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Mobility potential of latent antibiotic resistance genes: *novel mobile colistin resistance genes*

BACKGROUND

After their recent discovery, several variants of mobile colistin resistance (*mcr*) genes have been identified. These genes are closely related to bacterial chromosomal *eptA* genes. So the question is, are all mobile or plasmid-borne *eptA/mcr*-genes mobile colistin resistance genes? And could these genes pose a potential risk to human health? Our aim was to characterize the genetic diversity of *eptA/mcr*-genes in influent sewage and determine their genetic context to infer their mobility potential.

MATERIALS AND METHODS

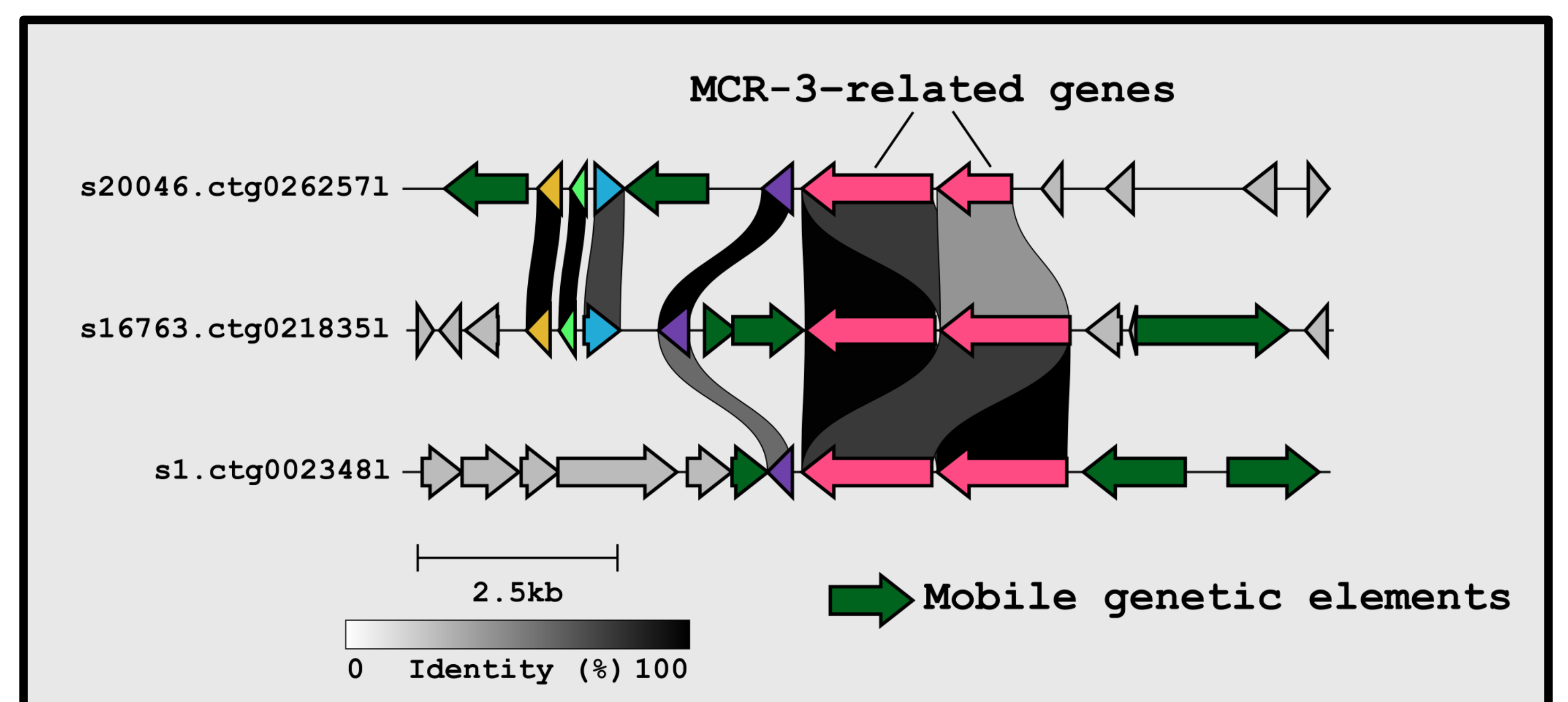
Influent sewage was sampled on three consecutive days and sequenced with PacBio Sequel II. Metagenomes were assembled with hifiiasm-meta. HMM-models were build from known *mcr*-gene variants and queried against the assembled metagenomes. Plasmid contigs were predicted with PlasX and mobile genetic elements within 5 kb up- or downstream region from the identified gene with MobileElementFinder. Phylogenetic tree was built with FastTree.

