

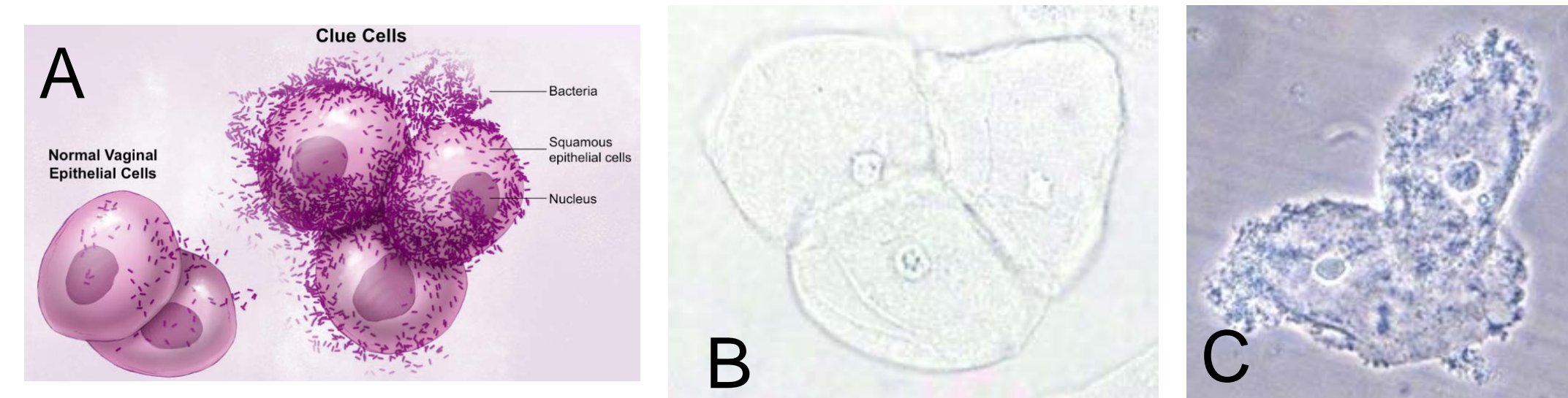


Chemokine Profiling of Vaginal Epithelial Cells Exposed to *Gardnerella vaginalis*

Betsy Schlehuser¹, Oladipupo Ogunbekun¹, Jonathan Lowery¹, Bryan Larsen¹
 Marian University College of Osteopathic Medicine¹

Introduction

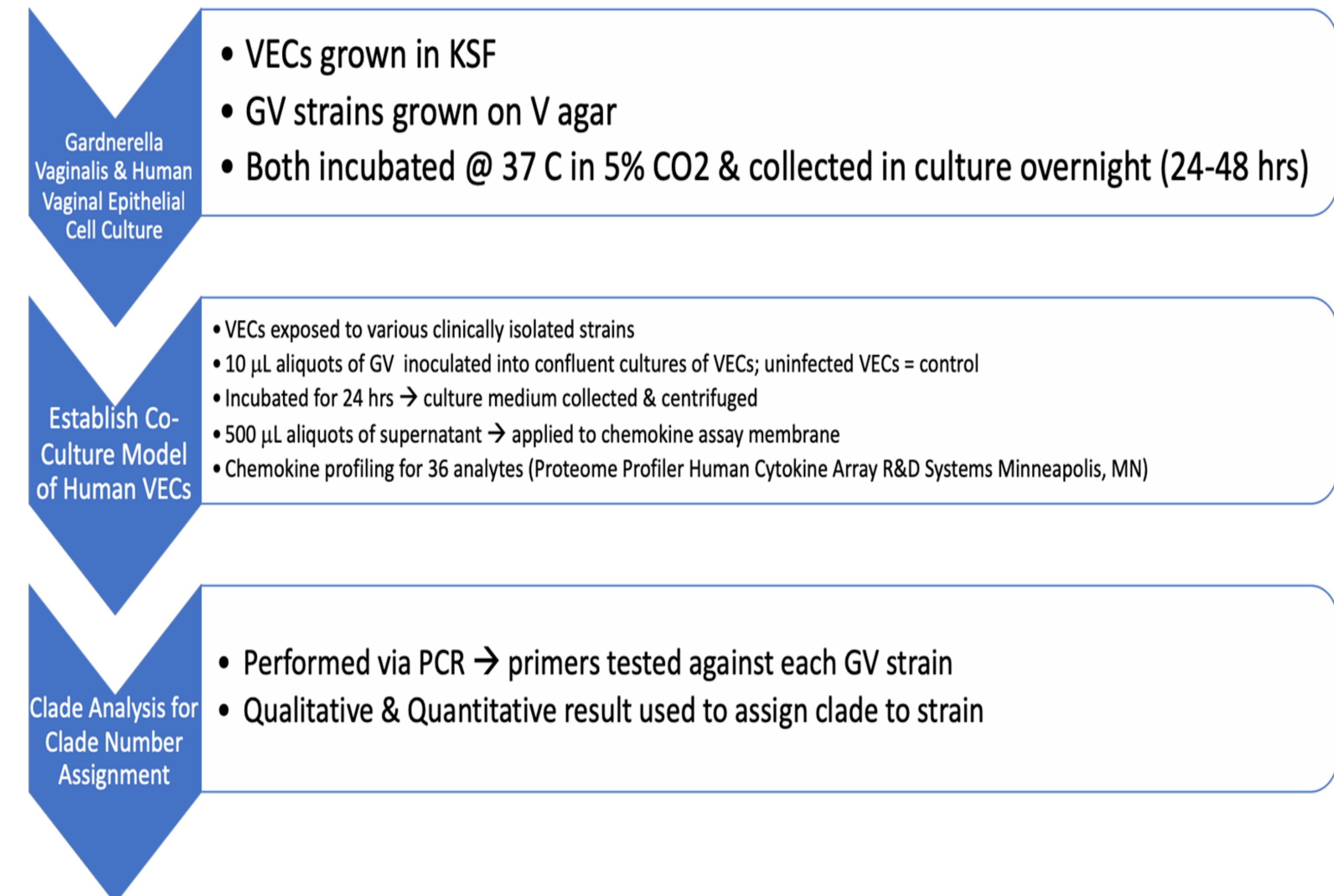
Gardnerella vaginalis (GV) is associated with bacterial vaginosis (BV) and when present in abundance, causes a dysbiosis characterized by increased pH, presence of clue cells, malodorous discharge, and a diversity of bacterial species other than *Lactobacillus*. BV predisposes to preterm labor and increased susceptibility to sexually transmitted infections. The potential role of cytokines elaborated by the vaginal epithelium may impact BV symptoms and hence, is the topic of this research.



