# CANCER IN MEAT WORKERS: A ROLE FOR INFECTIOUS ORGANISMS

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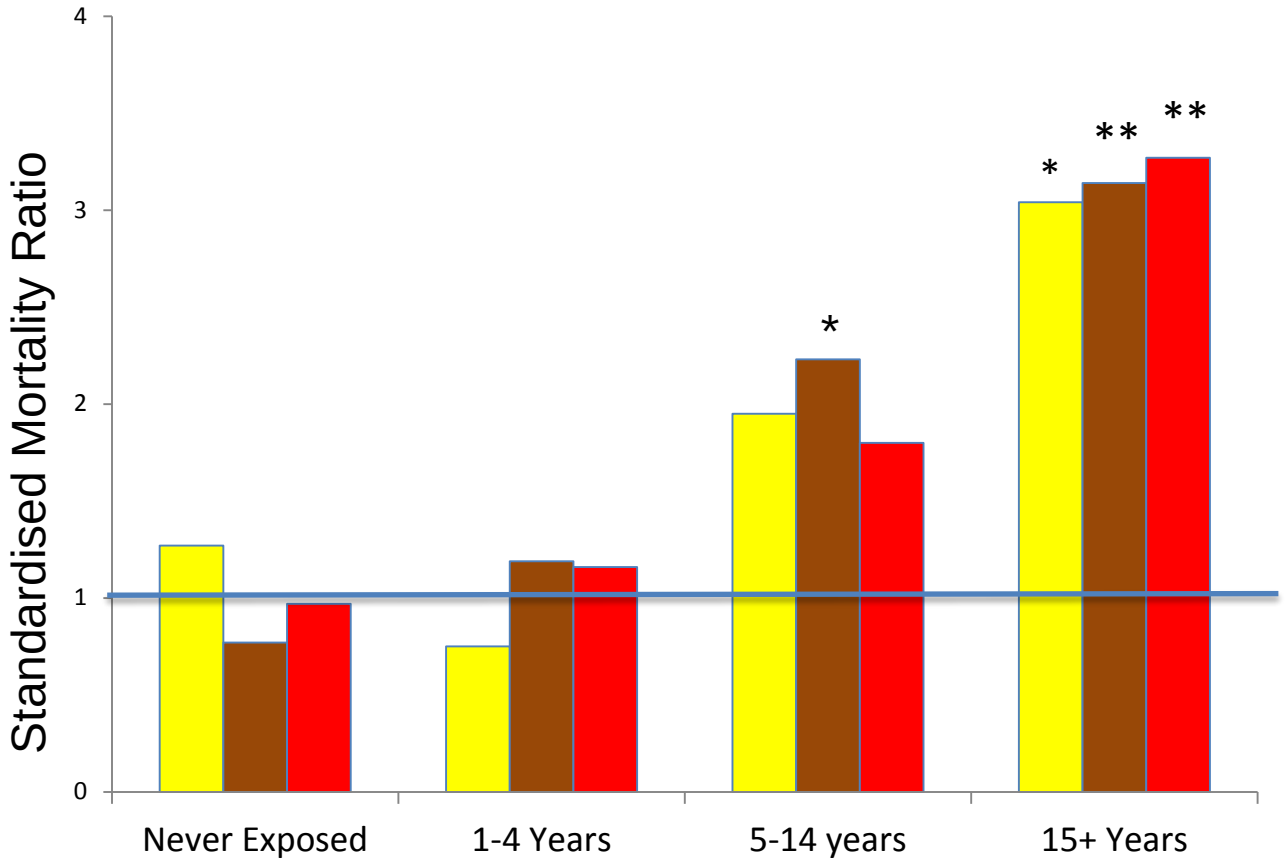
# MORTALITY AND CANCER INCIDENCE IN NZ MEAT WORKERS. MCLEAN *et al*. Occup Environ Med 2004;61:541-7

| Cause of death (ICD-9) | Observed | Expected | SMR | 95% CI |
|---|---|---|---|---|
| All Causes | 227 | 203.6 | **1.12** | 0.98 - 1.27 |
| All Cancer (140-208) | 69 | 61.4 | **1.12** | 0.88 - 1.42 |
| Lung (162) | 23 | 12.9 | **1.79** | 1.13 – 2.68 |
| Haematologic (200-208) | 6 | 6.3 | **0.96** | 0.35 – 2.09 |

