

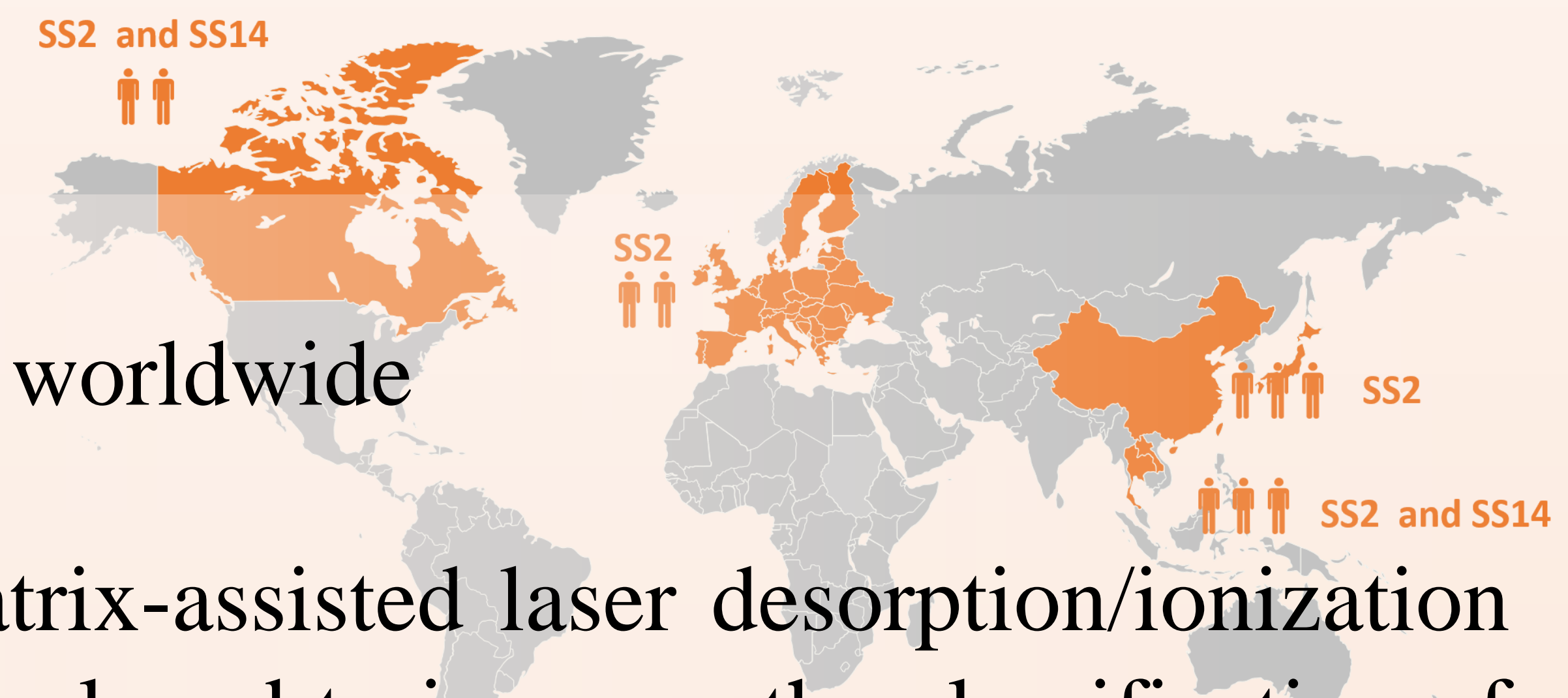
Streptococcus suis serotyping by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

Chadaporn Chaiden¹, Janthima Jaresitthikunchai², Anusak Kerdsin³, Nattakan Meekhanon⁴, Sittiruk Roytrakul², Suphachai Nuanualsuwan^{1,5,*}

¹Department of Veterinary Public Health, Faculty of Veterinary Sciences, Chulalongkorn University, Bangkok 10330, Thailand. ²Functional Proteomics Technology Laboratory, Functional Ingredients and Food Innovation Research Group, National Center for Genetic Engineering and Biotechnology, National Science and Technology for Development Agency, Pathum Thani, Thailand. ³Faculty of Public Health, Kasetsart University Chalermpkrakiat Sakon Nakhon Province Campus, Bangkok, Sakon Nakhon, Thailand. ⁴Department of Veterinary Technology, Faculty of Veterinary Technology, Kasetsart University, Bangkok 10900, Thailand. ⁵Center of Excellence for Food and Water Risk Analysis of Chulalongkorn University, Bangkok 10330, Thailand.

Introduction

- *Streptococcus suis*, particularly *S. suis* serotype (SS2)
- Important zoonotic pathogen causing meningitis in humans worldwide
- The current serotyping methods are significantly limited.
- In the present study, the peptide barcode generated by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (Maldi-TOF MS) was developed to improve the classification of *S. suis*.



