BIOAEROSOL COMPOSITION AT A FRUIT BEVERAGE BOTTLING FACILITY

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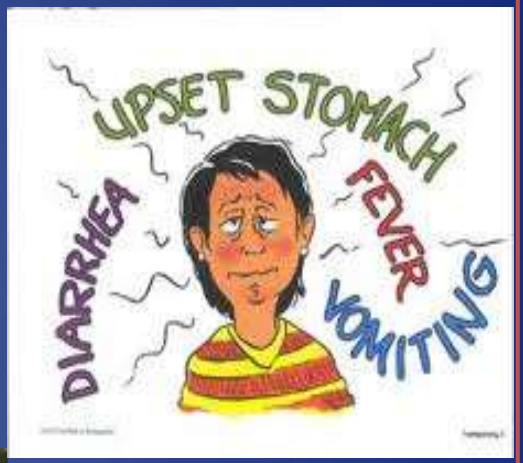
OUTLINE

- INTRODUCTION
- AIM
- MATERIALS AND METHODS
- RESULTS AND DISCUSSION
- CONCLUSIONS
- FUTURE RESEARCH

WHY THIS PROJECT



INTRODUCTION

- Pathogenic microorganisms in food
- Linked to numerous foodborne illness outbreaks
- Pasteurization, concentration or low-temperature storage

- South African legislation for consumption of fruit juices

Microorganisms	Legislation
Total viable colony count	10^4 CFU.ml^{-1}
Coliform count	10^2 CFU.ml^{-1}
Yeast and mould	10^3 CFU.ml^{-1}
E. coli	Not detectable in 25 ml
Salmonella spp.	Not detectable in 25 ml

- No legislation for air quality

(Act no 54 of 1972; Despres *et al.*, 2011)

INTRODUCTION

- Bioaerosols and organic dust
- Bioaerosols are defined as
- Two phase system

- Various methods available for detecting viable microorganisms

- Air sampling most effective

- Various factors influence the airborne contamination

- The features of this specific fruit juice bottling facility

(Després *et al.*, 2011)

INTRODUCTION

Culturable organisms

- Viable and culturable
- Reproduce under controlled conditions
- Underestimate the total quantity of organisms
- Some bacteria, moulds and yeast

Non-culturable organisms

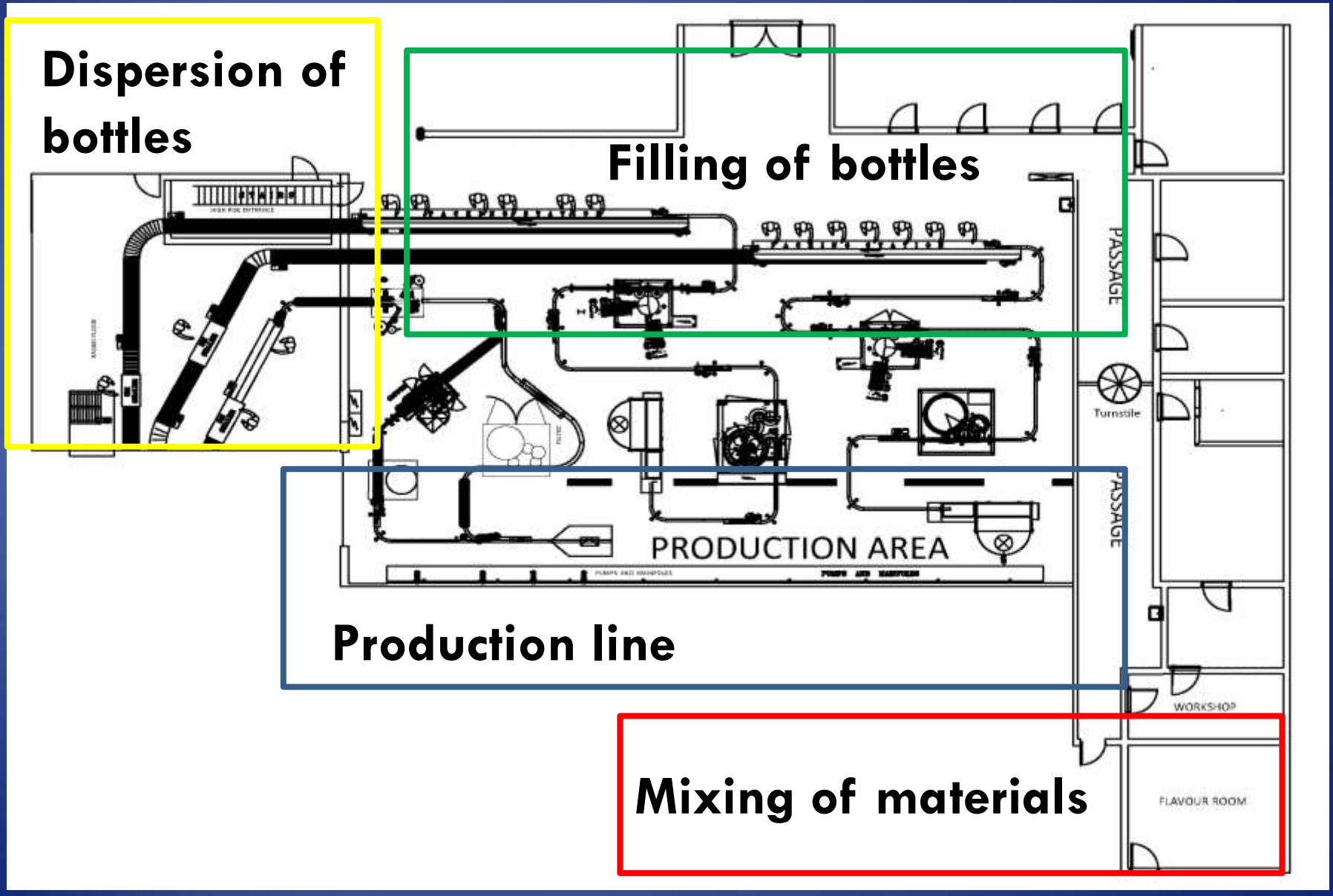
- Viable but non-culturable
- Not conductive to growth
- Difficult to estimate total quantity of organisms
- Some pathogenic bacteria, spores and allergens

