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Evolution of the nasopharyngeal bacterial microbiota of beef calves from spring processing to 40 days  
after feedlot arrival

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### Highlights

- Three groups of beef steer calves (n = 120) were sampled at three time points
- The bacterial microbiota of the nasopharynx was characterized (16S rRNA)
- Nasopharyngeal bacterial microbiota evolved over time in all calf groups
- Patterns of microbiota evolution differed across all time points and calf groups
- *Mycoplasma* was the most abundant genus and *M. dispar* was the most abundant species

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