

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

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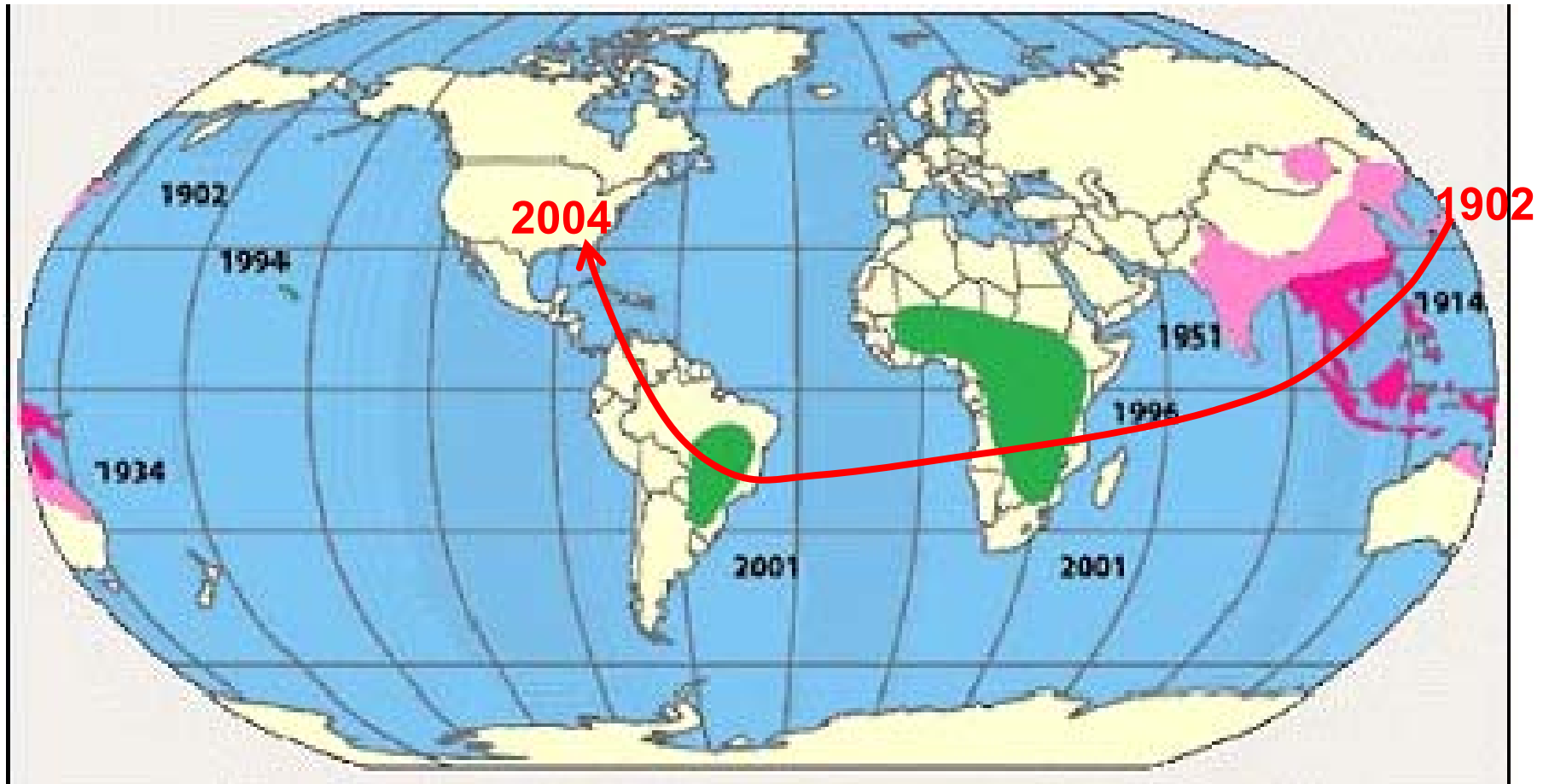
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MONSANTO



