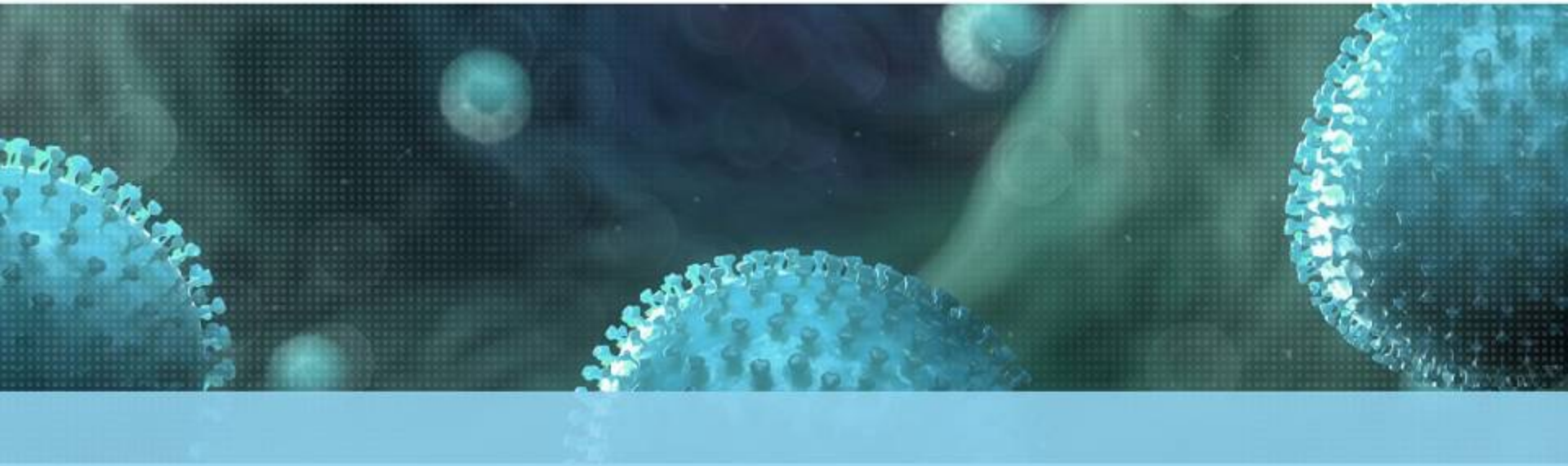
Erasmus MC

Viroscience lab

WHERE SKILLS MEET TO STUDY & PROTECT



The sequence of a predicted stem-loop in H5 hemagglutinin drives the emergence of highly pathogenic avian influenza

Monique Spronken

Conclusions

Why is a MBCS acquired in H5 and not in other HAs?

- H5 stem-loop sequence is more prone to indels than that of H6
- Indels in H5 loop were easily facilitated by increasing the adenine stretch length, but not in H6
- Intermediate H5 cleavage sites leading to increased indel frequency were detected in nature
- The most indel-prone H6 cleavage site was not detected in nature
- **Loop sequence** is a key determinant driving insertions at the hemagglutinin cleavage site.

Acknowledgments

Mathis Funk
Sacha Gultyaev
Anja de Bruin
Ron Fouchier
Mathilde Richard

Richard CEIRS Option 18J