WORLD VIEW

Distribution and shifting trends of bacterial keratitis in north China (1989–98)

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Aims: To study the distribution and shifting trends of bacterial keratitis.
Methods: The data of 2220 corneal isolates from 1 January 1989 to 31 December 1998 were reviewed retrospectively.
Results: Positive culture was recovered in 490 isolates. Gram positive cocci and Gram negative bacilli represented 51% and 39.4%, respectively. *Pseudomonas aeruginosa* was the most common pathogen (32.2%). A gradual increase in the percentage of Gram positive cocci coupled with a decrease of Gram negative bacilli.
Conclusion: *Pseudomonas aeruginosa* and coaculase negative *Staphylococcus* were the most common pathogens in bacterial keratitis in north China.

Keratitis caused by bacteria usually results in various corneal lesions, and even severe visual loss. In developing countries, bacterial keratitis has become the most common cause of corneal blindness.[1] Based on data over 10 years (1989–1998), we carried out a detailed aetiologic analysis.

MATERIAL AND METHODS

From 1 January 1989 to 31 December 1998, bacterial cultures were carried out on 2220 cases. Culture media: blood agar plate, routine culture media, and identified culture media. Specimens were inoculated on culture media in 35℃ for 24–48 hours.

RESULTS

Of the 2220 corneal isolates, mono-bacterial positive culture was recovered in 490 isolates (table 1). Gram positive cocci were found in 250 isolates (51.0%); most of these were coagulase negative *Staphylococcus*. Gram positive bacilli isolates accounted for 45 (9.2%). Gram negative bacilli isolates were found in 193 (39.4%), mainly *Pseudomonas* spp (see table 2).

The gradual increase in the percentage of Gram positive cocci (25% in 1991 *v* 70.8% in 1997, $p<0.01$), and decreasing trend in Gram negative bacilli (69% in 1990 *v* 23.4% in 1997, $p<0.01$), are shown in figure 1.

The percentage of *Pseudomonas* spp followed a trend of decrease (58.6% in 1990 *v* 24% in 1998, $p<0.01$), as shown in figure 2.

Table 2 Distribution of organisms in positive bacterial cultures (1989–98)

	No of bacterial isolates	% of total bacterial isolates
Gram positive cocci	250	51%
Staphylococcus epidermidis	91	18.6%
Micrococcus spp	54	11%
Staphylococcus aureus	27	5.5%
Streptococcus pneumococcus	59	12%
Streptococcus viridans	17	3.5%
Others*	2	0.4%
Gram positive bacilli	45	9.2%
Corynebacterium commune	36	7.4%
Bacillus spp	1	0.2%
Nocardia actinomycete	1	0.2%
Others*	7	1.4%
Gram negative cocci	2	0.4%
Branhamella catarrhalis	2	0.4%
Gram negative bacilli	193	39.4%
Pseudomonas spp	158	32.2%
Acinetobacter spp	7	1.4%
Moraxella spp	1	0.2%
Enterobacteriaceae	21	4.3%
Flavobacterium spp	2	0.4%
Others*	4	0.8%
Total bacterial isolates	490	

*Bacteria specimens not identified under the conditions of our laboratory.

DISCUSSION

According to our study, Gram positive cocci is still the leading causative organism of bacteria keratitis, and the percentage of Gram positive cocci showed an increased trend. *Pseudomonas* spp accounted for 32.2% of the total corneal positive cultures, but it decreased year by year. The data from

Table 1 Number and ratio of bacterial cultures by year

	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	Total
Corneal cultures	119	156	210	250	246	249	214	231	277	268	2220
Positive cultures	27	29	36	73	41	57	41	42	64	80	490
(% of corneal cultures)	22.7	18.6	17.1	29.2	16.7	22.9	19.2	18.2	23.1	29.9	22.1

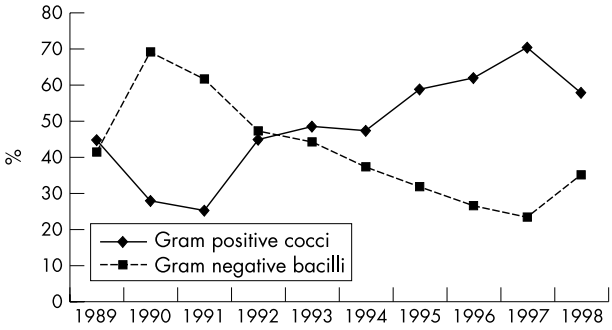

Figure 1 Shifting trends of different organisms by year.

America showed that *P aeruginosa* accounted for 25.7% of total positive bacterial isolates.[2]

A study in India showed that Gram positive organisms accounted for 82.4%, while Gram negative organisms 16.1%[3]. Compared with that study, our data from north China have shown a lower percentage of Gram positive bacteria and a relatively higher percentage of Gram negative for ketatitis.

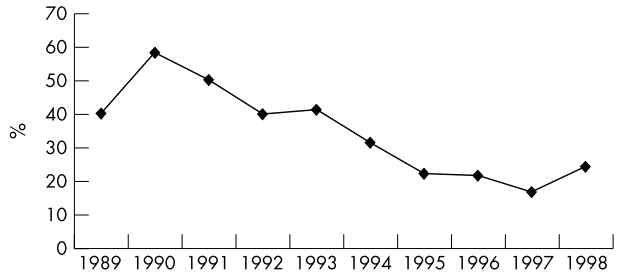

Figure 2 Shifting trend of *Pseudomonas* spp isolates by year.

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ECHO

New mutations in the PAX6 gene in patients with aniridia

Please visit the *British Journal of Ophthalmology* website [www.bjophthalmol.com] for a link to the full text of this article.

Three novel mutations in the PAX6 gene have been found in patients with aniridia, adding to the data base of more than 200 different mutations in this gene.

Overall, aniridia has an incidence of about 1/80 000, and mutations in the PAX6 gene on chromosome 11p13 are responsible for about 80% of cases, both sporadic and familial. Normal eye development is highly susceptible to the degree of PAX6 expression. Haploinsufficiency causes aniridia and overexpresssion leads to microphthalmia.

The three new recently reported mutations were found in patients who were all heterozygous for their mutation. In one instance the mutation was found in three members of the same family—brother, sister and mother.

The PAX6 gene encodes a transcriptional regulator and produces two alternative splice isoforms that have distinct DNA binding specificities. Mutations are found throughout the gene so that extensive investigation is required in each case. The new mutations reported are all from unrelated families, and all probably lead to a truncated PAX6 protein. The first family carried a nonsense mutation in exon 8, another patient had a mutation in exon 10 and the third patient had a mutation which lead to aberrant mRNA splicing.

These findings indicate further the need for comprehensive genetic counselling in patients with aniridia in whom PAX6 mutations are detected.

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