A. Cartoon depiction of normal vaginal epithelial cells versus VECs covered in GV, called clue cells. B. Normal vaginal epithelial cells under light microscope. C. Clue cells under light microscope.

Methods

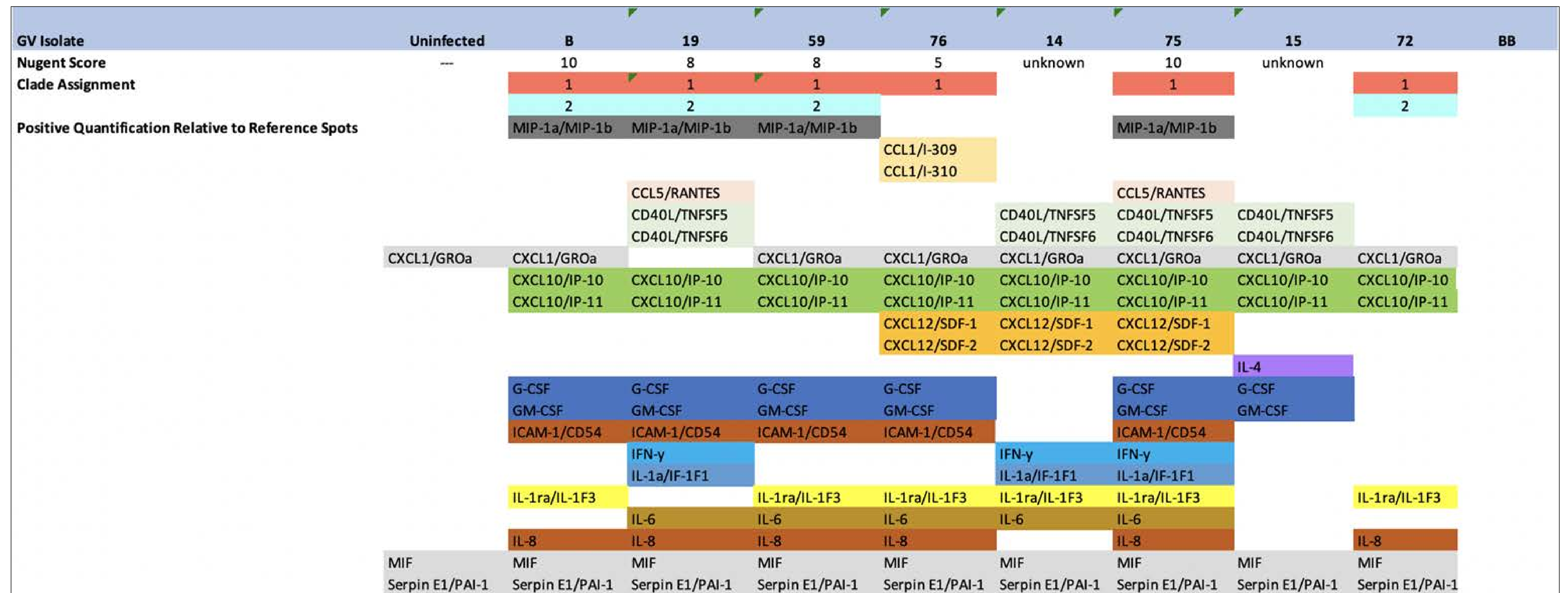
We hypothesized that host-derived chemokine expression will correlate with Nugent (Gram stain species diversity) severity scores obtained from women with GV colonization.



