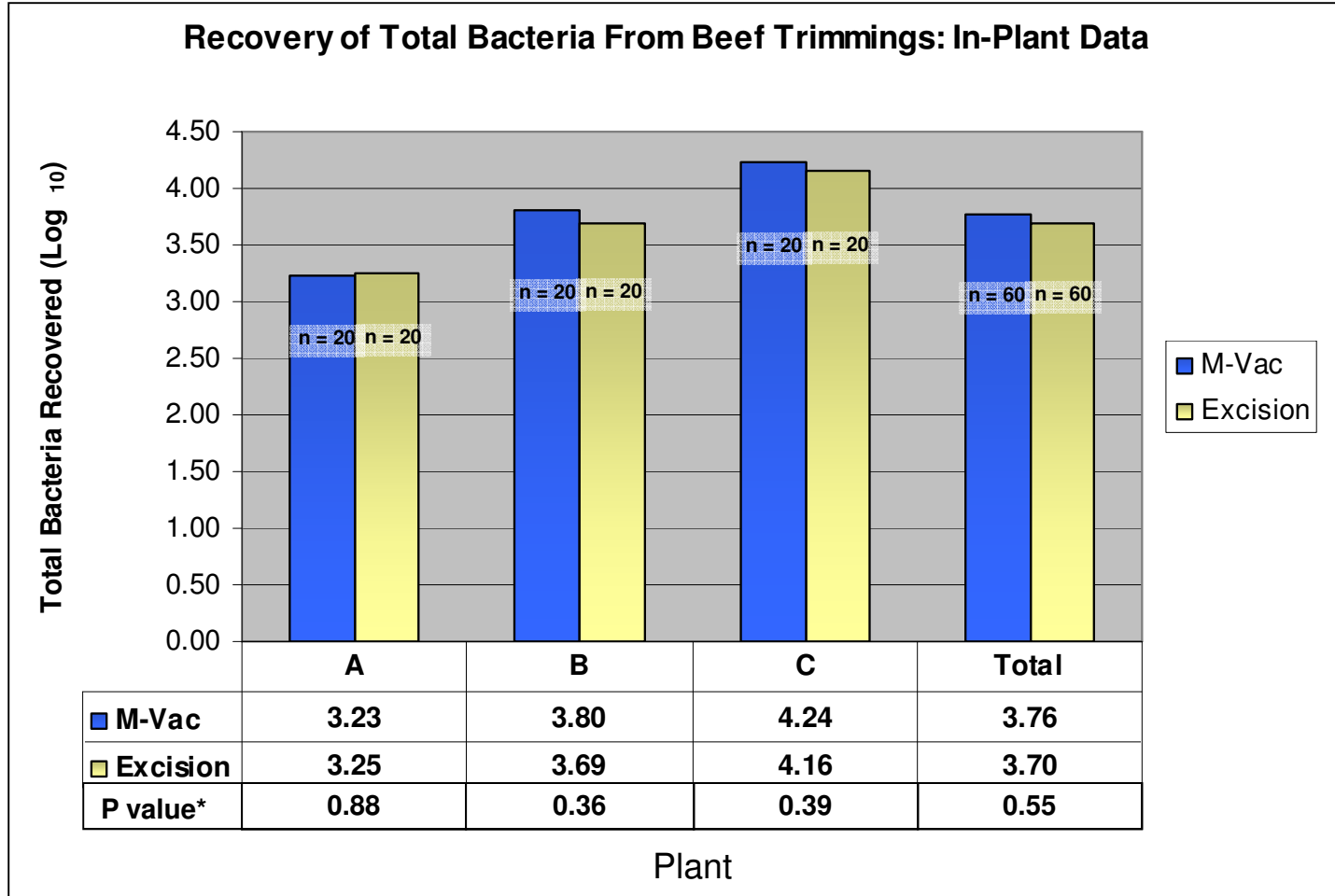


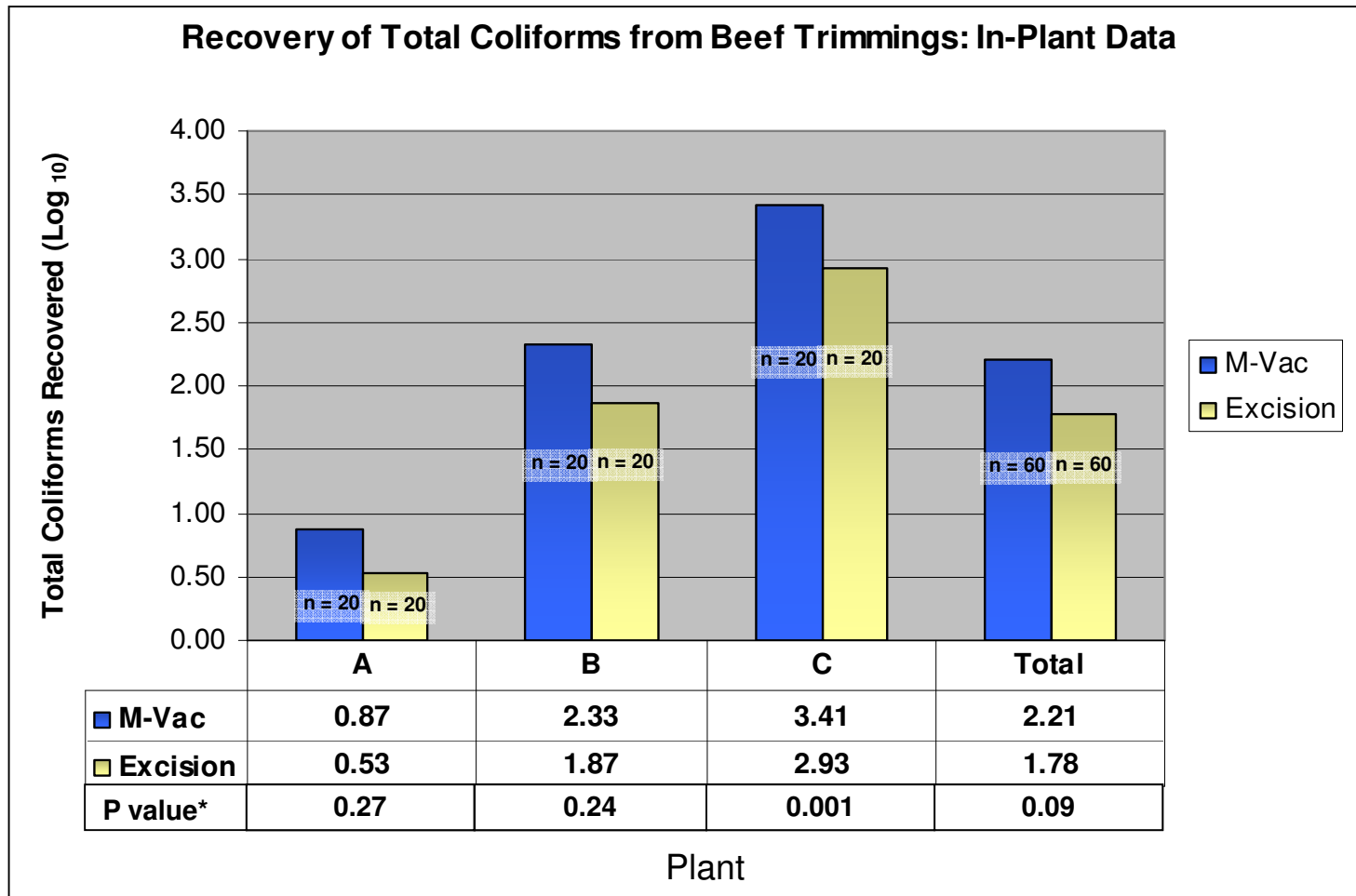
Combined In-Plant Validation Total Bacteria Count



*P values were calculated using an un-paired t-test. No significant differences were observed between the two sampling techniques in any plant or in the combined data ($P < 0.05$).

*Each individual sample consisted of 12 sites (i.e. $n = 20 \times 12$)

Combined In-Plant Validation Total Coliforms



*P values were calculated using an un-paired t-test. Significant differences were observed between the two sampling techniques in plant C (P<0.05).

