ It should be possible to develop specific genetic markers as a diagnostic tool to identify individual ASR genotypes.