The genome of Leishmania donovani from clinically isolated parasites in India and Nepal

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Visceral Leishmaniasis is a neglected parasitic disease with a global annual incidence of approximately half a million cases. Early treatment is critical for patient welfare and for broader reaching plans to control or eliminate the disease. Unfortunately, the repertoire of available drugs is limited and drug resistance is emerging. In this study we focus on a region of India and Nepal where the former first-line drug sodium stibogluconate (SSG) was recently replaced by miltefosine (MIL). MIL is an oral drug with a long half-life, and is available over-the-counter raising fears that resistance will rapidly emerge. We aim to understand the parasite-genetic basis for naturally acquired resistance to both drugs. As a first step. we have produced an essentially complete genome of cloned parasites isolated from a patient. The data were assembled de novo and aligned against the existing L. infantum sequence. We are using this reference sequence to explore the genome variation of 16 further clinical L. donovani isolates, identifying sequence polymorphisms and ploidy differences as well as laying down the foundations to understand the parasite population structure in this region