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# Mobile Genetic Elements associated with antibiotic resistance in clinical and commensal isolates of *Streptococcus salivarius*

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## Résumé

Mobile genetic elements (MGEs) largely contribute to evolution and diversity of bacterial genomes through horizontal gene transfer. Among them, Integrative and Conjugative Elements (ICEs) promote their own excision by site-specific recombination, their transfer by conjugation and their integration into a replicon of the recipient cell. MGEs usually encode adaptative functions that may cause drastic changes in the ecological and/or pathogenic properties of bacterial species. A variety of MGEs conferring antibiotic resistance has been described in pathogenic streptococci but little is known on MGEs present in commensal streptococci. Strains of *Streptococcus salivarius* (92 clinical and 46 commensal strains isolated from saliva and feces of healthy individuals) were studied for their resistance to tetracyclines, macrolides, lincosamides, aminoglycosides and phenicol antibiotics and the presence of associated resistance genes. Genetic linkage of these resistance genes with MGEs was then examined. Almost all the macrolide-resistant commensal strains harbor a *mef(A/E)* resistance gene carried by a MEGA element. A genetic linkage between a macrolide resistance gene (*erm(B)*) and genes of ICEs of the Tn916 family was detected in 23 clinical and 5 commensal strains with a predominance of Tn3872 elements (n=13) followed by Tn6002 elements (n=11) and Tn2009 elements (n=4). Four strains harboring a *mef(A/E)* gene are also resistant to chloramphenicol and carry a *catQ* gene. The genome sequencing of one of these strains revealed that these genes co-localize on an IQ-like element as already described in other viridans streptococci. ICESt3 related elements were also detected in half of the isolates. This work highlights the potential role of MGEs of *S. salivarius*, including various ICEs, in the spread of antibiotic resistance genes both in oral sphere and gut.

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