ASR global movement: a century-old tale



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

Adapted from source of USDA-ARS

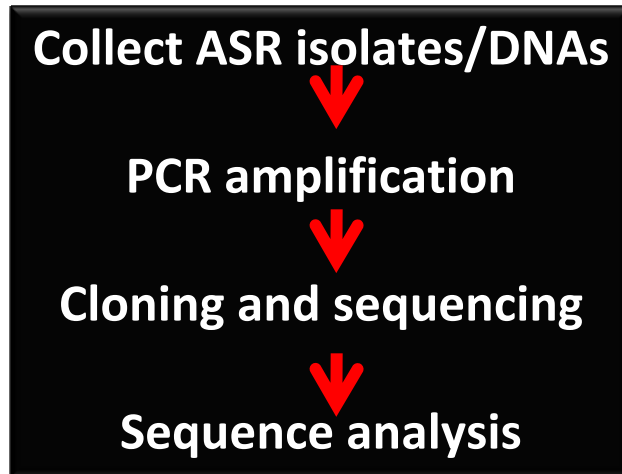
Origins and genetic diversity of ASR

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.

Experimental Plan



ITS
Polyubiquitin5
HistoneH4
Aldehyde dehydrogenase

ADP ribosylation factor
14-3-3
B-D-galactosidase
18s rRNA
unknown

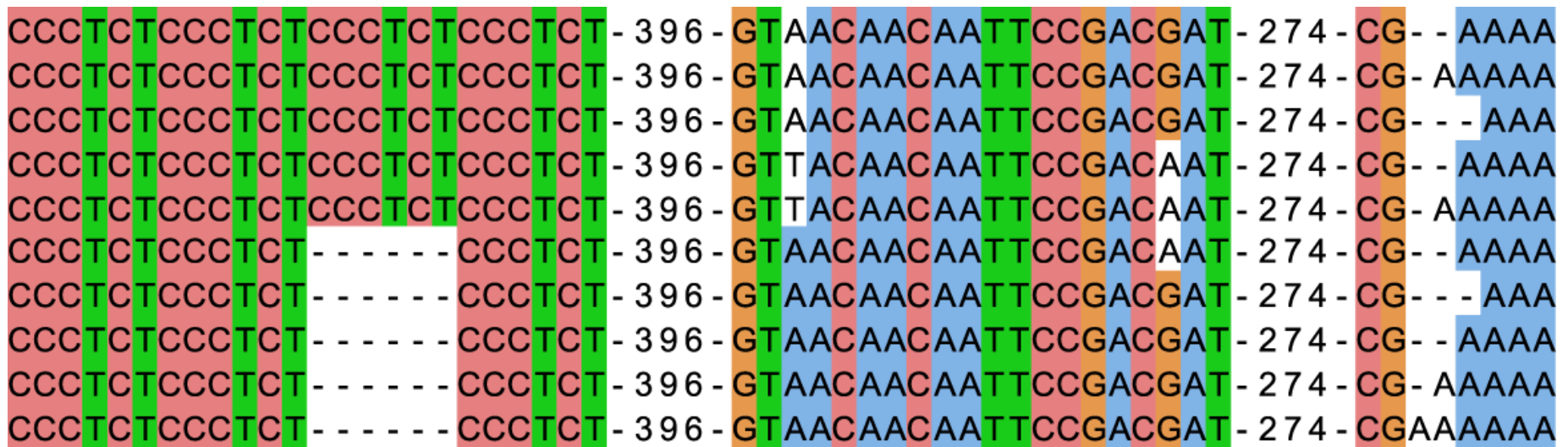
Mt cytochrome B

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

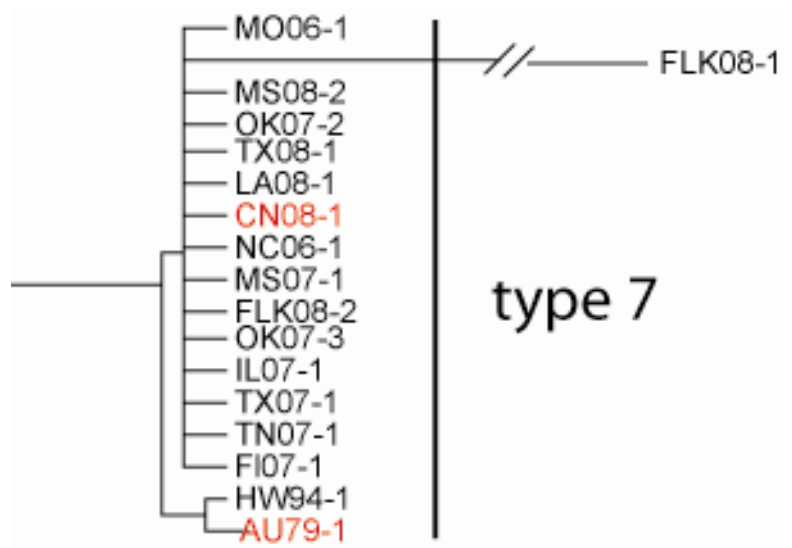
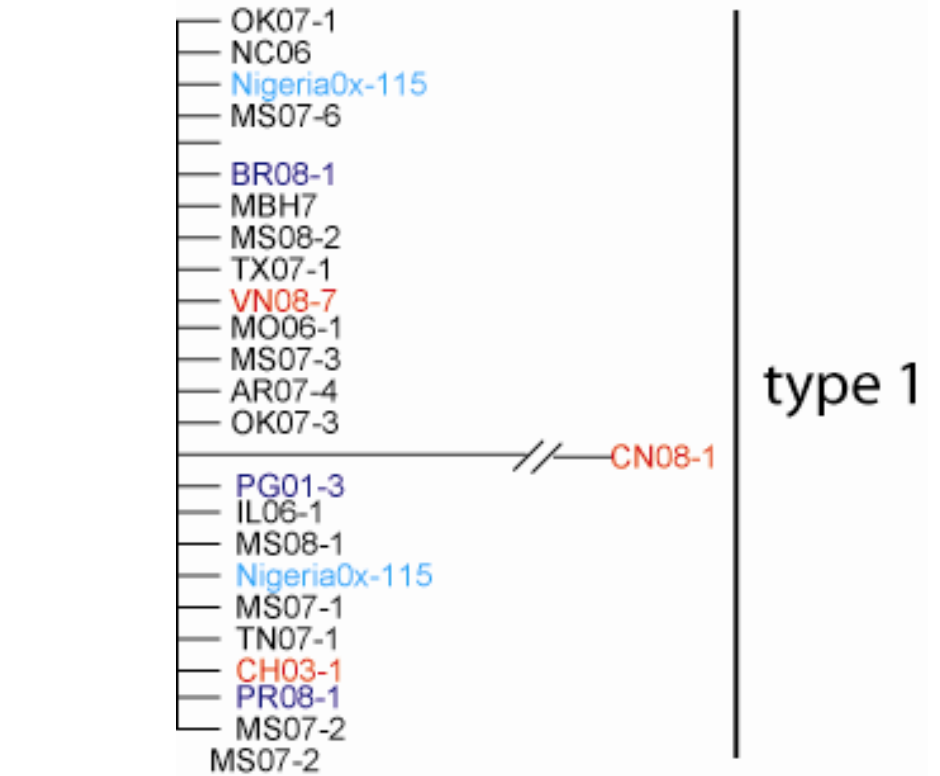
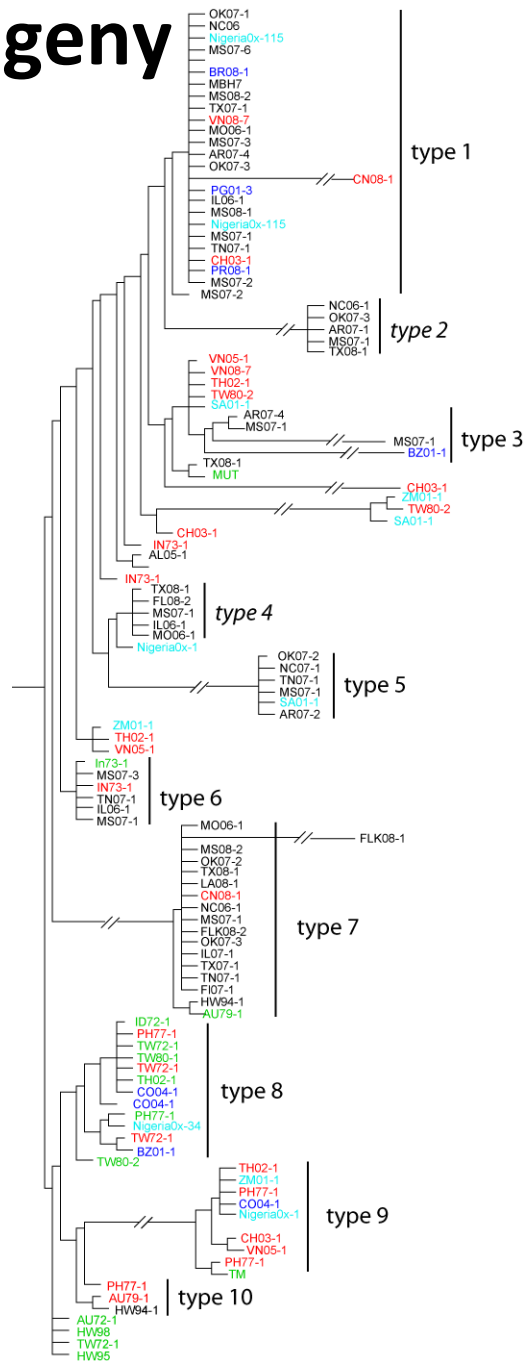
11 out of 29