*(n = 6,647)*

# Lung cancer mortality by employment duration in selected biological exposure categories




* $p<0.05$
** $p<0.01$



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# OVERALL CONCLUSIONS

Significant excess mortality from lung cancer.

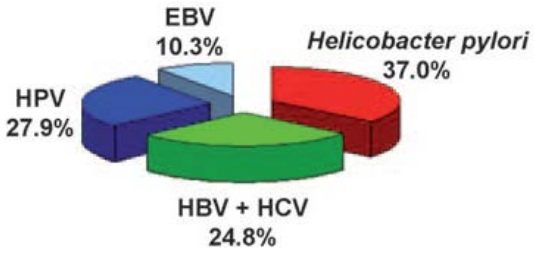
The excess was associated most strongly with increasing duration of exposure to animal urine/faeces/blood.

The excess is greater than could be attributed to smoking.

# CURRENT THEORIES ON CAUSATION

A **biological** exposure, although specific causal agents have not been identified.

Cancers due to 5 infections constitute 18.5% of total cancer incidence in humans.




Another strong possibility is **chronic antigenic stimulation**.

# MEAT WORKERS STUDY METHODS

Personal **bioaerosol** samples to measure:

- **Protein** levels as a proxy for chronic antigenic stimulation.
- **Urine**, **blood** and **faecal** markers.
- **Mutagenicity** of the bioaerosols *in vitro*.
- **Bacterial** and **viral** pathogens using culture methods, next-generation sequencing and specific PCR analysis.

**Blood** and **sputum** samples for evidence of past infection and current exposure.

Repeat **epidemiological analysis on cohort** using refined exposure estimates.