Materials and methods

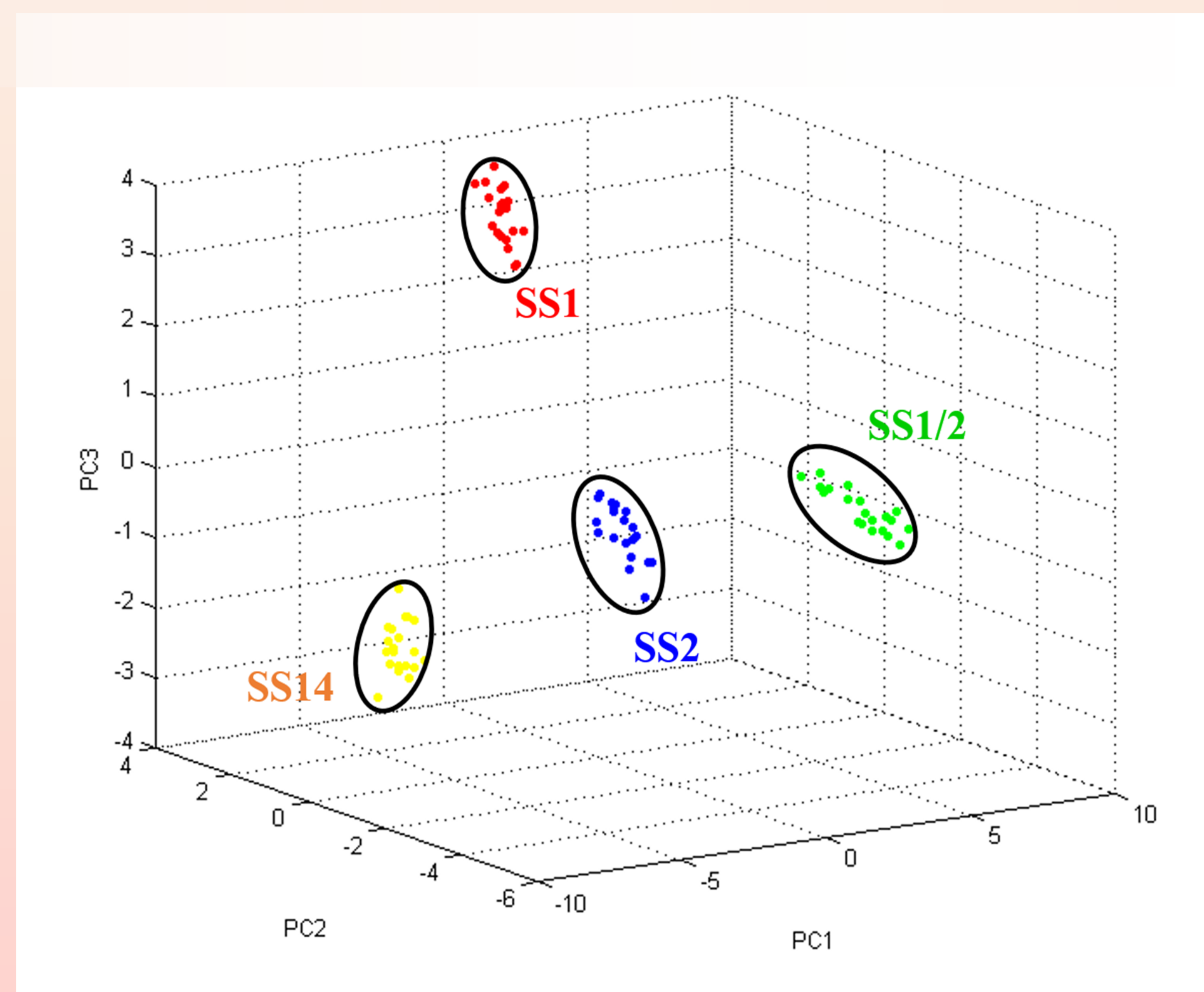
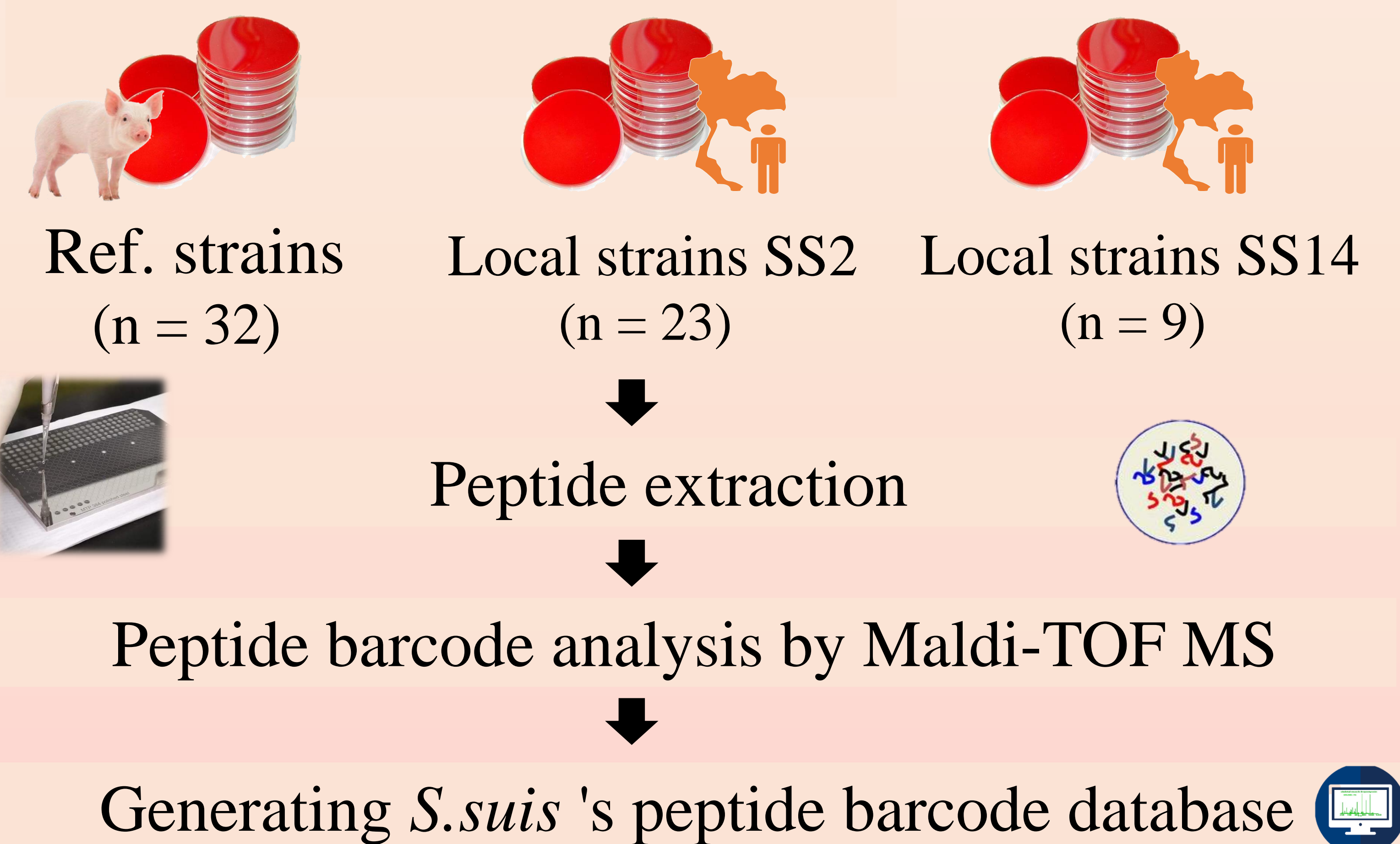