2 in coding region
9 in non-coding region

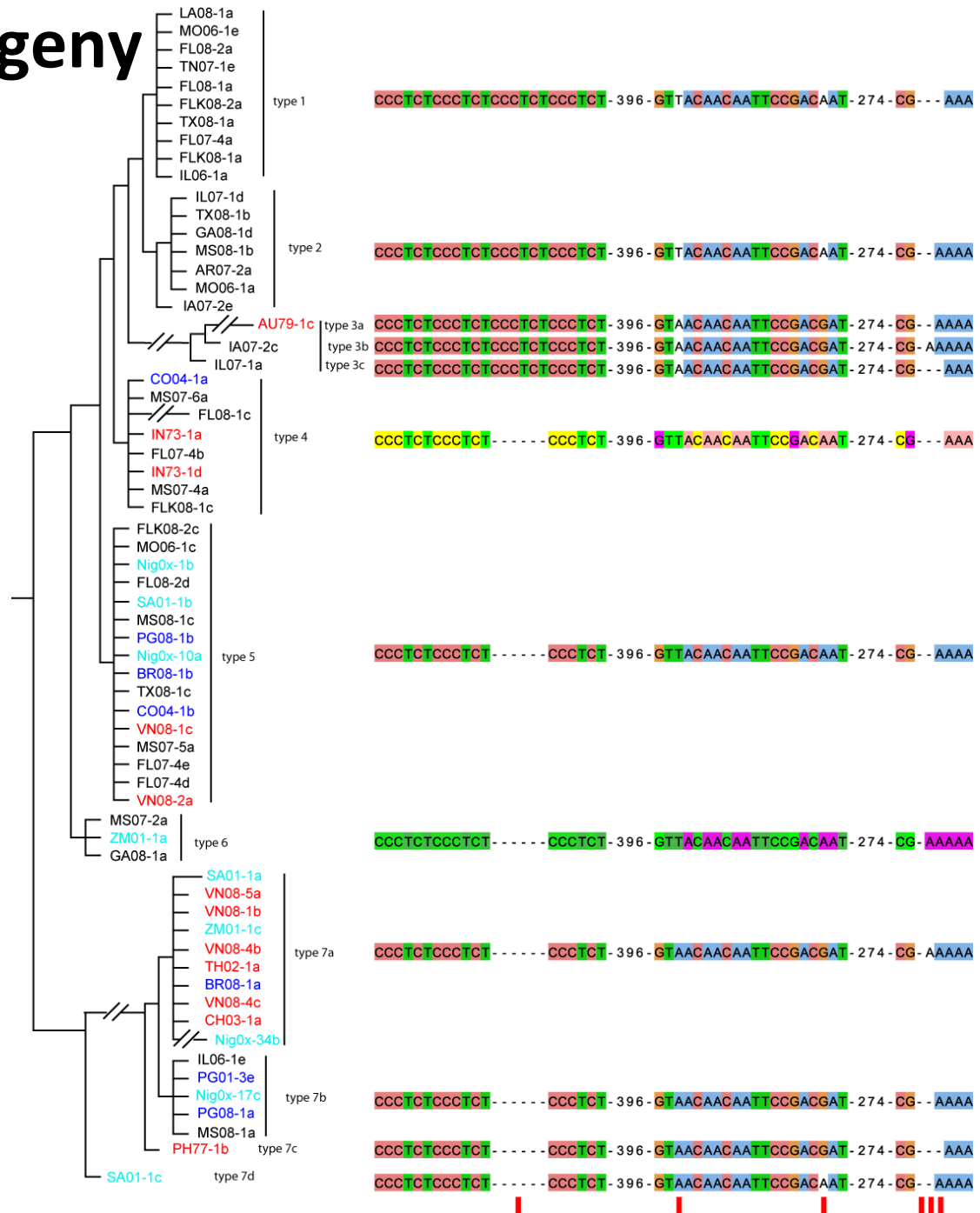
Most samples are a mixture of distinct isolates

