Authors' reply

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We appreciate the comments provided by Melano et al. regarding our publication. They found the PCR-MCA method to be simple and rapid. In addition, they agreed that all of the mis-sense mutations harbored in strains confirmed by PCR-MCA clearly demonstrated that the PCR-MCA method was able to detect mutations in the four QRDR positions (*gyrA*-81 and -85, *parC*-79 and -83). Melano et al. highlighted the fact that the presence of intermediate *Tm,* which resulted from silent mutations or mutations in other positions inside the sensor probe, could result in an overestimation of significant mutation. Although none of the 72 strains used in our study were shown to have silent QRDR mutations, 17 out of 175 strains were determined to have silent QRDR mutations in their study. We designed probes which target the four QRDR positions in order to maximally differentiate *Tm* from the wild-type strain and *Tm* from mutant strains.. To avoid any misinterpretation of PCR-MCA results of intermediate *Tm* (in other words, to differentiate *Tm* from the wild-type strain and *Tm* from mutant strains), we suggest that a *Tm* range be set in each QRDR positions using control strains. Unfortunately, not enough strains have been assayed to evaluate the different Tm values between strains with silent mutations (from mutant or wild-type strains). In addition, there is a current lack of information about variations of intermediate *Tm*. As mentioned by Melano et al., intermediate Tm should be interpreted with caution. As a result, further studies are needed for a more thorough evaluation.