(Nystrom, 2001)

AIM

To enumerate and identify the culturable and non-culturable bioaerosol microbiota associated with a fruit juice bottling plant in Bloemfontein, South Africa.

MATERIALS AND METHODS



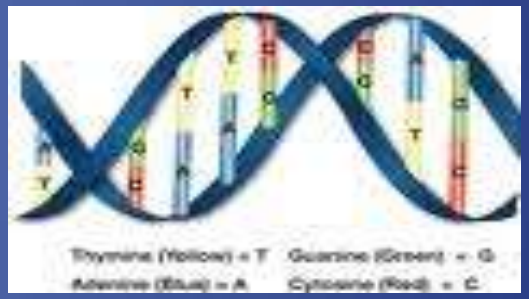
Sampling

Microbial enumeration

Concentration calculation

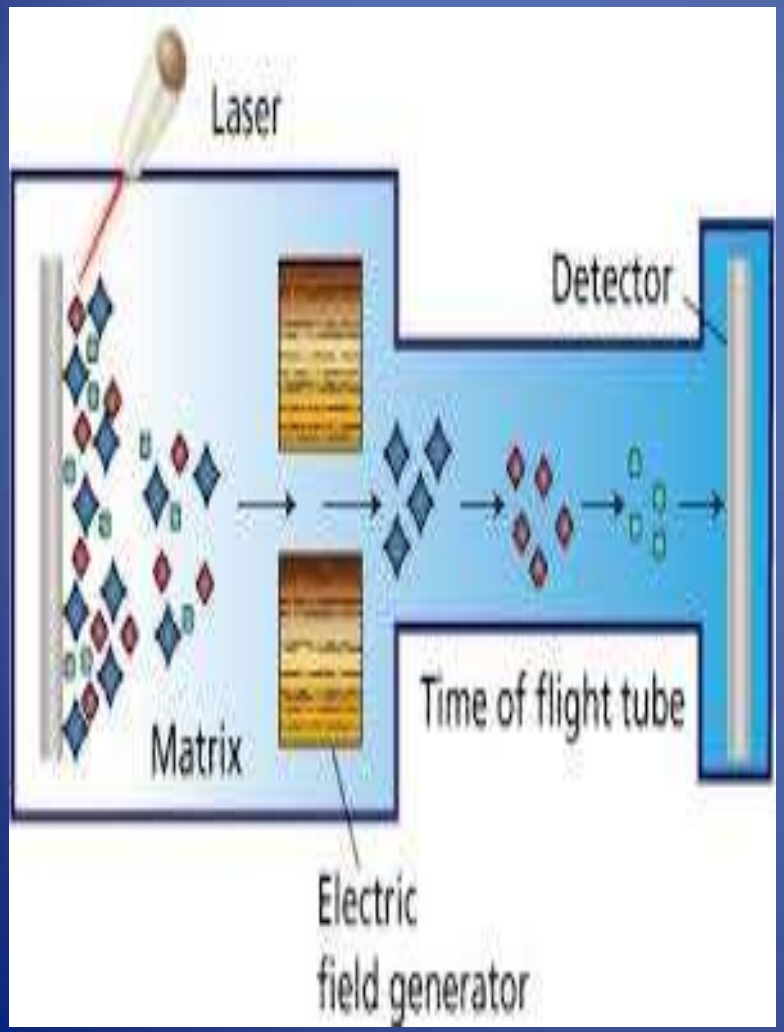
$$\frac{(\#CFUs\ [\text{after positive hole correction}])}{(sampling\ time\ min)(\frac{0.1m^3}{min})} = CFUs.m^{-3}$$

