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BACTERIA RESIDENT IN BOVINE UTERUS WITH SPECIAL REFERENCE TO REPEAT BREEDER COW IN THE SUDAN

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INTRODUCTION

Repeat breeding is an important problem that has a direct effect on the economy of dairy and beef industry. It results in great economical loss in terms of calf and milk production. In the tropics great loss should be anticepated due to poor management, nutrition and environmental stress factors (Boyd and Reed, 1961; Brett, 1979).

The aeteological factors of repeat breeding condition are multiple and complex, amongst which is the bacterial infections. Certain specific infections such as Brucellosis, Vibiosis and Trichomonosis have been found to induce patholotical changes that transfer a good breeding animal into an infertile one (Stableforth et al, 1937; Plastridge et al, 1947 Sojellema, 1949). There is also a broad category of non-specific bacterial infections, the role of which is still controversial. They have no predelection for the genital tract but still they have been as one of the causes of infertility (Gunter et al, 1955; Elliot et al, 1968; Hartigan et al, 1972; Sharma et al, 1978; Mohanty et al, 1980).

The present study was conducted to survey the bacterial flora resident in the bovine uterus with special reference to repeat breeders.

MATERIAL AND METHODS

This investigation was carried out on three dairy farms in Khartoum North during the period August, 1981-1983. A total of 113 cows were used in this study; they were divided into three groups. Group one: Repeat breeders composed of 26 animals.

Collection of Uterine Wash: Animals were anaethestised epidurally with 2% xylocaine solution. The perineal region was thoroughly cleaned with soap and water. The vulva and vagina were examined with speculum for any evidence of disease or abnormality. The external

os of the cervix was gently exposed using Richter tumour forceps. A sterile uterine catheter was introduced into the uterus for about ten/cms. ten cms. Hundred to 160 ml of sterile normal saline were injected into the uterus. Using another empty syringe 3-5 ml of saline were aspirated, transfered to a sterile universal bottle and stoppered pending laboratory examinations.

Media used: These included nutrient broth and agar, blood agar, brain heart infusion, T. C. B. S. , Vibrio media, Brucella agar medium and Mycoplasma broth.

Isolation and Identification of Bacteria; All uterine washes were cultured aerobically at 37C for 24 hours on all abovementioned media. Cultures in fluid media were checked for growth by turbidity, meat digestion or other alterations, then subcultured on solid media and incubated aerobically and anaerobically at 37C for 24 hours. Plates showing no growth after 24 hours incubation were reincubated for another 24 hours. Cultures on Brucella and Vibrio media were left for four to five days and then discarded as negatives, if not showing any growth. Different colonies obtained were studied and identified according to Cowan and Steel (1974). The results were analysed statistically.

RESULTS AND DISCUSSION

The incidence of positive cultures in group one, two and three were 79%, 84% respectively. Most specimens contained one, two or three organisms. Different types of organisms were isolated. These were summarised in table 1.

In group one (repeat breeders), the most frequent organisms isolated were Micrococcus spp. 35.5%). Staphlococcus (4%). Listeria spp. were the least in this group (4.8%).

In group two (normal breeders), Listeria spp. (36%) and Micrococcus spp. (28%) were the most frepuent organisms isolated from this group. The least frequent organisms isolated from this group. The least frequent organism isolated from this group was Streptococcus faecalis (4%).

In group three (virgin heifers), the predominent organisms isolated were Listeria spp. (38.4%), Baccillus spp. (34.5%), Micrococcus spp. (26.9%). The Streptococcus faecalis and Corynebacterium pyogenes were not isloated from this group.

The Aerococcus viridans, Bacclus firms, B. polymxa, Klebsiella ozaenae, Listeria monocytogenes, L. grai were found to be of significance.

Aeroviridans was isolated from the three groups of animals. It was significantly predominent in the uterus of haifers and has been isolated four times in the repeat breeders group.

Three species of the genus Bacillus were isolated; these were B. coagulans, B. firmus, and B. polymxa. According to Hartigan et al (1972) and Hartigan (1978) this organism is a common uterine flora.

Corynebacterium pyongenes was isolated from eight repeat breeders and two normal cows. It was absent in the heifers group. This organism is known to be pathogenic and cause edometritis (Dawson, 1960; Griffin et al, 1974). It was isolated from repeat breeder cows and baffaloes by Awad and Alhariri (1980). Nevertheless, Hartigan et al (1972) were unable to recover C. pyogenes from any of the 80 clinically normal repeat breeders examined. However, the same investigators (1974) succeeded to isolate this organism in 22.3% out of 763 samples from 93 cows.

