The ICE integration/excision module encodes a recombinase, frequently a tyrosine recombinase. This enzyme assists in the reaction between *attP*, a sequence on the recombination module of the ICE, and *attB* on the host chromosome, forming the attachment sites *attL* and *attR* that flank the element after successful integration (Burrus and Waldor 2004). In most cases of tyrosine recombinase-mediated reactions, an excisionase is needed for excision. Site-specific recombination between *attR* and *attL* forms again an *attP* site on the circularized ICE and an *attB* site on the host's chromosome. ICEs can exhibit high to weak integration specificity, depending on the respective integration/excision modules. ICEs harboring a tyrosine recombinase usually integrate into several specific sites, not only at the 3′ end of tRNAs but also at both ends of housekeeping genes (Burrus and Waldor 2004; Johnson and Grossman 2015).

SXT is a 100 kb ICE that was initially isolated from *V. cholerae* in India and codes for multiple ABR genes. SXT and related MGEs have become alarmingly widespread in Asian and African *V. cholerae* isolates. SXT is similar to the IncJ element R391 and both integrate into the same chromosomal site, the *prfC* gene, with the aid of a tyrosine recombinase (Hochhut and Waldor 1999; Hochhut et al. 2001). The mechanism of integration and excision was described to be similar to that in lambdoid phages. Both the integrase and the excisionase are needed for successful SXT excision (Burrus and Waldor 2003). These two genes are in a convergent orientation and further most probably not co-regulated. The proteins forming the conjugative machinery have significant homology with transfer (Tra) proteins from pCAR1 from *Pseudomonas resinovorans* and Rts1 from *Proteus vulgaris* (Murata et al. 2002; Maeda et al. 2003; Burrus et al. 2006). The SXT *tra*-genes are located in four clusters spanning more than 25 kb. These *tra*-genes are conserved among SXT-related ICEs. The R391 *tra*-genes reveal more than 94% identity to their counterparts in SXT (Beaber et al. 2002; Böltner and Osborn 2004). Both SXT and R391 harbor exclusion systems that prevent redundant transmission of these ICEs (Burrus et al. 2006).

Tn*916* is regarded as prototype of the Tn*916*-Tn*1545* family of ICEs and is one of the most studied conjugative transposons in G+ bacteria. Tn*916* was originally isolated from *Enterococcus faecalis* (Santoro et al. 2014). Conjugative processes of Tn*916* are again described to be similar to those of conjugative plasmids. Following conjugative transfer of the nicked single-stranded DNA and replication, Tn*916* integrates into A + T rich sequences. Thus, this MGE reveals a low specificity for integration, which results in frequent intracellular transposition (Jaworski and Clewell 1995; Roberts and Mullany 2009). In contrast, Tn*5276* from *Lactococcus lactis* reveals a higher integration specificity (Rauch and de Vos 1992). Tn*916* and related MGEs are regulated by tetracycline. Tn*916* encodes a tetracycline resistance gene and under exposure to this antibiotic drug, conjugative transfer increased 19-fold in *B. subtilis* (Showsh and Andrews 1992).