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

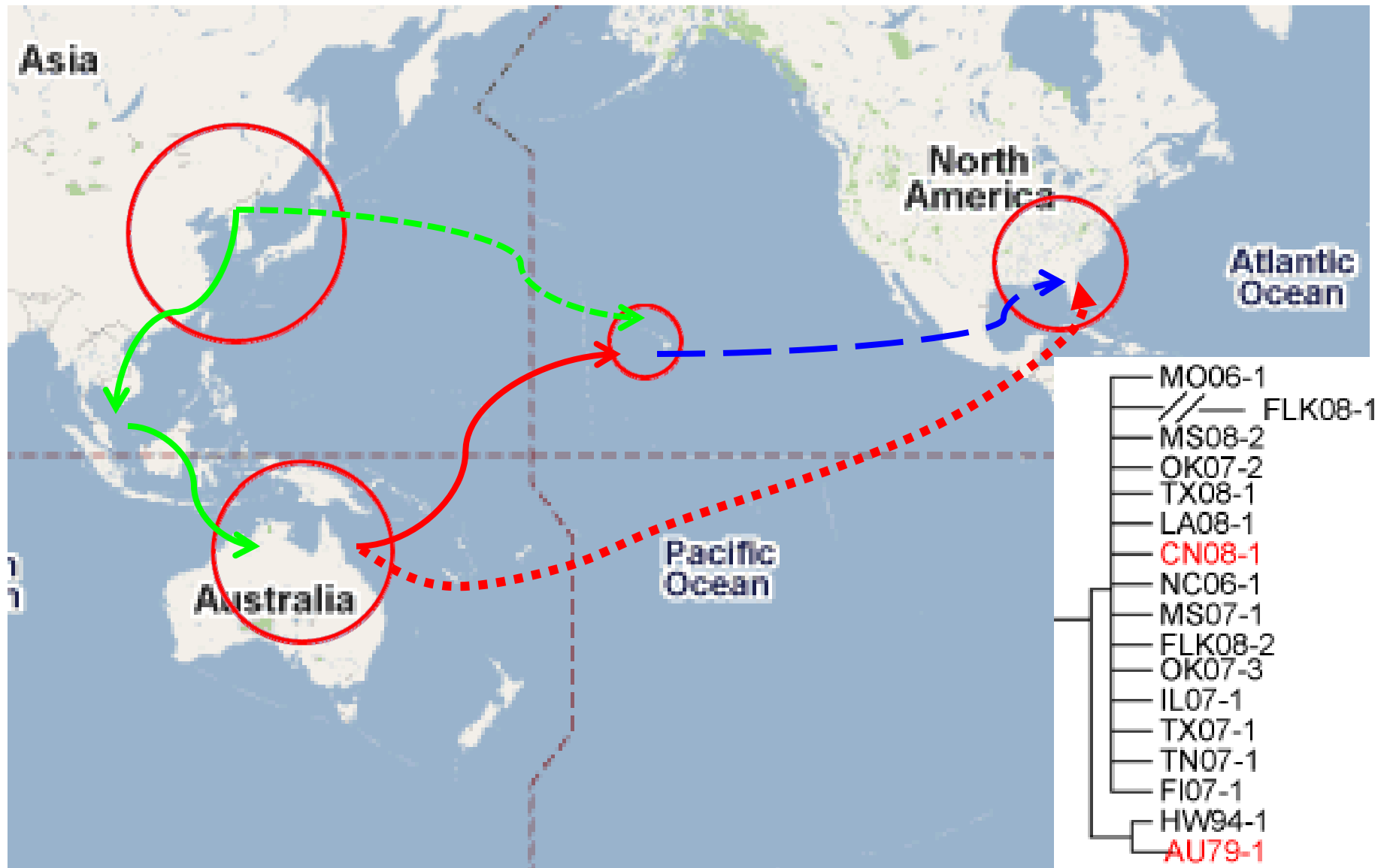


The prevalent ASR migration hypothesis



A path of ASR from East Asia to the USA