E. coli was found in all groups of animals in more or less similar proportions; so it may not be of significance in bovine infertility although Dawson (1960). suggested that it may be pathogenic.

Klebsiella ozaenae was not isolated from the repeat breeders group. However, this finding is in contrast with the results of Awad and Alhariri (1980).

Micrococcus viridans was isolated from only two repeat breeders. This is in agreement with the results of Lindley and Hatifield (1952), Ayalon (1969) and Panangala et al (1978).

Three spp. of the genus Proteus were isolated; these were P. mirabilis, P. morganii and P. vulgaris. The first spp. was recovered in repeat breeders and heifers, the second was absent in the repeat breeders group and the third spp. was isolated from two heifers and two normal breeders. Members of this genus were cnosidered as commensals of the uterus (Lindley and Hatifield, 1952). However, Awad and Alhariri (1980) were able to isolate Proteus spp. from repeat breeders only. Our findings could not septtle this dispute, since it was isolated from the three groups invstigated.

Two spp. of the genus Staphlococcus were isolated; these were S. aureus and S. epidermidis. Both were recovered from all animal groups. This is in agreement with the finding of Kiesel and Dacrees (1959); Bora et al (1978).

One spp. of the genus Streptococcus was isolated form repeat breeders and normal cows groups. Although this organism was considered as saprophyte (Panangala et al, 1978), yet it could be pathogenic if the animal resistance was lowered (Gunter et al, 1955; Kiesel and Dacrees, 1959).

In this study, two isolates of Mycoplasma were recovered in the repeat breeders group. Although the isolation of Mycoplasma from the geintal tract of cattle has been reported by many workers (Edward et al, 1947; Afshar, 1966; Langford, 1975), its recovery from repeat breeders raise the question of its significance in bovine infertility. According to Erno (1974), Mycoplasma in general seems to behave as commensals in the bovine genital tract and only infrequently it may cause disease in those organs.

SUMMARY

Uterine washes of repeat breeders, multiparous normal breeders and heifers were examined for bacterial flora. The predominant

organisms isolated from the uterus of repeat breeders were Micrococcus luteus, Staphylococcus aereus and Escherichia coli.

The bacteria isolated from the uterus of normal breeders were Listeria monocytogenes, Micrococcus luteus and Klebsiella ozaenae.

The organisms isolated fequently from heifers were Listeria grai, Micrococcus luteus and Bacillus polymxa. Two mycoplasma isolates were recovered from the uterus of repeat breeders. The results were discussed with special reference to possible role of non-specific bacteria in bovine infertility.

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Table 1

Frequency and percentage of organisms isolated from the uterine washes of the three animal groups

Organisms	Group 1		Group 2		Group 3	
	F	%	F	%	F	%
Aerococcus viridans *	4	6.5	3	12	4	15.4
Alcaligenes faecalis	0	0	0	0	1	3.8
Bacillus coagulans	6	9.7	0	0	2	7.7
Bacillus firmus *	0	0	4	16	1	3.8
Bacillus polymxa *	1	1.6	0	0	6	23.0
Chromobacter violacum	0	0	0	0	1	3.8
Citrobacter spp. *	0	0	0	0	2	7.7
Cornebact. pyogenes	8	12.8	2	8	0	0
E. coli	11	17.7	4	16	3	11.5
Klebsiella ozaenee *	0	0	6	24	4	15.4
Klebsiella spp. *	6	9.7	0	0	3	11.5
Listeria grai	0	0	0	0	7	26.9
List. monocytogenes *	3	4.8	9	36	3	11.5
Micrococcus luteus	20	32.5	7	28	7	26.9
Micrococcus viridans	2	3.2	0	0	0	0
Mycoplasma spp.	2	3.2	0	0	0	0
Proteus mirabilis	2	3.2	0	0	1	3.8
Proteus morganii	0	0	1	4	1	3.8
Proteus vulgaris	6	9.7	2	8	2	7.7
Staphlococcus aureus	13	21.0	3	12	3	11.5
Staph. epiermidis	8	12.8	2	8	3	11.5
Streptococcus faecalis	6	9.9	1	4	0	0
Sterile specimens	13	21.0	4	16	4	15.4

F = frequency

* = significant result ($P < 0.05$)