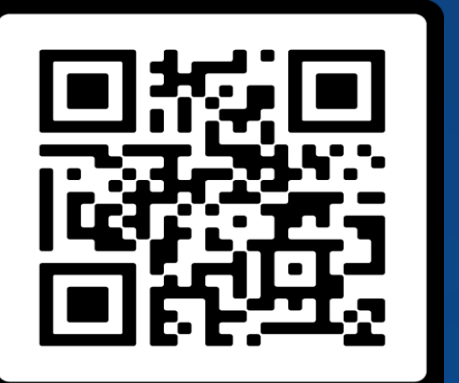




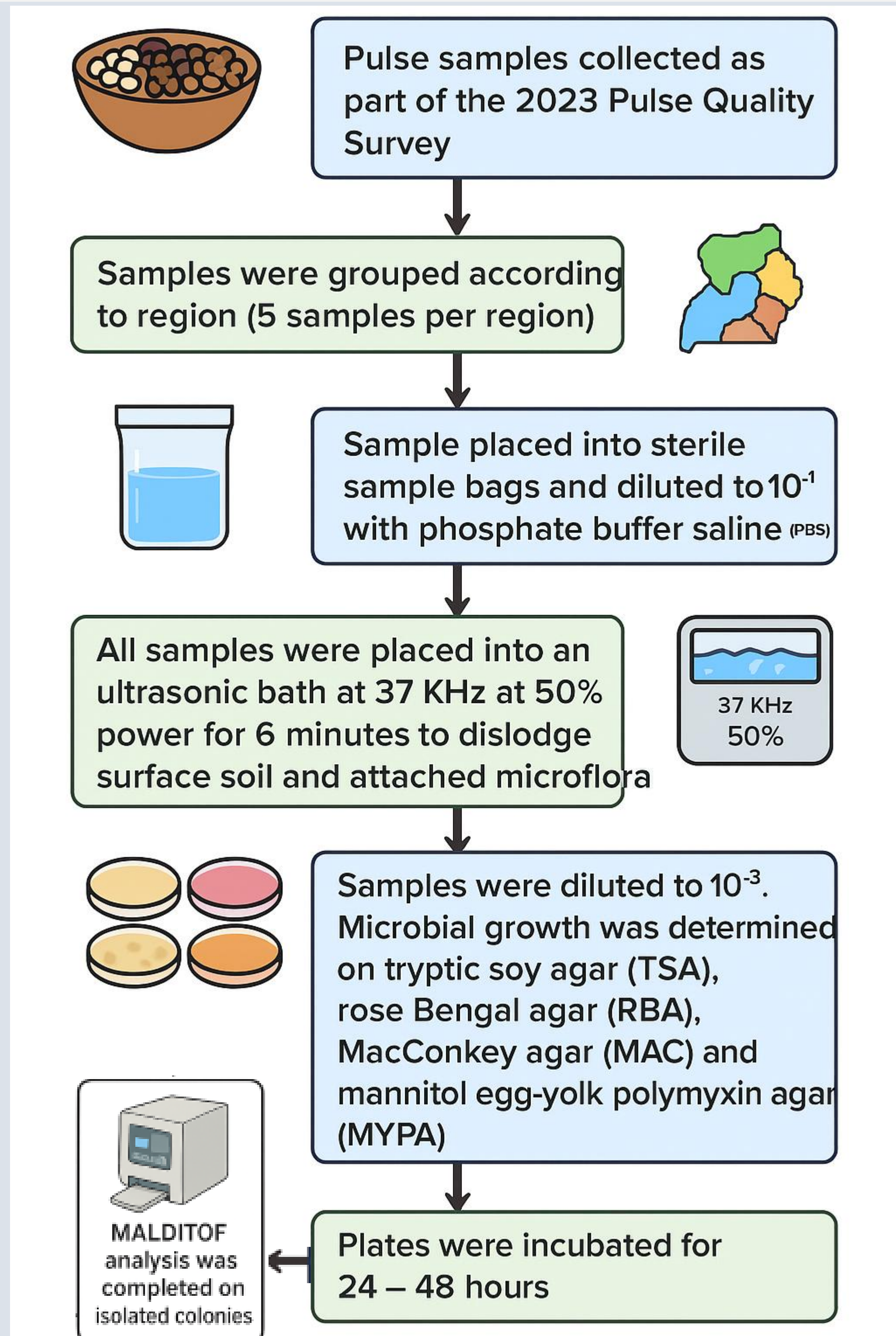
Justification

- Many microorganisms (MO) exist naturally or as possible contaminations near pulse farms.
- Limited information is available about the MO prevalent on pulse crops (chickpea, pea, lentil).
- This study was undertaken to characterize the MO present on chickpea, pea, and lentils.

