

Article of Significant Interest Selected from This Issue by the Editors

Characterization of ICE6013 Elements in *Staphylococcus aureus*

Integrative conjugative elements are understudied stock in the inventory of mobile genetic elements of *Staphylococcus aureus*. Sansevere et al. (e00629-16) have characterized the function and diversity of this species' ICE6013 elements. ICE6013 is unique in using its IS30-like transposase as a recombinase for excision. The element horizontally transfers by conjugation, efficiently for some recipients. Study of rare chromosomal integrations of ICE6013 in transconjugants revealed that nonrandom sequences flank a more arbitrary target site, reminiscent of IS30 integration. ICE6013 is distributed widely across the *Staphylococcus* genus, which indicates that the element is an agent of horizontal gene transfer.

Transposase-Mediated Excision, Conjugative Transfer, and Diversity of ICE6013 Elements in *Staphylococcus aureus*

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ABSTRACT

ICE6013 represents one of two families of integrative conjugative elements (ICEs) identified in the pan-genome of the human and animal pathogen *Staphylococcus aureus*. Here we investigated the excision and conjugation functions of ICE6013 and further characterized the diversity of this element. ICE6013 excision was not significantly affected by growth, temperature, pH, or UV exposure and did not depend on *recA*. The IS30-like DDE transposase (Tpase; encoded by *orf1* and *orf2*) of ICE6013 must be uninterrupted for excision to occur, whereas disrupting three of the other open reading frames (ORFs) on the element significantly affects the level of excision. We demonstrate that ICE6013 conjugatively transfers to different *S. aureus* backgrounds at frequencies approaching that of the conjugative plasmid pGO1. We found that excision is required for conjugation, that not all *S. aureus* backgrounds are successful recipients, and that transconjugants acquire the ability to transfer ICE6013. Sequencing of chromosomal integration sites in serially passaged transconjugants revealed a significant integration site preference for a 15-bp AT-rich palindromic consensus sequence, which surrounds the 3-bp target site that is duplicated upon integration. A sequence analysis of ICE6013 from different host strains of *S. aureus* and from eight other species of staphylococci identified seven divergent subfamilies of ICE6013 that include sequences previously classified as a transposon, a plasmid, and various ICEs. In summary, these results indicate that the IS30-like Tpase functions as the ICE6013 recombinase and that ICE6013 represents a diverse family of mobile genetic elements that mediate conjugation in staphylococci.

IMPORTANCE Integrative conjugative elements (ICEs) encode the abilities to integrate into and excise from bacterial chromosomes and plasmids and mediate conjugation between bacteria. As agents of horizontal gene transfer, ICEs may affect bacterial evolution. ICE6013 represents one of two known families of ICEs in the pathogen *Staphylococcus aureus*, but its core functions of excision and conjugation are not well studied. Here, we show that ICE6013 depends on its IS30-like DDE transposase for excision, which is unique among ICEs, and we demonstrate the conjugative transfer and integration site preference of ICE6013. A sequence analysis revealed that ICE6013 has diverged into seven subfamilies that are dispersed among staphylococci.