# MEAT WORKERS STUDY METHODS

## Personal sampling

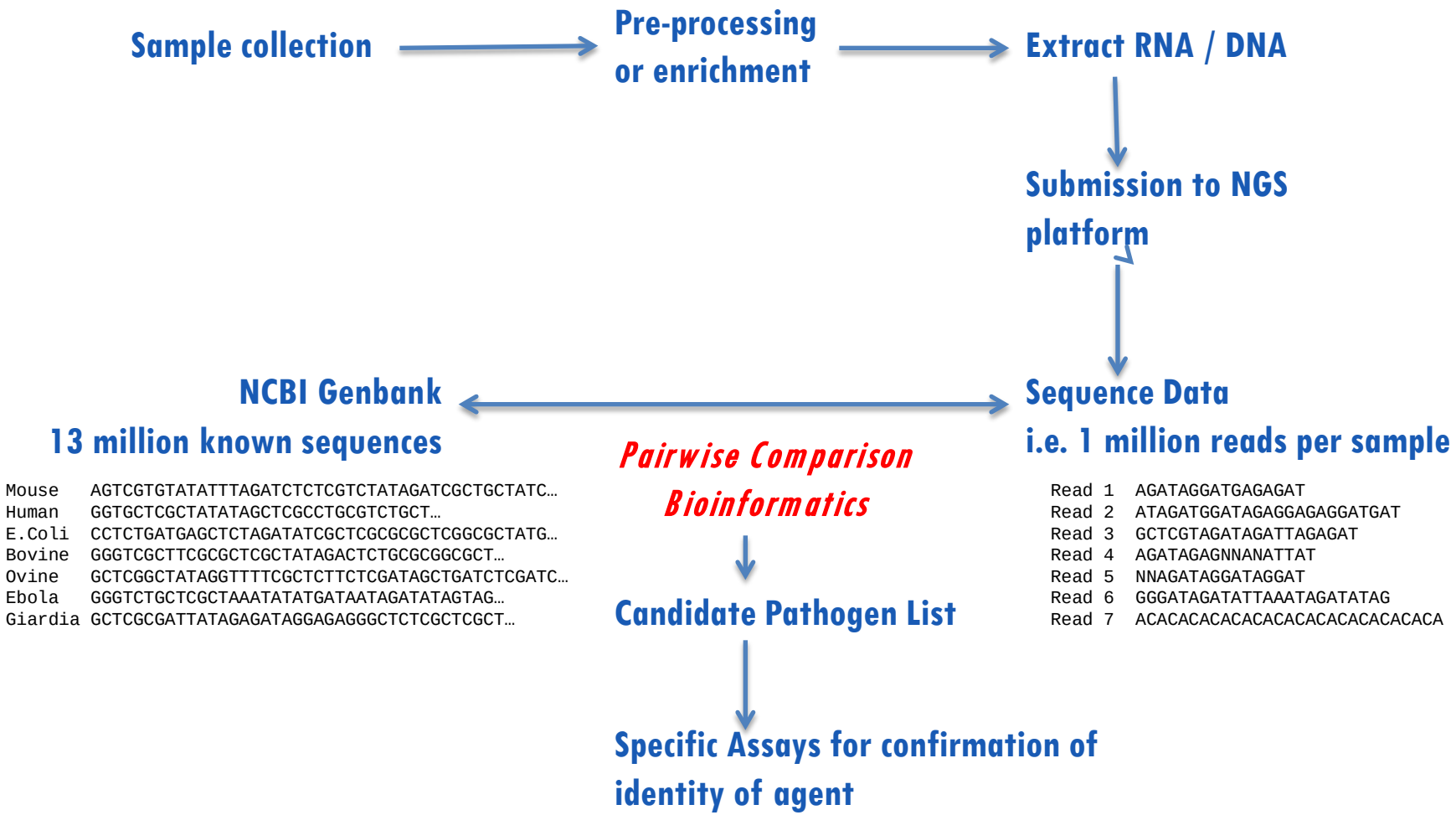

## Viable culture plates

MAS-100
100LPM

## Bulk sampling

SASS 3100
50 to 300 LPM

# PATHOGEN DISCOVERY USING DEEP-SEQUENCING



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# RESULTS: VIABLE BACTERIAL CULTURE



# RESULTS: NGS ON POOLED PERSONAL SAMPLES

Bacterial species made up the majority of sequences identified.

Bovine and Ovine sequences detected, confirmed by real-time PCR detection of the cytochrome b gene.

Human viral sequences detected, confirmed by specific PCR on the amplified samples: **HPV – 120**

**WU PyV**

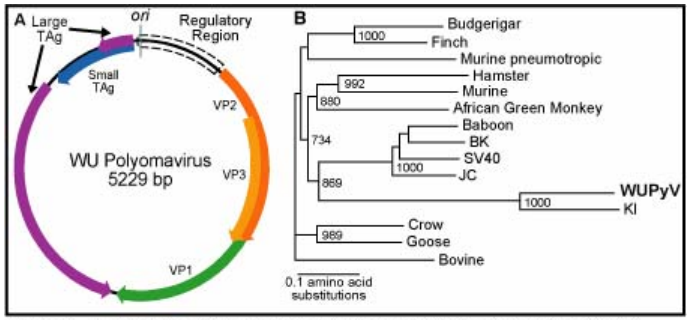


Figure 1. A. Genomic organization of WUV. B. Phylogenetic analysis of VP1 capsid protein



