# 6. Summary

A 25 kb region covering *tbpAB* to *opaA* was sequenced from *Neisseria meningitidis* serogroup A, subgroup IV-1 strain Z2491 from The Gambia. 18 open reading frames and several repetitive elements could be identified and analysed. Comparative sequencing of the *N. meningitidis* serogroup C, ET37-complex strain Z4400 showed that the general order of this region was very similar between both strains, but many polymorphisms were detected. Most differences could be found in the repetitive elements. The results also indicate that the *tbpAB* operon from ET37-complex is probably an import from unrelated bacteria.

Analysis of four gene fragments (*potF*, *tbpB*, *amiC*, *opaA*) in old isolates of the serogroup III (1966), IV-1 (1966) and IV-2 (1917) showed that they were identical to the sequence in Z2491 with minor differences. In order to determine the frequency of horizontal genetic exchange within different countries, the same gene fragments were sequenced from 100 serogroup , subgroup IV-1 meningococci isolated during and after the epidemic in The Gambia in the 1980s and from 100 serogroup C, ET37-complex meningococci isolated from endemic disease in Mali in the early 1990s. Among the ET37-complex strains only 1 point mutation in the *opaA* gene was found. In contrast to that finding roughly 50% of the alleles in the 100 IV-1 strains were imported or mutated. Most of these recombinations in the IV-1 strains took place around the *tbpAB*-operon, the size varied between 5-11 kb. This leads to the assumption of different recombination pathways in both subgroups.

In the IV-1 strains a group of bacteria could be identified where the *tbpAB* operon is probably an import from a foreign organism.

All these data support the concept of the "Global Gene Pool" in Neisseria and show that recombination events even among very far related members of a gene family are possible.