

A study of the epidemiology of *Salmonella bareilly* in India using a new phage-typing system

By G. SINGH, N. C. SHARMA, M. JAYASHEELA AND S. N. SAXENA

*National Salmonella and Escherichia Centre, Central Research Institute,
Kasauli-173 205 (HP), India*

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SUMMARY

A total of 637 strains of *Salmonella bareilly* received from different parts of India between 1959 and 1985 were phage typed using five locally isolated wild phages. The overall typability was 94.5% and 11 different phage types could be defined. Phage types 10 and 1 were the most prevalent and the geographical and source distribution is described.

INTRODUCTION

Salmonella bareilly was isolated for the first time in 1928 (Bridges & Scott, 1931). Although identified in India for many years (Ganguli, 1958) its importance as a human pathogen causing both gastroenteritis (Raichowdhuri *et al.* 1983; Agarwal *et al.* 1983) and nosocomial infections (Panhotra & Agarwal, 1982) has only been recently recognized. As part of the investigation into the epidemiology of this serotype the distribution of different phage types in the country was likely to prove useful. Majumdar & Singh (1973) first developed a phage-typing system for this serotype but did not use their data to study its epidemiology. Sharma *et al.* (1984) developed a further phage-typing system based on lysogeny in order to study the epidemiology of the organism (Saxena *et al.* 1985) but the system proved too elaborate and insensitive for general use (Jayasheela *et al.* 1987).

In the present study a total of 637 strains received by the National Salmonella and Escherichia Centre, Kasauli, India during the past 27 years were phage typed using a new system based upon five wild phages isolated from sewage to study the occurrence and distribution of different phage types in the country.

MATERIALS AND METHODS

Bacterial strains

A total of 637 strains of *S. bareilly*, received at the National Salmonella and Escherichia Centre, Kasauli, India between 1959 and 1985 and preserved in a lyophilized state, were used in the study.

Phage-typing method

The bacterial strains were phage typed using five wild phages as described by Jayasheela *et al.* (1987).

Table 1. *Source distribution of S. bareilly phage types*

Phage types	Human	Animal	Others	Unknown	Total
1	123	33	77	4	237
2	2	1	4	—	7
3	—	1	1	—	2
4	—	1	—	—	1
5	—	1	—	—	1
6	—	—	1	—	1
7	3	—	—	—	3
8	1	—	4	—	5
9	—	—	4	—	4
10	151	66	55	26	298
11	8	34	1	—	43
UT*	28	2	4	1	35
Total	316	139	151	31	637
Typability	91.1%	98.6%	97.3%	96.2%	94.5%

* UT, untypable.

Table 2. *Distribution of S. bareilly phage types amongst different animals*

Animal	Phage types							UT	Total
	1	2	3	4	5	10	11		
Food animals*	5	—	—	—	—	30	24	1	60
Rodents†	6	1	—	—	1	21	8	1	38
Cold-blooded animals‡	16	—	—	—	—	5	2	—	23
Others§	6	—	1	1	—	10	—	—	18
Total	33	1	1	1	1	66	34	2	139

* Includes goat, poultry, fish, sheep, pig, calf.

† Includes rat, guinea pig, wild rodents, shrew.

‡ Includes tortoise, lizards, toad, snake, cockroach, earthworm.

§ Includes birds, bat, jackal, dog.

RESULTS

Of the 637 strains studied, 316 (49.6%) were from human sources, 139 (21.8%) from animal sources and 151 (23.7%) were from other sources. The origin of the remaining 31 (4.9%) strains was not recorded. A total of 602 strains (94.5%) could be phage typed. The most common overall phage types were 10 (46.8%) followed by phage type 1 (37.2%). Of human strains 288 (91.1%) could be typed (Table 1).

Phage type 1 was represented in all clinical sorts of sample, i.e. stool, blood, urine and CSF as was phage type 10 except for CSF. Types 2, 7 and 8 were all from stool samples.

Of the 139 strains obtained from 20 different species of animals 137 (98.6%) could be phage typed (Table 2). Phage type 10 was the commonest and was present in 17 animal species, followed by phage type 1 found in 9 different animals and phage type 11 which was found in 6 different animals. Phage types 6-9 were not found amongst animals sources.

