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Authors: Marshall, M. M., Songer, J. Glenn, Chilelli, C. J., and deVos, James C.

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ISOLATIONS OF AEROBIC BACTERIA FROM WILD DESERT BIGHORN SHEEP (*OVIS CANADENSIS NELSONI* AND *O. C. MEXICANA*) IN ARIZONA

M. M. Marshall,[1] J. Glenn Songer,[1] C. J. Chilelli,[1] and James C. deVos[2]

ABSTRACT: Nasal, pharyngeal, cervical and vaginal swab specimens were obtained from 74 desert bighorn sheep for the purpose of investigating the normal aerobic bacterial flora of wild sheep. A total of 281 isolates was obtained and identified by standard microbiologic tests. One hundred seven of these isolates were gram positive and included *Bacillus* sp. (36%), *Staphylococcus epidermidis* (8%), *S. aureus* (4%), *Corynebacterium* sp. (diphtheroids, 4%), and *Streptococcus* sp. (48%). Gram negative isolates totaled 174 and included *Neisseria* sp. (18%), *Citrobacter* sp. (3%), *Enterobacter* sp. (2%), *Escherichia coli* (2%), *Proteus* sp. (2%) and nonfermentative bacilli (NFB) (73%). Of the NFB isolates, *Pseudomonas* sp. (25%), *Acinetobacter* sp. (18%), *Moraxella* sp. (15%) were identified.

INTRODUCTION

The study of the bacterial flora of most wild ruminants has received little attention in the published literature, although the flora of domestic animals has been studied in depth (Carter, 1973). No work has apparently been done on the bacteria of desert bighorn sheep; the related Rocky Mountain bighorn sheep (*O. c. canadensis*) has been studied to a limited extent (Post, 1962; Woolf and Kradel, 1973; Spraker, 1977). Most data relate to diseased rather than normal animals and to captive rather than wild animals (Marsh, 1938; Rosen, 1970; Rosner, 1971; Taylor, 1976; Spraker, 1977; Spraker and Hibler, 1977; Foreyt and Jessup, 1982). The purpose of this report is to present data on the aerobic bacterial flora of wild desert bighorn sheep.

MATERIALS AND METHODS

Seventy-four bighorn sheep were captured by personnel of the Arizona Game and Fish Department for the purpose of transplant from six geographic locations in Arizona (Fig. 1). Calcium alginate swabs (Calgiswab Type III, Inolex, Glenwood, Illinois 60425, USA) were used for collection of nasal and pharyngeal specimens and Teigland swabs (Haver-Lockhard Lab., Shawnee, Kansas 66203, USA) were used for collection of cervical and vaginal specimens. Inoculated swabs were placed immediately into Stuart's Transport Medium (Difco, Detroit, Michigan 48232, USA) and held at 4 C; all were processed within 48 hr. The swabs were streaked on Tryptose-agar (Difco, Detroit, Michigan 48232, USA) containing 5% sheep blood and on MacConkey agar (Difco, Detroit, Michigan 48232, USA); plates were then incubated aerobically at 37 C for 24–48 hr. Identification of isolates was by standard microbiologic tests (Carter, 1973; Harris and Oetjen, 1973; Rubin et al., 1980) and included use of the API-20E Profile Recognition System (Analytap Products, Plainview, New York 11803, USA).

RESULTS

A total of 281 isolates (Table 1) was obtained from 49 nasal, 48 pharyngeal, 33 cervical, and 30 vaginal swab-specimens secured from trapped bighorn sheep. Of these isolates, 107 were gram positive and 174 were gram negative. The *Staphylococcus aureus* isolates were hemolytic and one isolate of *E. coli* isolated from a cervical swab was also hemolytic.

The NFB isolates included 25% *Pseudomonas* sp. of which 10% were *P. aeruginosa* obtained only from pharyngeal swabs. Eighteen percent were *Acinetobacter* sp. Fifteen percent were *Moraxella* sp. of which 22% were *M. urethalis* obtained from cervical and vaginal swabs and 11% *M.* group M6 obtained from pharyngeal swabs. The remaining NFB were either unidentifiable by presently available techniques (30%) or could not be maintained in vitro (12%).

There were no apparent differences in the bacterial flora in sheep from different locations (Fig. 1).