RESULTS

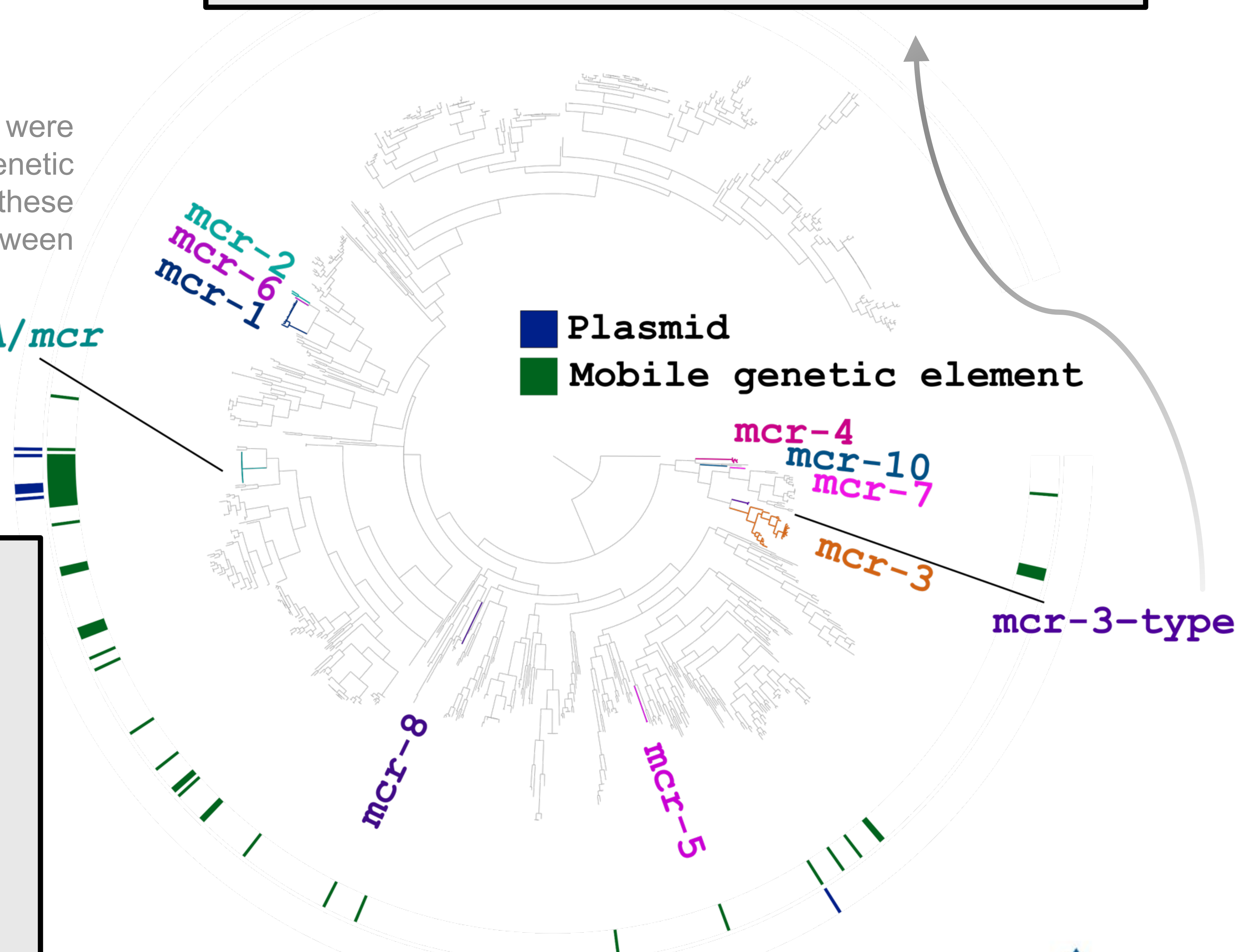
We identified several novel *eptA/mcr*-genes that were plasmid-borne and/or associated with mobile genetic elements. The diverse genetic context of some of these genes suggests that they are actively moving between different genetic locations.

CONCLUSION

Sewage hosts a diverse pool of *eptA/mcr*-genes. Some of these genes could be considered novel mobile colistin resistance genes based on their mobility potential. Further work is needed to link these genes to their hosts, determine their phenotypic resistance patterns and get better insights of the possible horizontal transfer routes of these genes.



Acinetobacter eptA/mcr



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