*Each individual sample consisted of 12 sites (i.e. n=20*12)

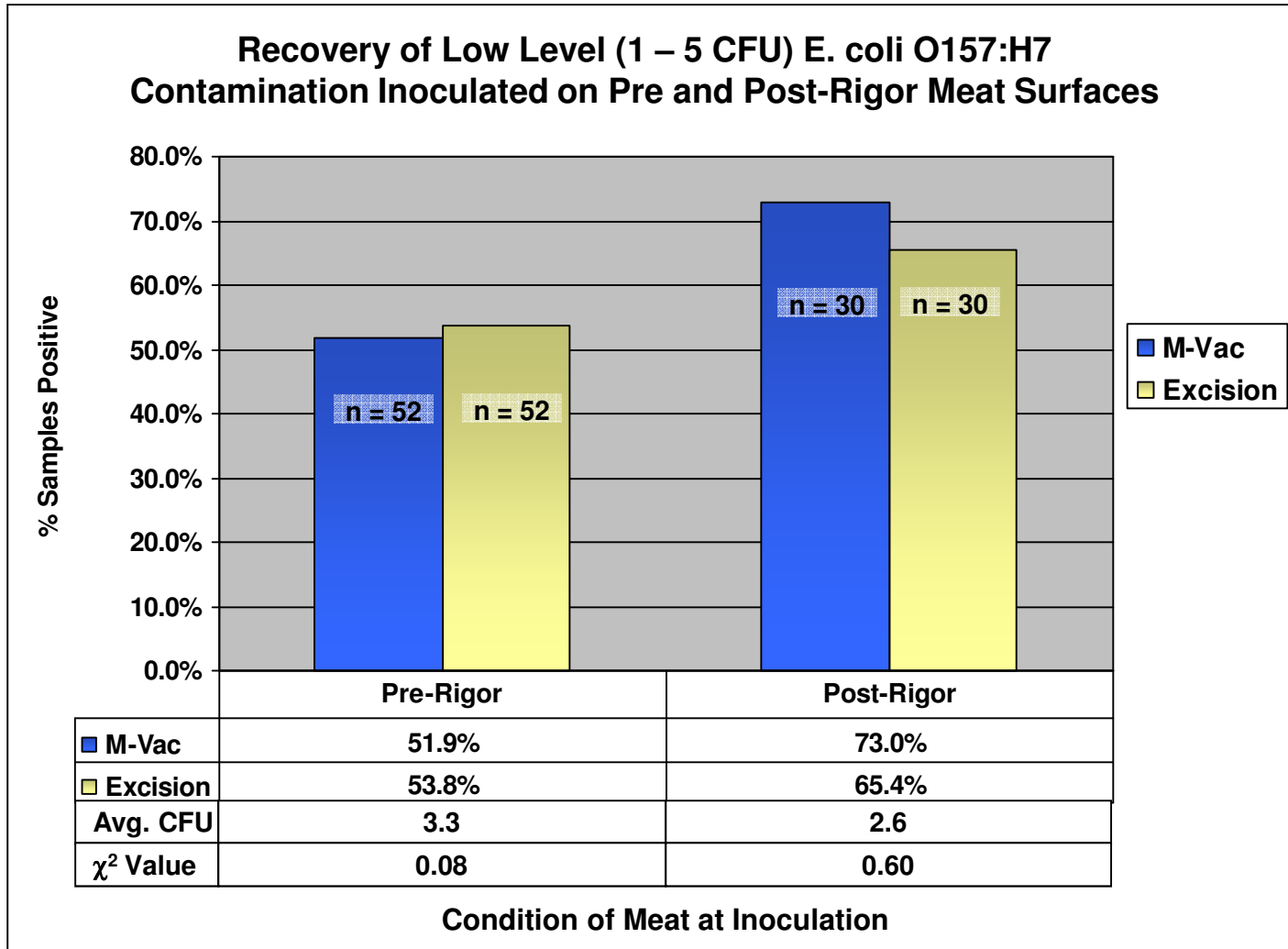
Combined In-Plant Validation Generic *E. coli*

Plant	Method	% of Samples <i>E. coli</i> +
Plant A n=20	M-Vac	0.0% (0/20)
	Excision	0.0% (0/20)
Plant B n=20	M-Vac	35.0% (7/20)
	Excision	35.0% (7/20)
Plant C n=20	M-Vac	25.0% 5/20
	Excision	0.0% (0/20)
Total n=60	M-Vac	20.0% (12/60)
	Excision	11.7% (7/60)

No significant differences were observed within each plant at the 5% probability level. Given the variability between plants, doing statistics on the pooled data, which would suggest a significant difference exists, would be an unfair test.

*Each individual sample consisted of 12 sites (i.e. n=20*12)

Low Level Contamination Data



No significant differences were observed in either treatment at the 5% probability level. A χ^2 value > 3.84 would have suggested a significant difference at the 5% probability level.

*Each individual sample consisted of 12 sites (i.e. n=52*12)