Yeast and mould were identification by D1/D2 domain sequencing and ITS1/ITS4 respectively

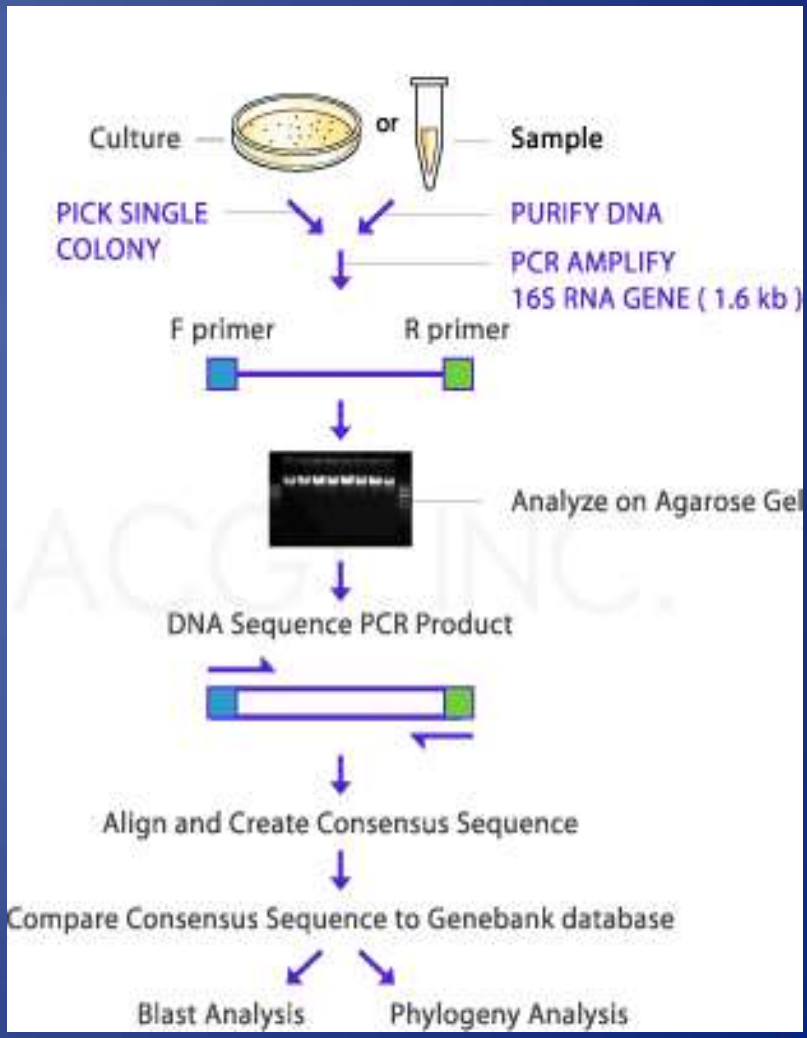


Bacteria

MALDI-TOF
Mass spectrometer



16S rRNA Gene Sequencing



RESULTS AND DISCUSSION

Total microbes - 52 to 1269 (CFUs).m^{-3}