Fig 2. The PCA, based on the peptide barcodes, of the ambiguous serotypes of *S. suis* SS2, SS1/2, SS1, and SS14.

Results and Discussions



- Repeatability = 68.8% (22/32)
 - Validation = 56.5% and 77.8% (SS2 and SS14)
 - Reproducibility = 56.3%
 - Degree of test agreement unweighted Kappa score = 0.522
- Theoretically, in order to improve the score, more peptide barcodes of *S. suis* should be included.

Fig 1. The peptide mass spectra from each individual serotype generated a particular peptide barcode that contained their individual unique mass(es) and so differentiated each serotype from one another. Overall, 4420, 5337, 5965, 6634, 6748, 6834, and 8260 Da peptide masses were commonly found in most of the *S. suis*.

Acknowledgment

1. Chulalongkorn University for supporting the Center of Excellence for Food and Water Risk Analysis of Chulalongkorn University, Bangkok 10330, Thailand
2. The 100th Anniversary Chulalongkorn University Fund for Doctoral Scholarship; The 90th Anniversary of Chulalongkorn University Fund (Ratchadaphiseksomphot Endowment Fund); The Scholarship from the Graduate School, Chulalongkorn University to commemorate the 72nd anniversary of his Majesty King Bhumibol Adulyadej; The Agricultural Research Development Agency (Public Organization).

Conclusion

- Successfully differentiated the ambiguous serotypes of *S. suis*
- Providing an alternative method for *S. suis* classification
- Useful for *S. suis* infection diagnosis and epidemiological study of this zoonotic pathogen