

**British Society for Parasitology (BSP) Spring Meeting 2026:
ABSTRACT**

**IN VIVO SELECTION OF A LEISHMANIA COSMID LIBRARY REVEALS
CANDIDATE GENES INVOLVED IN SAND FLY TRANSMISSION**

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INTRODUCTION: Due to the absence of a protective human vaccine and the various challenges related to vector control, the management of leishmaniasis currently relies heavily on early and effective diagnosis and treatment. Despite compelling evidence of the importance of the vector, research has predominantly focused on parasite interactions with the vertebrate host. Studies in the invertebrate host have been limited and mostly based on loss-of-function approaches. The development of *Leishmania* promastigotes inside the sand fly vector is a complex, yet critical step in the parasite life cycle, shaped by intricate parasite-vector interactions that may offer interesting novel targets for disease management strategies.

METHODOLOGY: A genome-wide cosmid library of *Leishmania donovani* was subjected to *in vivo* selection through *Lutzomyia longipalpis* sand flies and subsequent mouse macrophage infection. This approach was used to identify candidate genes that provide a gain-of-function and enhance the parasite transmission potential.

RESULTS: Preliminary screening identified several genomic regions potentially conferring an advantage to parasite survival, metacyclogenesis and transmission.

CONCLUSIONS: This unique approach provides a genome-wide strategy for identifying parasite genes essential for vector transmission, deepening our understanding of parasite-vector interactions and offering potential targets for transmission-blocking interventions.

Current efforts focus on narrowing down candidate genes and validating their contribution to sand fly infection establishment, differentiation and macrophage infection through targeted mutagenesis.