Presumptive positive *Staphylococcus aureus* - 11 to 138 (CFUs).m^{-3}

Presumptive positive *Salmonella* spp. - 2 to 6 (CFUs).m^{-3}

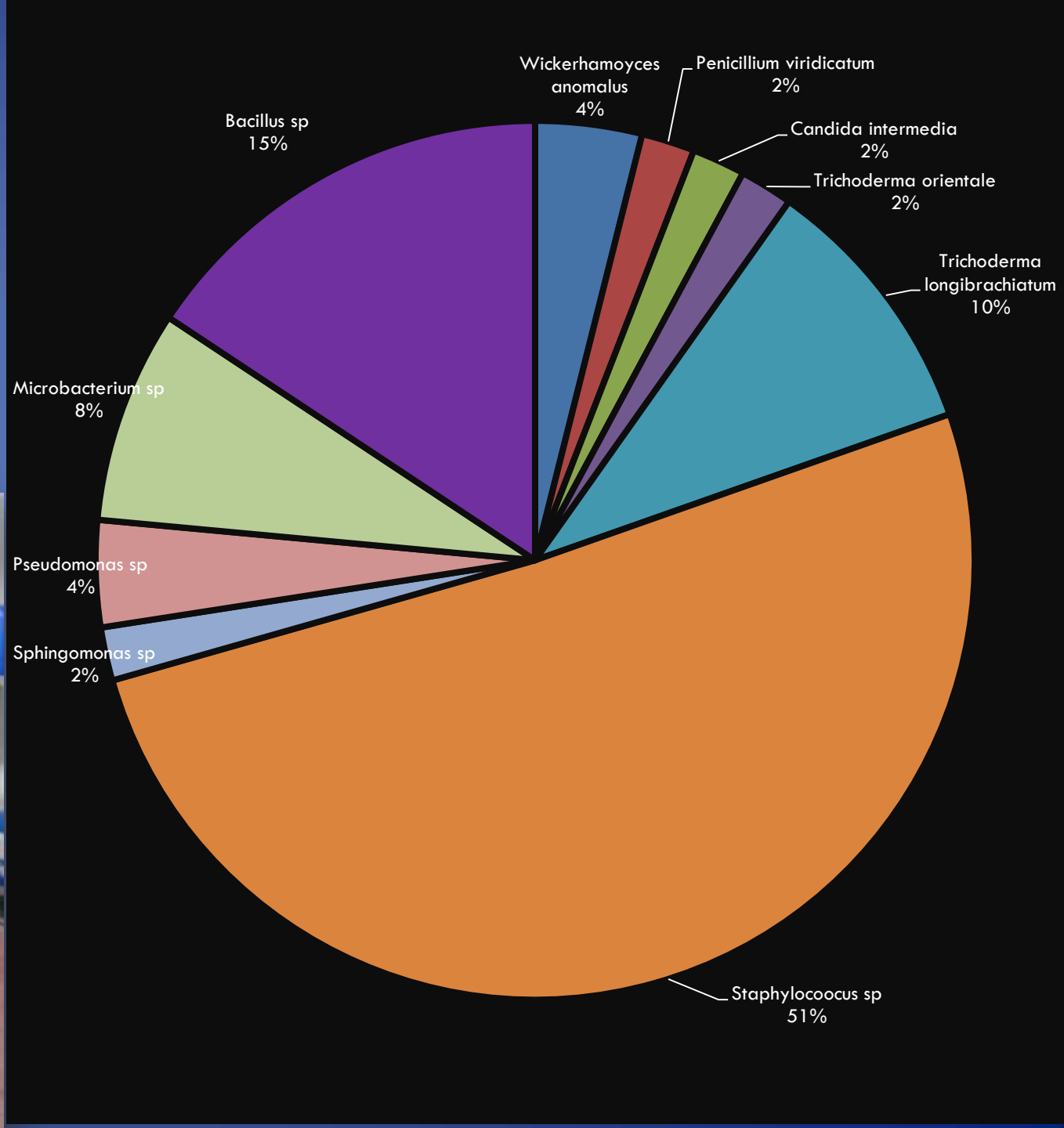
Coliforms - 1 to 18 (CFUs).m^{-3}

Presumptive positive *Escherichia coli* - 1 to 5 (CFUs).m^{-3}

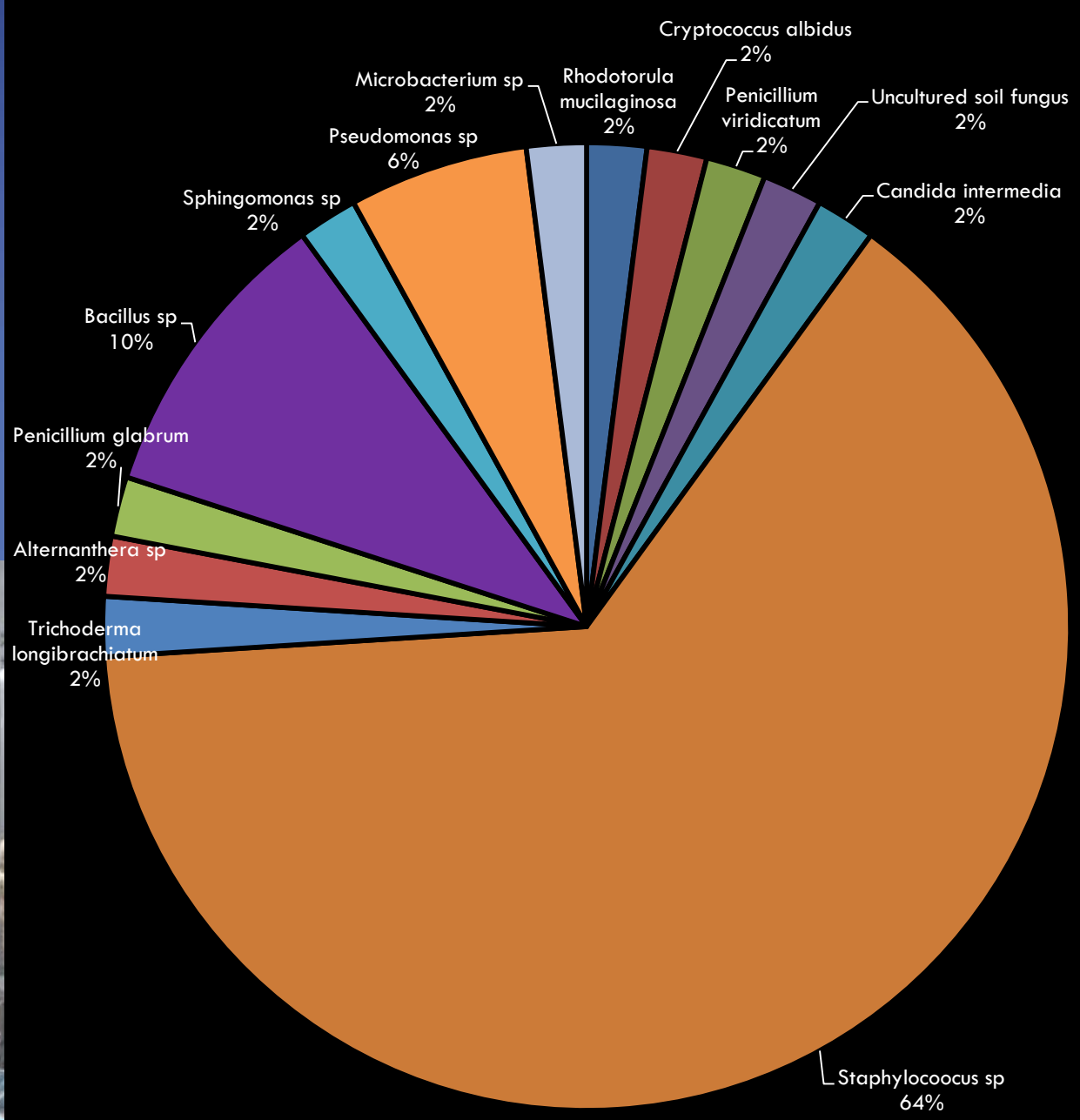
