might contain other resistance determinants, being particularly relevant the association of *qnr* genes with genes coding for extended-spectrum ß-lactamases and AmpC ß-lactamases (Strahilevitz et al. 2009). These co-resistance associations, in addition to the presence of other resistance genes in *qnr*-encoding plasmids, have likely favored the dissemination of *qnr* genes even when quinolones are not used for therapy.

Although less prevalent at the moment, other transferrable mechanisms of quinolone resistance besides Qnr proteins have been described. Among them, two quinolone efflux pumps, QepA (Yamane et al. 2007) and OqxAB (Hansen et al. 2004, 2007), have been found to be encoded in different plasmids. In addition to quinolones, QepA extrudes a narrow range of substrates, including erythromycin, ethidium bromide, and acriflavine. OqxAB (almost exclusively present in organisms causing animal infections) however presents a wider substrate range that includes tetracycline, chloramphenicol, benzalkonium chloride, and triclosan (Hansen et al. 2007).

A quinolone-inactivating enzyme (ciprofloxacin and norfloxacin), encoded by the *aac(6′)-Ib-cr* gene, has been described more than 10 years ago. This enzyme evolved toward quinolone resistance from an original aminoglycoside acetyltransferase through the acquisition of two amino acid changes (Trp102Arg and Asp179Tyr) (Robicsek et al. 2006), which allow the inactivation of quinolones at the cost of reducing the efficacy of the enzyme against aminoglycosides (Robicsek et al. 2006). This modification strongly suggests that the new evolved enzyme has been selected under strong quinolone selective pressure, likely during antimicrobial treatment. Since association of *aac(6′)-Ib-cr* with genes encoding the ß-lactamase CTX-M-15 or extended-spectrum ß-lactamases has been reported (Coque et al. 2008; Pitout et al. 2008), co-selection of this determinant by other antibiotics besides quinolones is a suitable possibility.

It has been stated that the risk for the dissemination of resistance is lower in the case of mutations than in the case of HGT-acquired genes. For the first, spread is achieved through clonal expansion, whereas for the second both clonal expansion and gene transfer are both at work. While this is the most common rule, there are some exceptions, and one of them consists in antibiotic resistance mutations in genes encoding bacterial topoisomerases. Indeed, it was described that *parC* and *gyrA* mutations, and the associated phenotype of resistance to quinolones, can be transferred by transformation in *Streptococcus pneumoniae* clinical isolates (Ferrandiz et al. 2000). Further, mutation-acquired resistance to quinolones can be transferred from the viridans group streptococci to *S. pneumoniae* (Balsalobre et al. 2003), indicating that commensal bacteria might contribute by means of transferring target mutations to the development of quinolone resistance, at least in the case of *S. pneumoniae*.