

Abstract Number: 596

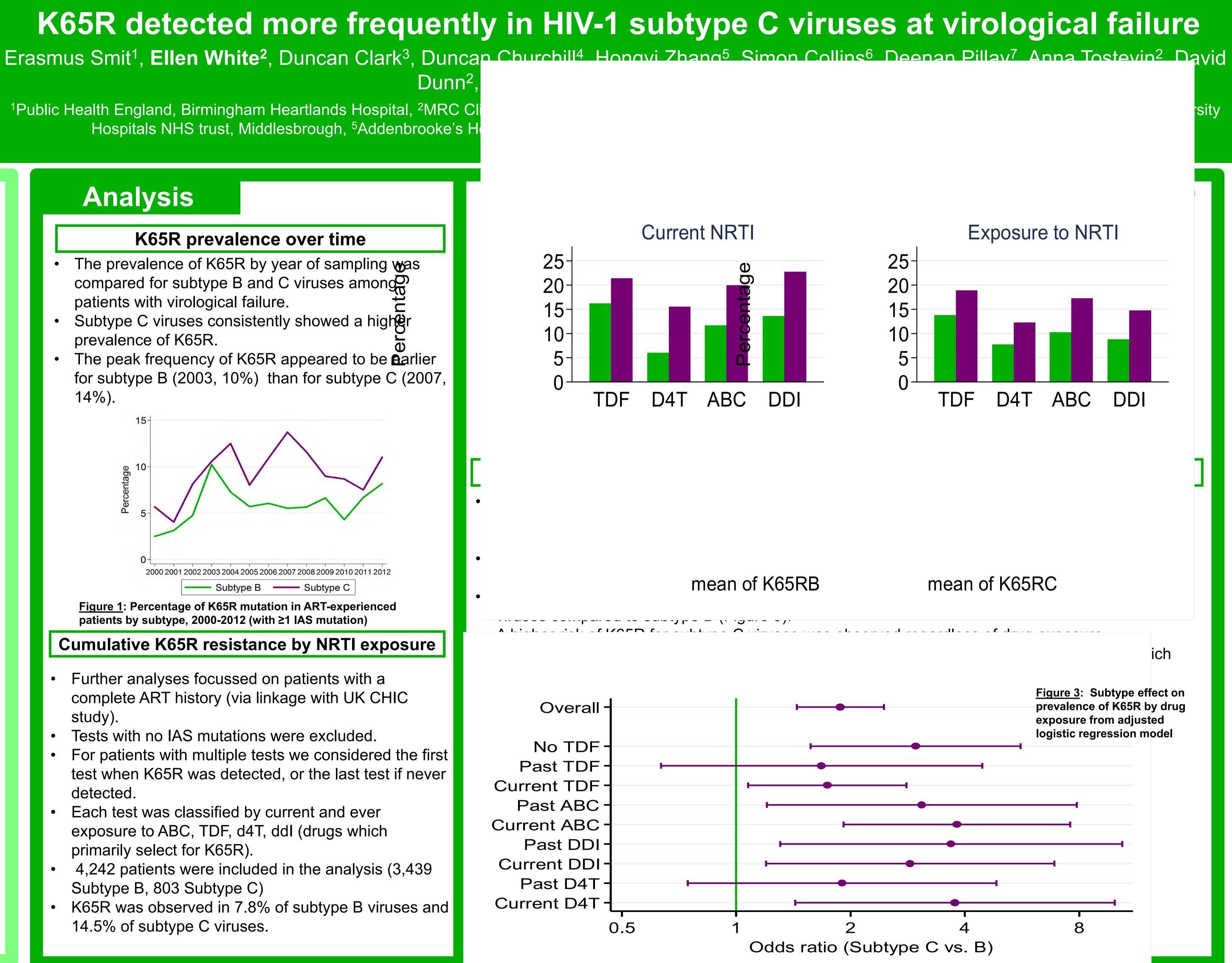
Background

- Cell culture experiments have shown that subtype C viruses have a greater propensity to develop the K65R mutation [1].
- This appears to be due to different codon usage:

Subtype B AAG AAA AAA Subtype C AAA AAG AAG **65 66** Codon 64

- The clinical relevance of this finding has not been elucidated. A high prevalence of K65R has been documented in several cohort studies in Southern Africa, where subtype C is the predominant subtype [2,3]. However, prolonged virological failure could also account for this observation.
- A retrospective European study found that K65R selection was significantly higher in subtype C but included a limited number of subtype C viruses [4].
- We have performed a similar analysis using the results of routine genotypic tests reported to the UK HIV Drug Resistance Database, with a much larger number of subtype C viruses and a range of different regimens.

- 14%).



- study).
- detected.

ſSIťY

Contact information: Miss Ellen White Email: ellen.white@ucl.ac.uk www.hivrdb.org

Summary

- These are the strongest clinical data yet to show an increased risk of selection of the K65R mutation among subtype C viruses.
- This effect was observed across a range of different NRTI exposure histories.
- Preliminary analysis (not shown) suggest that non-B non-C subtypes have a similar prevalence of K65R to subtype B.
- A key unresolved clinical question is whether patients infected with subtype C viruses are at a higher intrinsic risk of virological failure on first-line TDF-containing regimens. We are currently undertaking such analyses.

References

- Brenner et al; AIDS 2006, 20:F9-F13
- Sunpath et al; AIDS 2012, 26(13) 1679-1684
- Skhosana et al; PLoS ONE, 2015, 10(2): e0118145
- Theys et al; Antimicrob Agents Chemother, 2013 57(2): 1053-1056

Acknowledgments

We would like to acknowledge all contributors to the UK HIV Drug Resistance Database and the UK CHIC Study (listed at www.hivrdb.org and www.ukchic.org.uk).