A tale of two settings: The role of the Beijing genotype in the rise of multidrug resistant tuberculosis

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Body: Background The Beijing genotype of Mycobacterium tuberculosis (M. tb) has been associated with higher rates of drug resistance when compared with strains from other genotypes in some settings. This has led to speculation that the rise of Beijing will contribute to worsening of multi-drug resistant (MDR) tuberculosis (TB) epidemics. We sought to determine the relative importance of Beijing in two epidemiologically contrasting countries with differing MDR-TB challenges: the UK and Peru. Objectives 1) Identify any associations between Beijing and MDR in these two settings and 2) examine if rising trends in Beijing might explain increases in MDR-TB prevalence. Methods We utilised epidemiological, drug sensitivity and strain typing data from England and Lima, Peru, to examine the role of Beijing in these distinct settings, using descriptive analysis, logistic regression and time trend techniques. Results Whilst Beijing strains currently constitute a minority of lineages types in both countries (England: 8%, Peru: 7%), in England Beijing is strongly associated with being at least MDR (OR 7.83 (95% CI 4.46-13.76), p <0.005) and is nearly entirely responsible for more severe forms of resistance (e.g. extensively drug resistant TB). In contrast to the situation in England, the Beijing genotype is not associated with being at least MDR in Lima. Conclusions The absence of an association between MDR and Beijing in Peru reflects the fact that drug resistance there is highly prevalent among strains of several different genotypes. Migration is the main source of new strains in the UK, thus the proportion of TB that is MDR could decline rapidly if less Beijing importation occurred.