Mould - 11 to 33 (CFUs).m^{-3}

Yeasts - 23 to 120 (CFUs).m^{-3}

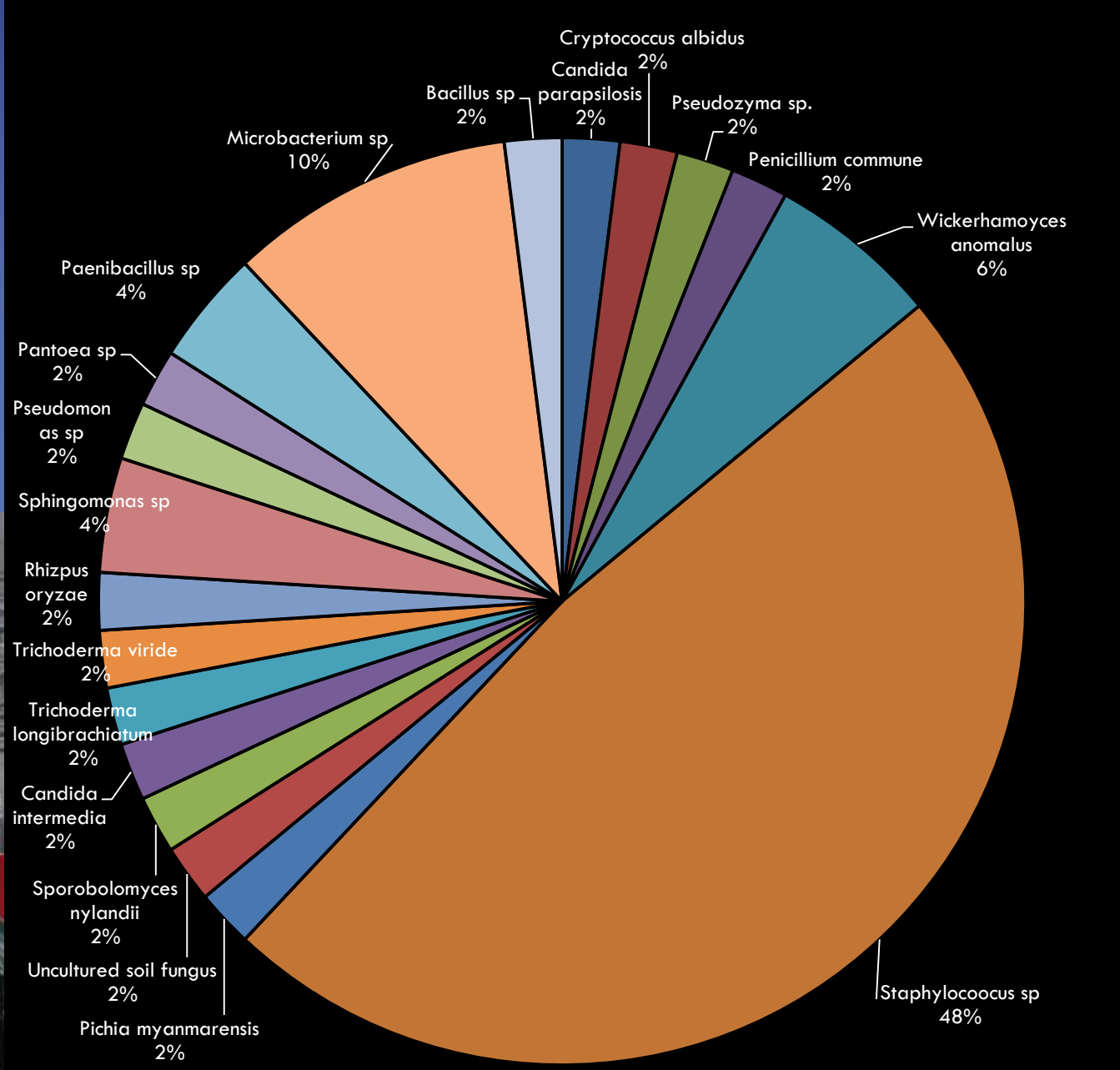
Mixing of materials



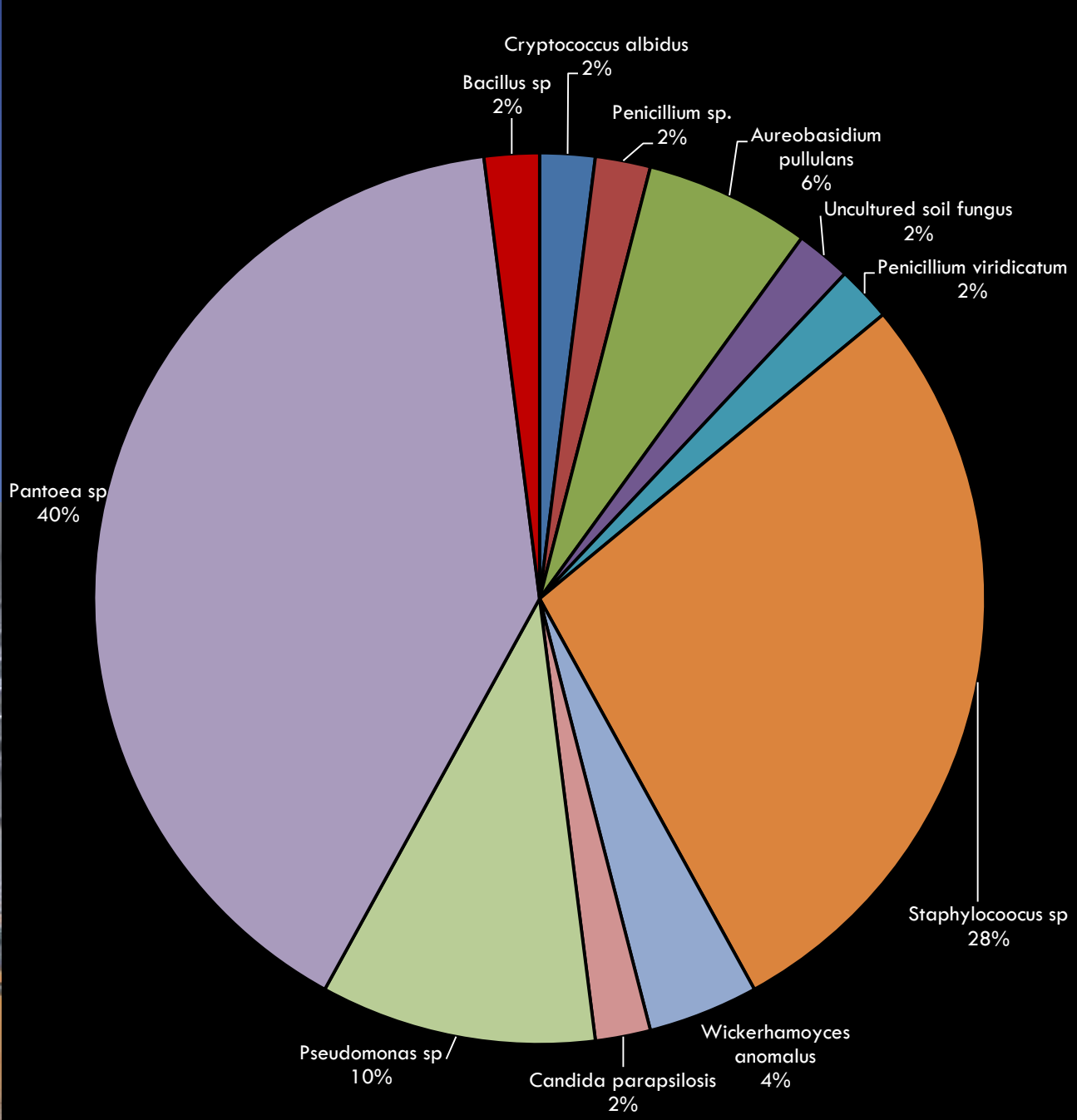
Production line

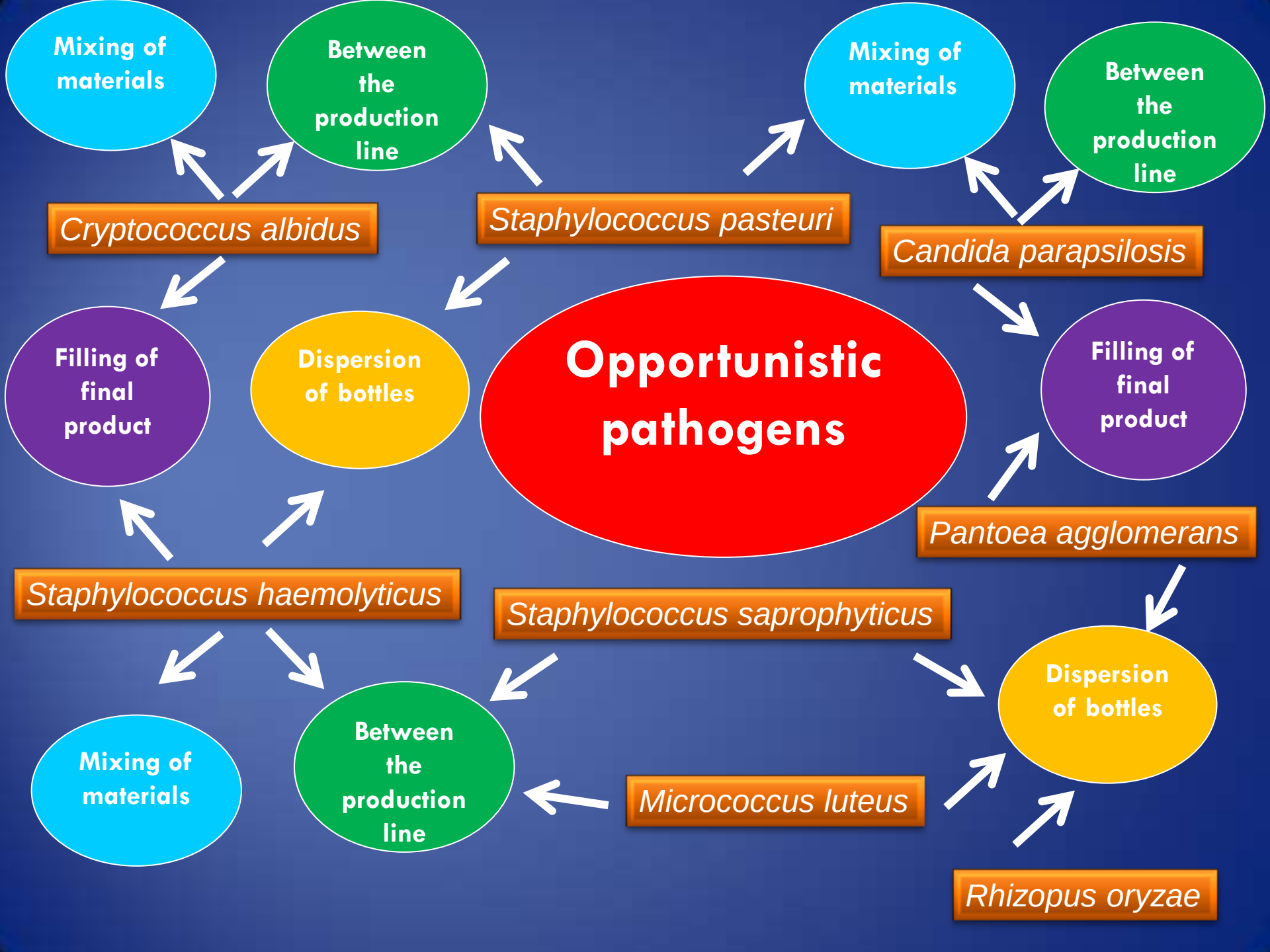


Dispersion of bottles



Filling of final product




Opportunistic pathogens
Cryptococcus albidus
Mixing of materials
Between the production line
Filling of final product
Dispersion of bottles
Staphylococcus pasteuri
Candida parapsilosis
Mixing of materials
Between the production line
Filling of final product
Pantoea agglomerans
Staphylococcus haemolyticus
Mixing of materials
Between the production line
Staphylococcus saprophyticus
Micrococcus luteus
Dispersion of bottles
Rhizopus oryzae

CONCLUSION

- 15 Different yeast species, 6 different mould species and 63 different bacteria species were identified
- There is a need for control of bioaerosols
- IDEAL – to collect all viable microorganisms
- Culture independent method

FUTURE RESEARCH

- Compare MALDI-TOF against 16S rRNA gene sequencing

- Culture independent analysis

THANK YOU


...WHY CAN'T IT EVER BE BRUSSELS SPROUTS?!
HEALTH
PISTACHIO WARNING
RED MEAT WARNING
PEANUT