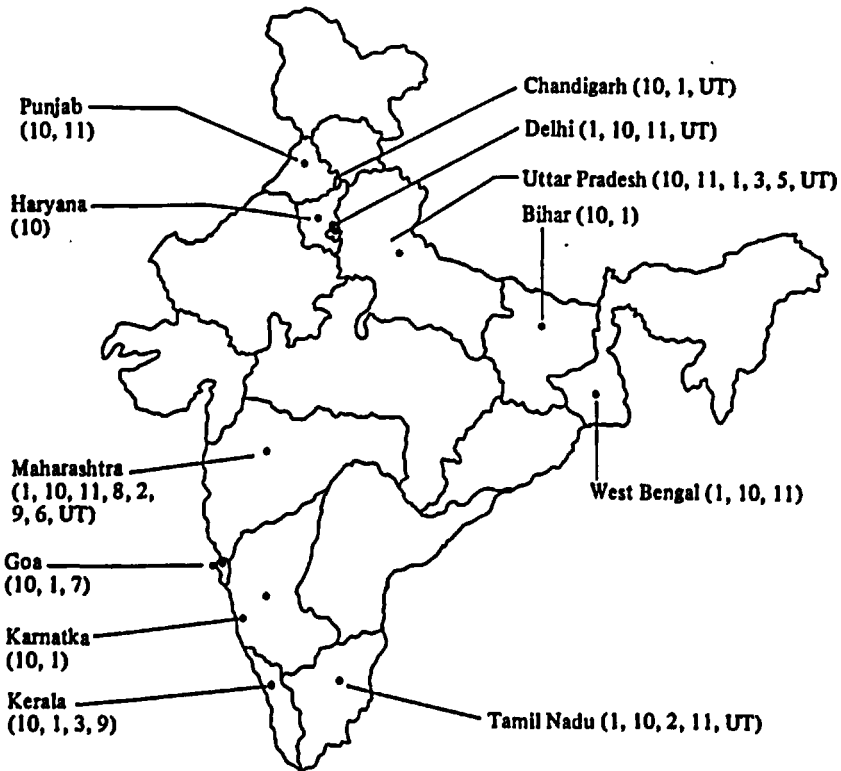


Fig. 1. Geographical distribution of phage types of *S. bareilly* in India.

Of the 151 strains from other sources, i.e. meat, frozen frog legs, bone meal, animal by-products, cheese, water, sewage, seabeach sand, floor of ship, mint and a knife, 147 (97.3%) were typable. Phage types 10 and 1 were again the most commonly isolated.

Geographical distribution of S. bareilly phage types

The distribution is presented in Fig. 1. The largest number of strains were received from the State of Maharashtra (29.7%) and Delhi (18.2%). Type 10 was found in all 12 states and Union territories, type 1 in 10 and type 11 in 5. Phage type 5 was restricted to the State of Uttar Pradesh, types 6 and 8 to Maharashtra and type 7 to Goa.

DISCUSSION

In India the incidence of *S. bareilly* infections in man is increasing. Because of its wide host range (Saxena *et al.* 1987) an attempt was made to develop a new and more generally useful system of phage typing in order to study its epidemiology. Of previous studies that of Majumdar & Singh (1973) was small, involving only 21 isolates. However, Sharma *et al.* (1984) studied 378 strains from a variety of sources and phage typed them on the basis of lysogeny. The value of the method was limited in that only 70.3% of strains turned out to be typable (Saxena *et al.*

1985). Phage types 1 and 10 account for over 84% of isolates from all sources. Of the other types defined, only type 11, found predominantly in animals, occurred in any significant numbers. A great many more human strains than others were typable. Thus, while the level of typability was high, discrimination was of a fairly low order.

The animal data is of interest in that the organisms from many of the domestic animals, i.e. sheep and poultry, were of the same phage types as those isolated from man. However, in India the goat is the main food animal and from them only phage type 11 was isolated. In view of the very small proportion of human isolates of this type (2.5%), this animal seems unlikely to be of much importance in infections in man.

It is not possible to read much into the data on the geographical distribution of types throughout the country. While it has been noted that certain phage types were found only in certain areas, the numbers are too small to attach any significance to the findings. Strains were not evenly distributed throughout the country (82% came from 5 of the 12 states) which, while it might reflect true incidence, could well be more associated with the availability of facilities.

The limitations of epidemiological analysis based on stored bacterial isolates is well known, but further prospective studies using this typing system may well provide more clues to the origins and transmission of *S. bareilly* in this country.

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