Objectives

- To complete a microbial analysis of pulses from the Palouse and Northern Plains regions of the United States.
- Use matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry to characterize individually isolated microbial colonies.

METHODS



- One-Way ANOVA Analysis was performed with Prism software on individual region samples.
- Two-way ANOVA Analysis was performed to test the variable influence of pulse type (fixed effect) and geographical region (random effect) on total microbial growth using Rstudio.

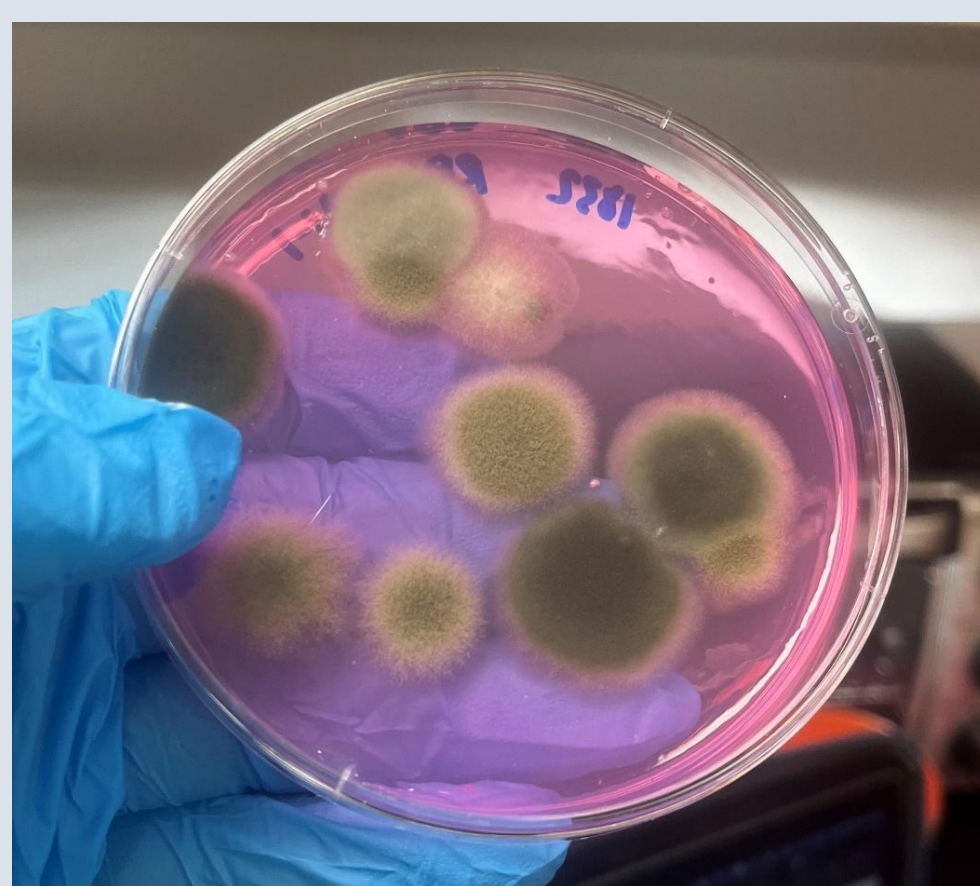
Results

Table1: Comparison of the Different Pulses in a Two-Way ANOVA Analysis (Region Growth x Pulse Type)

Microbial Indicator	Chickpea vs. Pea	Chickpea vs. Lentil	Pea vs. Lentil
Total Count	P=0.546	P=0.040*	P=0.006*
Yeast and Molds	P=0.777	P=0.897	P=0.509
Coliforms	P=0.174	P=0.505	P=0.02*
<i>Bacillus spp.</i>	P=0.344	P=0.726	P=0.117

*Indicates significant difference between pulses at p≤0.05.

Figure 1: Examples of microorganism growth in Pulses.



RESULTS (cont.)

Table 2: Average Microbial Population of Different Microbiome Types.

