**DNA modifications impact natural transformation of *Acinetobacter baumannii***

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**Presenter:** Pei-Qi Chen                    **Date/Time:**2023/09/21, 15:10 -16:00

**Commentator:**Pei-Jane Tsai Ph.D.   **Location:** Room 601, Med College Building

**Background:***Acinetobacter baumannii* is a dangerous hospital-acquired bacterium known for rapidly acquiring new traits, like antibiotic resistance genes (ARGs). This happens through a process called natural transformation, one of the primary modes of horizontal gene transfer (HGT). HGT drives bacterial evolution and allows bacteria to take up and use DNA from their environment. Natural transformation has been experimentally demonstrated in several strains of *A. baumannii*. However, these studies reported considerable variation in the transformation frequencies obtained in the different strains.

**Objective/Hypothesis:**This study aims to understand how the source of the transforming DNA affects transformability in *A. baumannii.*

**Results:**Several DNA features play a role in the transformability of certain naturally competent bacteria. The variability in DNA methylation patterns among *A. baumannii* strains influenced their ability to serve as efficient DNA donors. The authors identified a restriction-modification (RM) system in strain A118 that can prevent DNA uptake if it lacks the right methylation on RGATCY recognition sites. The restriction endonuclease (RE) degrades foreign DNA lacking specific epigenetic marks and the methylase (MT) protects self-DNA from the RE-mediated degradation by adding specific methylation marks. RM systems in competent cells can limit the acquisition of new genetic traits from different strains. While increasing methylase levels in the cell partially counteracted the RM-dependent effect on transformation. DNA with overlapping DNA adenine methyltransferase (Dam) methylation marks on GATC sites was not affected, indicating a preference for DNA with similar epigenetic patterns.

**Conclusion:**This study suggests that that DNA exchanges between bacteria that share similar epigenomes are favored and could therefore guide future research into identifying the reservoir of dangerous genetic traits for this multi-drug-resistant pathogen.