**Genome Sequence of *Helicobacter pylori* hpEurope Strain N6**

**Wiebke Behrens, Tobias Bönig, Sebastian Suerbaum, and Christine Josenhans**

Institute for Medical Microbiology and Hospital Epidemiology, Hannover Medical School, Hannover, Germany

*Helicobacter pylori* colonizes about half of the world’s population. It is a causative agent of stomach diseases, including malignant tumors. We report the genome sequence of strain N6, which is widely used in *H. pylori* research and appreciated for its large cell size and high transformation efficiency.

*Helicobacter pylori* strain N6 was isolated in 1989 in Nantes, France, from a patient with gastritis (8). It belongs to the phylogeographic population hpEurope (14). N6 was one of the first *H. pylori* isolates used in research and is still widely used. N6 was the first *H. pylori* strain in which isogenic mutants were constructed by allelic exchange-mediated gene disruption, a major step in the development of genetic tools for this organism (8). The strain exhibited a very high transformation efficiency when plasmids or DNA fragments were introduced (12,13), and it has provided important data about mechanisms introducing genetic flexibility in the species. N6 was later employed to develop novel genetic tools for the construction of conditional *H. pylori* mutants in essential genes (3). In addition to being naturally transformable, N6 is capable of infecting gnotobiotic piglets, allowing the demonstration that urease is essential for *H. pylori* colonization (5,6). It has served to elucidate regulatory and phenotypic features of the *H. pylori* flagellar apparatus (10,11,15,17), energy taxis (18), and the role of UreI in acid adaptation (4). However, analyses of data generated with *H. pylori* N6 were hampered by the lack of a genome sequence.

Here we report the draft genome sequence of *H. pylori* strain N6. A low-passage-number stock culture from 1991 was used for preparation of DNA. A total of 180,048 reads with an average length of 256 nucleotides were obtained with 454 FLX pyrosequencing technology (Roche), corresponding to ~28-fold coverage. The contig assembly from single reads was performed with the Roche Newbler Assembler (release 1.1.03.24), yielding 54 contigs (46 large contigs). Genome annotation and alignment were performed with KODON (Applied Maths, Sint Martens-Latem, Belgium) using *H. pylori* 26695 (19), J99 (1), and B8 (7) finished genome sequences as scaffolds. The automatic annotation was manually curated, and the RAST automated annotation and genome comparison pipeline were used for comparisons (2).

The *H. pylori* N6 genome sequence (all contigs) comprises 1,657 kbp in total and 1,738 coding sequences (GLIMMER2, RAST), as well as 36 tRNA and 3 RNA coding loci. The average GC content of all contigs was 38.7%, similar to those of the 26695 (38.9%) and J99 (39.2%) genomes. The RAST pipeline predicted *H. pylori* HPAG1 and G27 (both of the hpEurope type) to be the closest overall neighbors of N6.

The N6 genome carries a complete *cag* pathogenicity island (*cag*PAI), which is functional (our unpublished data); *cag*4A, coding for the secreted virulence factor CagA (EPIYA motifs ABC2, Western type), is located separately in a different genome region, close to the *cag*-1 open reading frame (ORF) and not to the *cag*-25 gene as in most other strains (16). The vacuolating cytotoxin gene vacA was assigned to type s1m2. Several genes associated with plasticity zones (PZ), transferable genome regions with high genetic variability found in all *Helicobacter pylori* genomes (9), were identified. The availability of the genome sequence for *H. pylori* strain N6 will be helpful for novel analyses and the reevaluation of a large number of experimental data already available for this strain.

**Nucleotide sequence accession numbers.** The N6 sequences are accessible at ENA EMBLBank (accession numbers CAHX01000001 to CAHX01000054).

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**REFERENCES**