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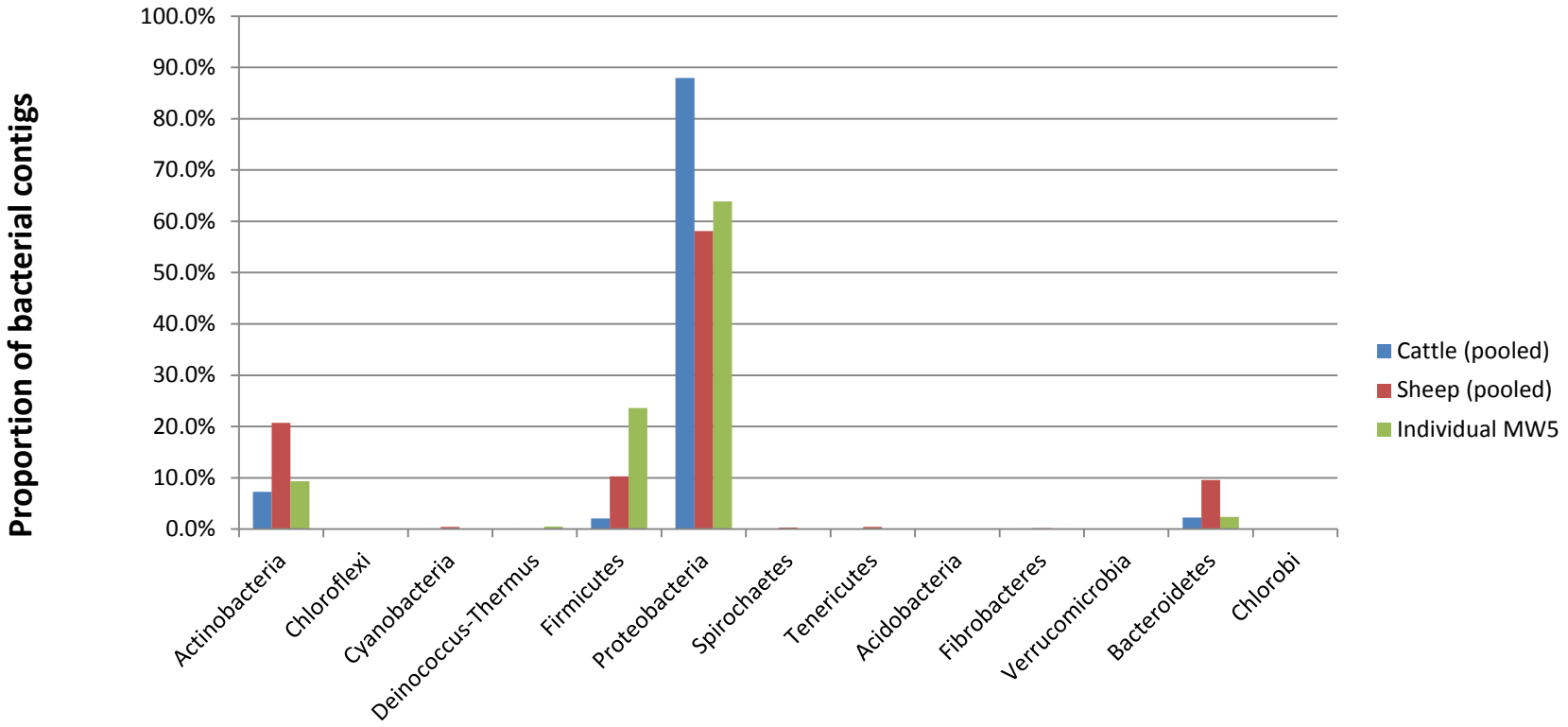
# Bioaerosol bacterial *de novo* metagenome of personal air samples (for assembled contigs)

Number of sequence reads
Cattle 83,536,320
Sheep 62,929,646
MW5 72,680,960



# CONCLUSIONS

- Full-shift personal samples collect insufficient genetic material for NGS, so have pooled samples and done bulk sampling using the SASS 3100.
- Have detected:
    - Mostly bacterial sequences.
    - Human, bovine and ovine DNA.
    - Numerous retroviruses, but probably endogenous retroviral sequences from the host genome.
    - WU PyV and HPV-120.
- Beginning to identify contrast in microbial composition of different environments – for epidemiological analyses.