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AUTHOR'S CORRECTION

Carried Meningococci in the Czech Republic: a Diverse Recombining Population

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Volume 38, no. 12, p. 4492–4498, 2000. We described the genetic characterization of 156 *Neisseria meningitidis* isolates obtained from healthy young adults in the Czech Republic during 1993. Subsequent work has established that a further 61 isolates collected during that year had been stored separately and had been overlooked. These isolates were not a random sample of those collected, as isolates with a phenotype resembling the strain responsible for a disease outbreak that year were overrepresented. All but one of the additional meningococci were isolated from individuals who were 20 to 24 years old, giving a total of 190 isolates from this age group, rather than the 130 isolates originally reported; the other isolate was from the younger cohort (age range, 15 to 19 years).

The revised multilocus sequence typing (MLST) data are available at the *Neisseria* MLST website (http://neisseria.mlst.net/links.htm). These data show a total of 88 sequence types (STs), which were resolved into 16 clonal complexes (lineages), with the remaining STs not presently assigned to clonal complexes. The six most prevalent clonal complexes were the ST-11 complex (33 isolates [15.2%]), the ST-44 complex (31 isolates [14.3%]), the ST-92 complex (21 isolates [9.7%]), the ST-106 complex (20 isolates [9.2%]), the ST-116 complex, (13 isolates [6%]), and the ST-53 complex (12 isolates [5.5%]). Since the original publication, some minor changes have been made to the assignment and names of the clonal complexes; for example, the ST-41 complex has been renamed the ST-44 complex. The present assignments are available at the PubMLST isolate database website (http://neisseria.mlst.net).

The principal conclusions of the paper, that the population was diverse and that this diversity was principally generated by recombination, are unaltered (Table 1; Fig. 1). However, the revised data show that the prevalence of meningococci belonging to the ST-11 (ET-37) complex was almost six times higher than that calculated on the basis of the data from the 156 original isolates and much greater than any previously measured prevalence of this complex among carriage isolates. This affects estimates of the overrepresentation of ST-11 complex meningococci among isolates from invasive disease. Of the 27 meningococcal isolates carried by members of the younger cohort (age range, 15 to 19 years), 3 (11.1%) belonged to the ST-11 complex. As 10 (22.7%) of the 44 cases of invasive disease in this age group were caused by ST-11 complex organisms, this clonal complex was overrepresented approximately twofold among disease-causing meningococci, as originally reported. However, meningococcus carriage data for individuals in the older cohort (age range, 20 to 24 years) indicated that a total of 30 (15.8%) of the 190 isolates belonged to the ST-11 complex, with 2 out of 9 cases of disease having been caused by ST-11 complex organisms (22.2%). This clonal complex was therefore overrepresented by approximately 1.4-fold (not the originally reported 16-fold) among the disease-associated meningococci isolated from this age group. The ST-11 complex meningococci were found in five of the geographical regions sampled, suggesting that the distribution of these meningococci was widespread. At present, it is unclear why the levels of carriage of the ST-11 complex meningococci (all but two of the isolates expressed serogroup C capsular polysaccharide) were so high in the Czech Republic during 1993, although it could have been a consequence of this clonal complex spreading through the Czech population after a period of absence.

TABLE 1. Genetic Variation in MLST loci[a]

Locus	Size (bp)	218 Czech carriage isolates			107 isolates isolated worldwide			No. (%) of alleles shared	No. (%) of polymorphic sites shared
		No. of alleles (no./100 isolates)	No. (%) of polymorphic sites	d_N/d_S	No. of alleles (no./100 isolates)	No. (%) of polymorphic sites	d_N/d_S		
abcZ	432	21 (9.6)	75 (17.4)	0.074	15 (14)	75 (17.4)	0.05	10 (47.6)	65 (86.7)
adk	465	19 (8.7)	25 (5.4)	0.011	10 (9.4)	17 (3.7)	0.02	8 (42.1)	15 (60.0)
aroE	489	21 (9.6)	135 (27.6)	0.295	18 (16.8)	166 (34)	0.293	11 (52.4)	126 (93.3)
fumC	465	29 (13.3)	48 (10.3)	0.010	19 (17.8)	38 (8.2)	0.024	13 (44.8)	38 (79.2)
gdh	501	19 (8.7)	26 (5.2)	0.049	16 (15)	28 (5.6)	0.05	9 (47.4)	24 (92.3)
pdhC	480	25 (11.5)	83 (17.3)	0.068	24 (22.4)	80 (16.7)	0.07	15 (60.0)	76 (91.6)

[a] d_N/d_S, the proportion of nonsynonymous to synonymous nucleotide substitutions.

