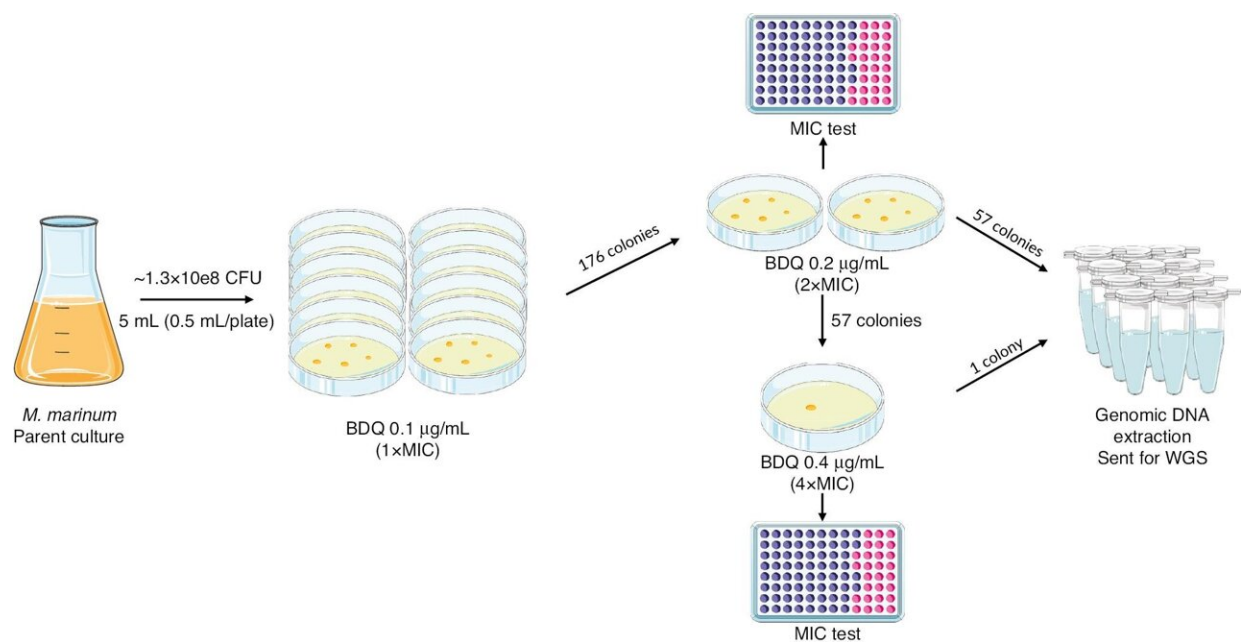


# Identification of novel mutations associated with bedaquiline resistance in *Mycobacterium marinum*

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In vitro selection of bedaquiline-resistant isolates in *M. marinum*. Credit: *Zoonoses* (2023). DOI: 10.15212/ZOONOSES-2022-0042

As infections caused by nontuberculous mycobacteria (NTM) are rapidly increasing globally, a need exists for developing novel antibiotics and discovering the mechanism of resistance. New research reported in *Zoonoses* is aimed at understanding the mechanism of bedaquiline

resistance in the model NTM species *Mycobacterium marinum* (*M. marinum*).

The *Mycobacterium marinum* strain was subjected to mutant selection with different concentrations of BDQ. After three rounds of evolution, 58 BDQ-resistant mutants were isolated and subjected to WGS. The results were confirmed through PCR and Sanger sequencing.

Seven [genetic mutations](#) among these mutants were identified. The highest drug resistance (6–10× MIC) was associated with a mutation in *AtpB*, the primary biochemical target of BDQ in *Mtb*. Numerous mutations and insertions mapped to the gene *MMAR\_1007*(46/58), which encodes the homolog of *Rv0678* (*MmpR*) in *Mtb*. More than 93% of mutants (54/58) contained a single mutation (G563A) in *MMAR\_4049*, which encodes the integral membrane protein *YrbE3A-1*.

Both target-based and efflux-based actions contribute to BDQ resistance in *M. marinum*. These findings may aid in developing novel potent anti-NTM (BDQ-based) drug regimens and diagnostic assays for the detection of BDQ-resistant *M. marinum*.

**More information:** Longlong Wang et al, Identification of Novel Mutations Associated with Bedaquiline Resistance in *Mycobacterium Marinum*, *Zoonoses* (2023). [DOI: 10.15212/ZOONOSES-2022-0042](https://doi.org/10.15212/ZOONOSES-2022-0042)

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