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Title: Genotyping mycobacterium avium has a clinical potential to predict therapeutic responses of the lung infection

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Body: For Mycobacterium avium lung infection, the lack of reliable predictors other than the relatively uncommon macrolide resistance represents a major limitation to clinical management. To investigate a potent predictor for the therapeutic response, we evaluated variable numbers of tandem repeats (VNTR) at 16 minisatellite loci of M. avium clinical isolates from 59 subjects with the lung infection. The disease of 30 subjects was defined as responsive for the microbiologic and radiographic improvement after clarithromycin-containing treatments, while that of the remaining 29 subjects was defined as refractory even after the similar treatment. When calculating the genotypic distance aggregated from 16-demensional VNTR data, we observed the genetic diversity of 59 M. avium isolates divided into 3 clusters in neighbor-joining phylogenetic tree, which revealed the nearly significant association with therapeutic responses ($P = 0.06$). In principal component analysis using the raw VNTR data without the distance calculation, we detected a significant correlation between the therapeutic responses and the scattering pattern of 59 M. avium isolates ($P < 0.05$). In further analysis by logistic regression, we examined the effect of each minisatellite locus on a predictive model of the therapeutic response. This led us to construct the highest likelihood multivariate model, adjusted for age, with a sensitivity and specificity both greater than 70%, using VNTR data from only four minisatellite loci ($P < 0.01$). Genotypic characterization of M. avium isolates may be a useful strategy for predicting the clinical outcome of medication.