	Chickpea	Pea	Lentil
Microbial Indicator	Mean Log CFU/g ± Standard Deviation		
Total Count	2.61 ± 0.58	2.21 ± 0.51	3.14 ± 1.17
Yeast and Molds	1.04 ± 0.44*	0.86 ± 0.64*	1.32 ± .99
Coliforms	1.92 ± 0.67*	1.55 ± 0.80	2.55 ± 1.18
<i>Bacillus spp.</i>	1.69 ± 0.68	1.53 ± 0.59	2.04 ± 1.00

* Indicates significant difference between the five regions within the specified pulse.

Non-*Bacillus spp.* Microbial Isolates (Chickpea, Pea, Lentil)

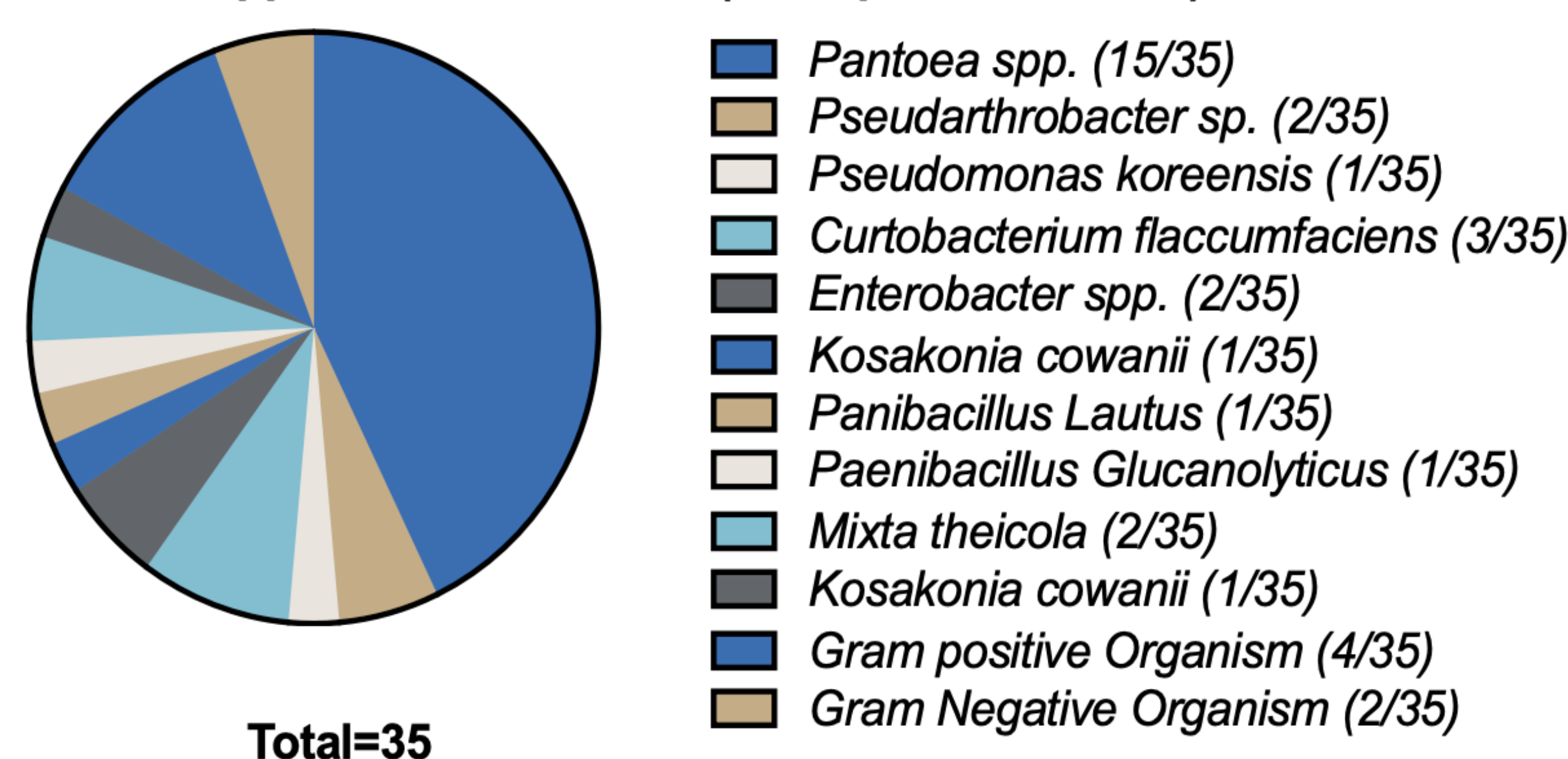


Figure 4: Yeast and Mold spp. in Pulse Samples.