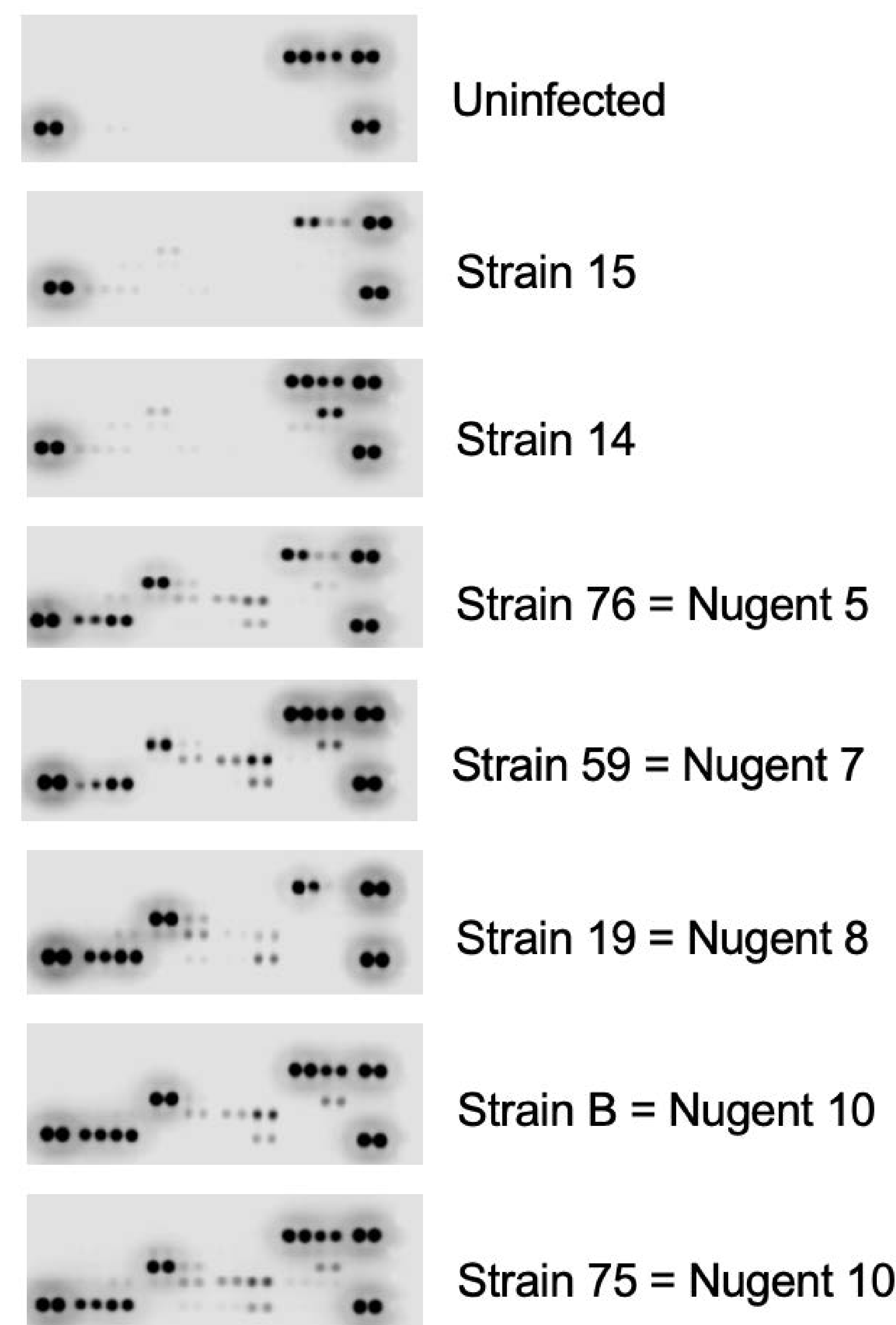
Results

Membrane profiling results showed that 23 cytokines and chemokines were variously upregulated following exposure of VECs to GV, while others are down-regulated relative to the control. Continued investigation will attempt to correlate Nugent scores and placement of strains into clades 1-4.

Cytokine/Chemokine Upregulation



Representative Images of Cytokine Arrays



Conclusions

Our results indicate that co-culture with GV induces release of numerous chemokines from VECs. Future work will determine if these chemokines signal in an autocrine/paracrine manner and/or participate in the recruitment and activation of immune cells in response to GV colonization.

Acknowledgements

A special thanks to Dr. Jonathan Lowery and Dr. Bryan Larsen for their assistance and guidance.