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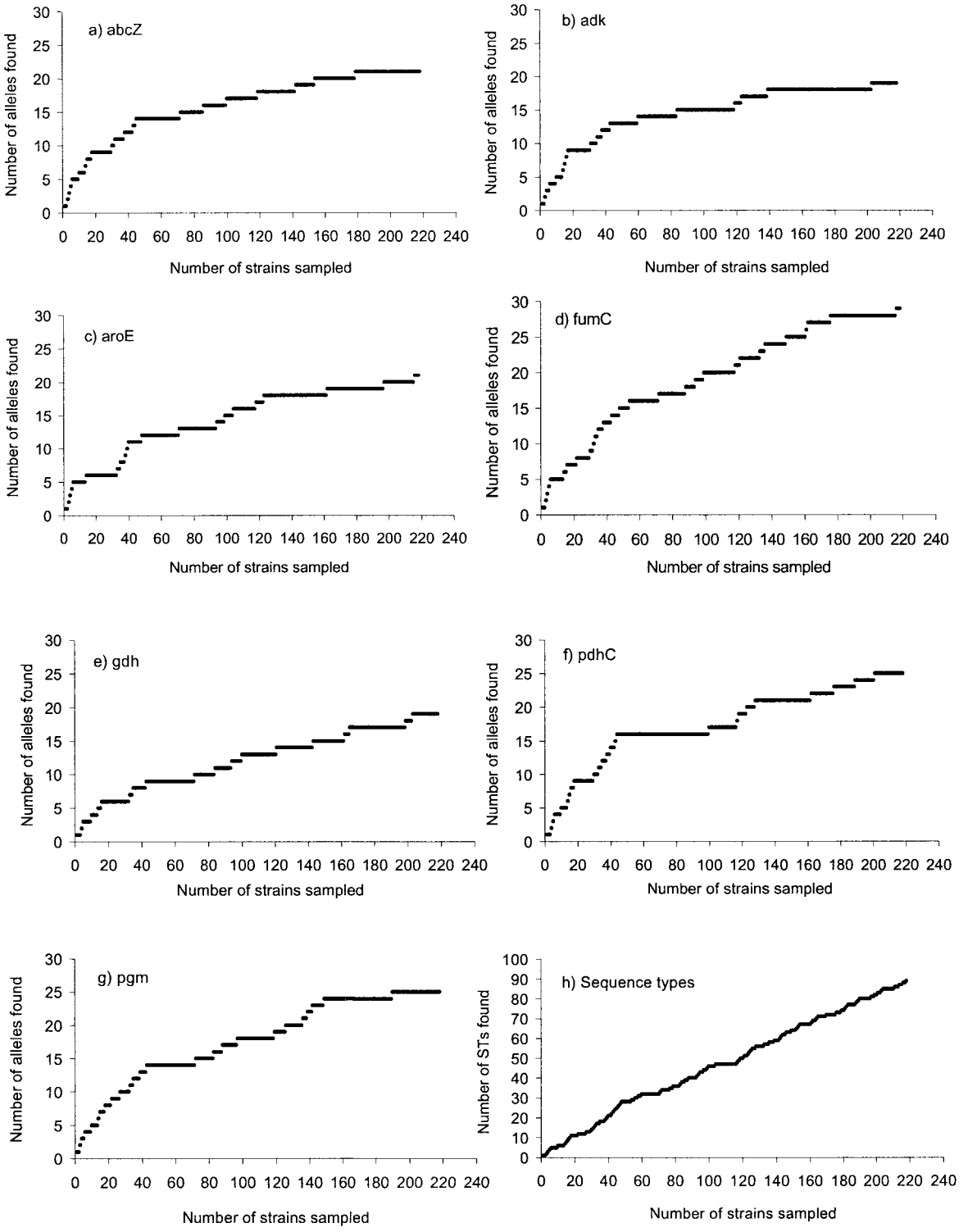

FIG. 1. The number of alleles present at the loci *abcZ* (a), *adk* (b), *aroE* (c), *fumC* (d), *gdh* (e), *pdhC* (f), and *pgm* (g), as well as the number of sequence types (h), plotted against the number of isolates sampled, given in numerical order of isolation.