Total *Bacillus spp.* Microbiome (Chickpea, Pea, Lentil)

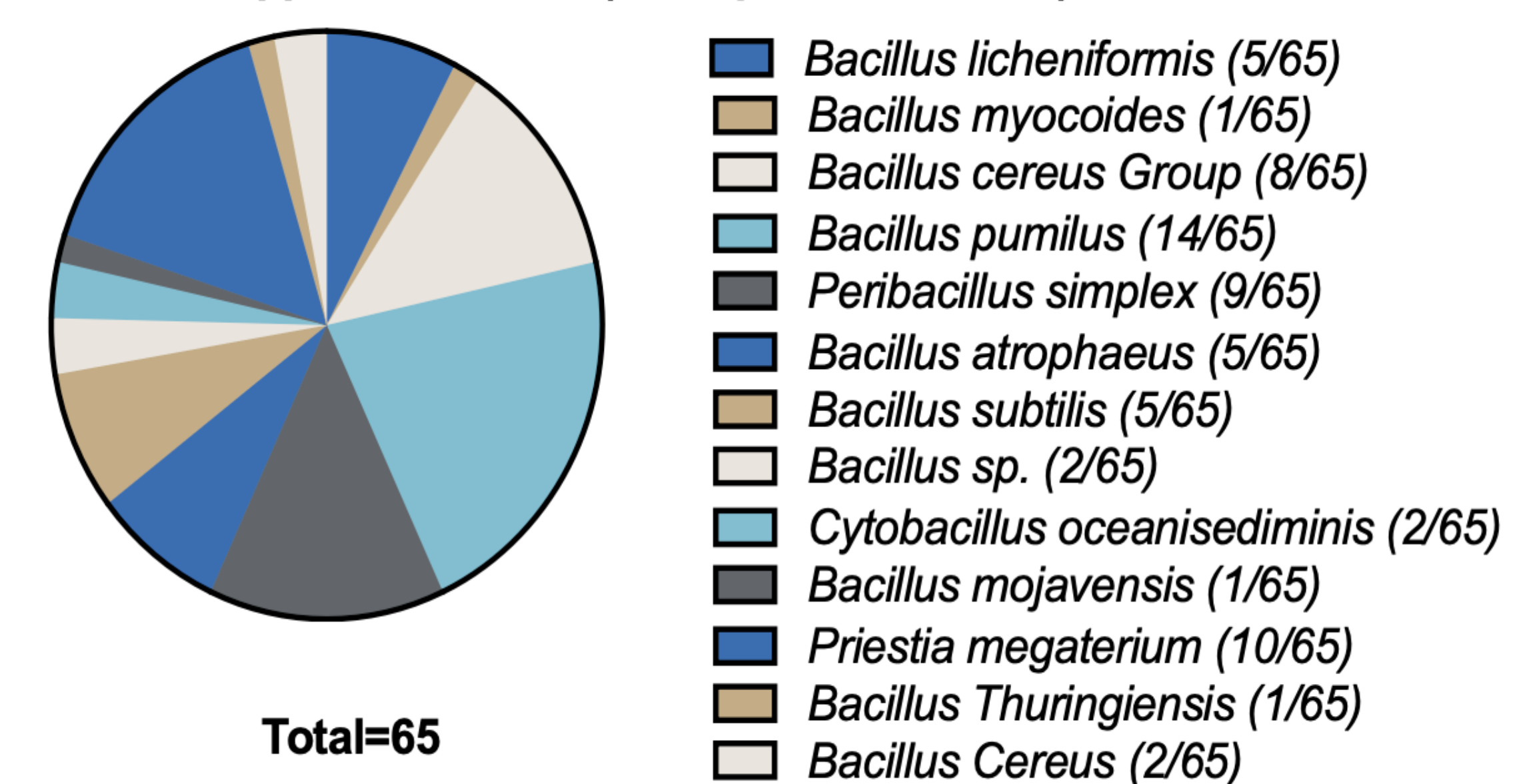


Figure 2: Total *Bacillus spp.* Isolated from Pulse Samples.