DISCUSSION

In the absence of other published data, it is difficult to determine the significance of our

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[1] Department of Veterinary Science, University of Arizona, Tucson, Arizona 85721, USA.
[2] Arizona Game and Fish Department, 2222 W. Greenway Road, Phoenix, Arizona 85723, USA.

FIGURE 1. Sites at which desert bighorn sheep were captured in Arizona. 1, Lake Mead Area; 2, Black Canyon Area; 3, Kofa Mts.; 4, Trigo Mts.; 5, Castle Dome Mts.; 6, Plomosa Mts.

findings. Several points of interest are, however, worth noting.

The lack of isolates of *Pasteurella* sp. from nasal and pharyngeal specimens is of interest. This organism has been cited as one which is commonly found in the lungs of diseased bighorn sheep (Marsh, 1938; Post, 1962; Rosen, 1970; Woolf and Kradel, 1973; Taylor, 1976; Spraker, 1977; Spraker and Hibler, 1977; Foreyt and Jessup, 1982), and it has been suggested that organisms of this genus may be part of the normal bacterial flora of the upper respiratory tract of animals (Post, 1962; Rosen, 1970; Rosner, 1971; Spraker, 1977). However, one study (Post, 1962) reported 7% recovery of *Pasteurella* sp. from normal nasal swabs, and 12% recovery from hunter-killed lung specimens but did not report other bacterial flora present, and in another study (Woolf and Kradel, 1973), nasal cultures were negative for *Pasteurella* sp. while lung specimens were positive. Lungs were not examined in this study. *Pasteurella hemolytica* has been isolated from a pneumonic lung of a desert bighorn sheep in Arizona (Bicknell, pers. comm.). Hence, although the organism is apparently not common in desert bighorn sheep (Table 1) it does occur and produces disease. Whether *Pasteurella* is part of the normal flora and an opportunistic pathogen or is indeed, a primary pathogen, deserves further study, since the occurrence of disease produced by *Pasteurella* sp. could present serious management problems (Taylor, 1976; Foreyt and Jessup, 1982).

The presence of β-hemolytic streptococci is also interesting. Similar findings from nasal swabs have been reported (Woolf and Kradel, 1973) and the presence of these organisms in cervical cultures (60%) should be noted, since certain members of this genus have been shown to be associated with disease in Arizona wildlife; Songer (unpubl. data) isolated *S. zooepi-*

TABLE 1. Aerobic bacteria isolated from desert bighorn sheep in Arizona.

Isolate	Percentage of total gram positive or gram negative organisms isolated from specimen swabs				
	Nasal Swab	Pharyngeal Swab	Vaginal Swab	Cervical Swab	Totals
Gram positive organisms					
Bacillus sp.	22.4	7.4	2.8	0.9	33.5
Staphylococcus epidermidis	5.6	2.8	0	0	8.4
Staphylococcus aureus	3.7	0	0	0	3.7
Corynebacterium sp.	3.7	0	0	0	3.7
Alpha-hemolytic *Streptococcus*	14.9	21.4	4.6	1.8	42.7
Beta-hemolytic *Streptococcus*	0	1.8	0	2.8	4.6
Non-hemolytic *Streptococcus*	0	0.9	0	0	0.9
Gram negative organisms					
Neisseria sp.	5.7	12.6	0	0	18.3
Citrobacter sp.	0.5	0.5	1.1	1.1	3.2
Enterobacter sp.	1.1	0.5	0	0	1.7
Escherichia coli	0	0	1.7	0.5	2.2
Proteus sp.	1.7	0	0	0	1.7
Non-fermentative bacilli (NFB)	22.4	28.7	9.7	11.4	72.4

demicus from tissues, primarily lung, of feral burros following a disease outbreak in which several animals died.

The significance of the NFB is uncertain. Knowledge of this entire group is expanding and their overall importance in animal disease needs further study.

Other potentially pathogenic bacteria were isolated. These included *S. aureus* and hemolytic *E. coli*; Songer (unpubl. data) isolated hemolytic *E. coli* from a feral burro with purulent vaginitis. Both *S. aureus* and hemolytic *E. coli* have been reported as causes of disease in domestic lambs (Carter, 1970). Continued monitoring of normal as well as diseased animals should eventually reveal the significance of these organisms to the health of desert bighorn sheep.

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