China--Australia—Hawaii---USA



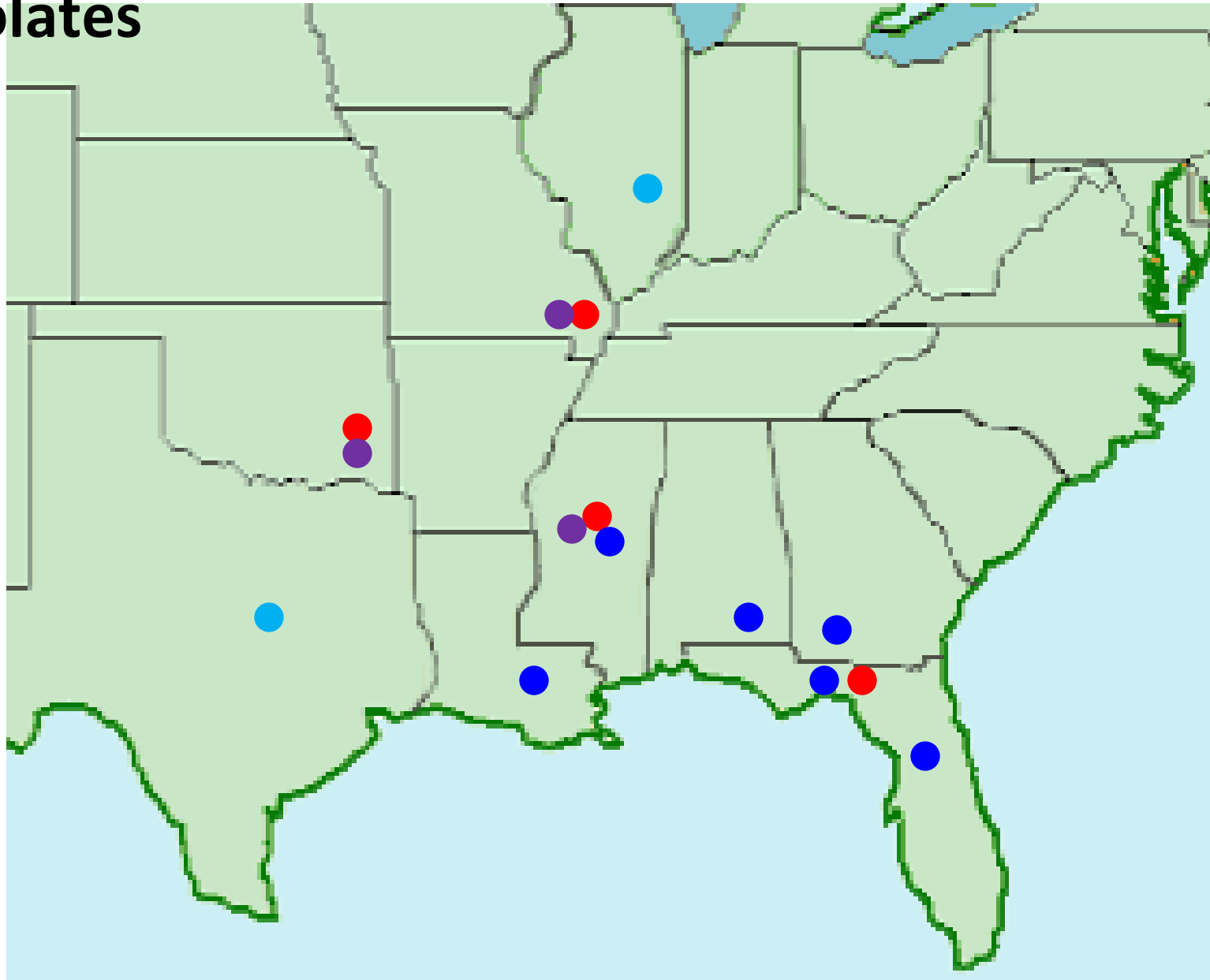
Sessile ASR



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.**