Yeast and Mold spp. (Chickpea, Pea, Lentil)

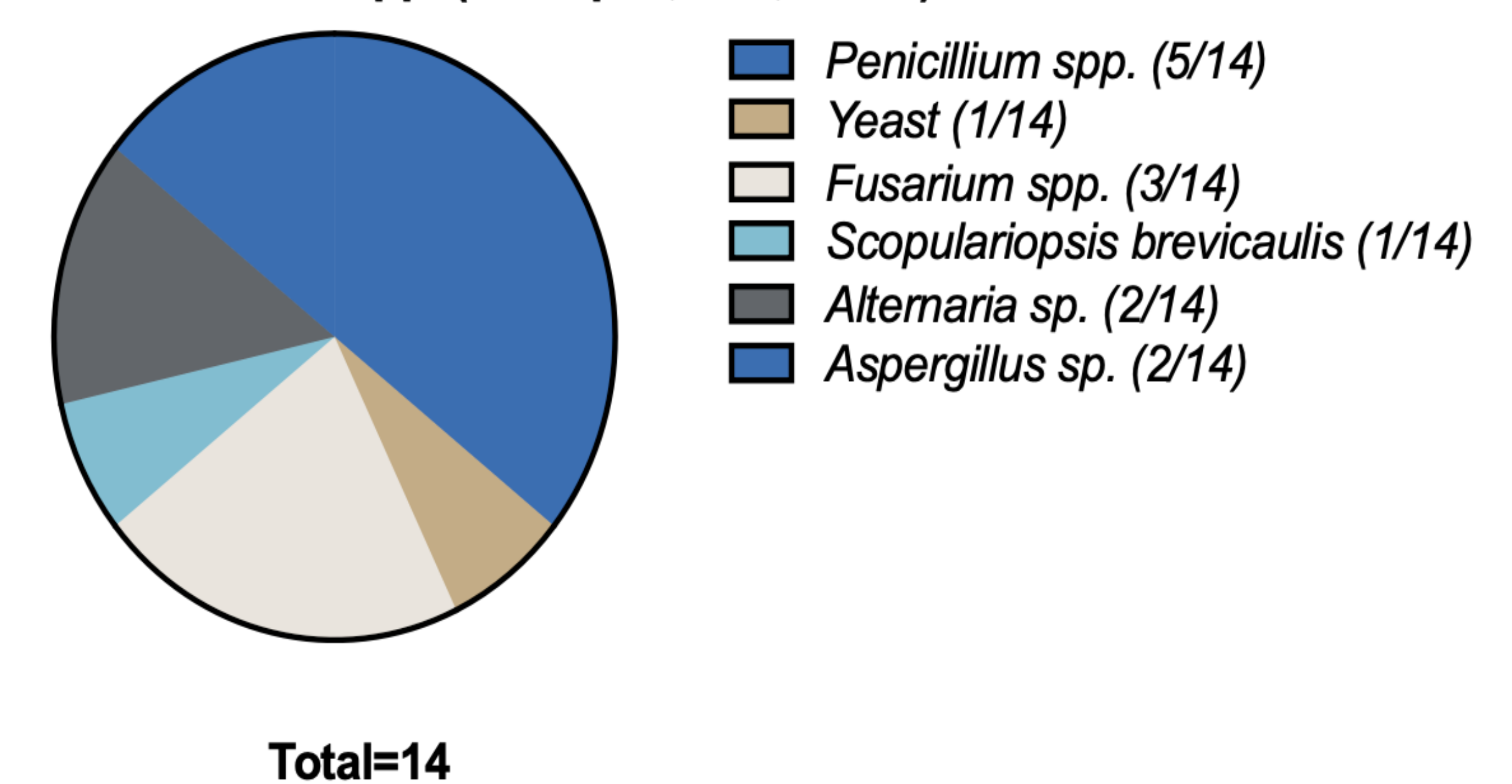


Figure 3: Total Non-*Bacillus spp.* in Pulse Samples.

IMPLICATIONS

- 29 total microbial species isolated
- Spoilage microorganism: *Alternaria spp.*, *Mucor circinelloides*, and *Penicillium spp.*
- Pathogenic organisms: *Fusarium spp.*, *B. cereus*.
- *Bacillus spp.* were characterized in 73%, 77.5%, and 38% of microbial isolates in chickpea, pea, and lentil, respectively.
- Lentil had statistically (Table 2) higher microbial population than chickpea and pea.
- *B. pumilus* (15/114) and *P. agglomerans* (14/114) were the most common microorganisms among samples.
- Geographical region and pulse type influence microbiome and microbial population

Conclusion

- Systematic analysis of chickpea, pea, and lentil samples provided evidence of geographical region and pulse type impacting microbial population.
- MALDI-TOF samples confirm presence of spoilage and pathogenic organisms in pulses. Analysis provides insight for microorganism to consider for future safety protocols.

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