

O1207 High genetic heterogeneity of *Blastocystis* spp. in the northeastern area of Spain

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Background: *Blastocystis* spp. is an anaerobic enteric parasite that infects humans and animals around the world, even though it is more frequently found in developing countries. The infection may be either asymptomatic or symptomatic; however, its pathogenicity remains uncertain. A total of 17 subtypes (ST) are known, nine of them are found in humans (ST1 - ST9). The aim of the study was to evaluate the genetic variability of *Blastocystis* spp. isolated from the same geographical area and from the same patient in order to define strategies for larger epidemiological studies.

Materials/methods: Seventeen stool samples from 11 patients infected with *Blastocystis* spp. were collected from May 2017 to June 2018 at Lozano Blesa Hospital, Zaragoza-Spain. DNA was extracted using commercial kits. Single and nested PCR techniques were used to amplify a ~500 bp fragment containing highly variable regions of the SSU-rRNA gene, which was then sequenced. Sequences were compared and analyzed to determine their genetic diversity.

Results: The results indicated that nested PCR was effective for those samples that could not be amplified with a one-step PCR. Using genotyping and phylogenetic analysis, five different subtypes were identified, namely ST1 (3 samples, 2 patients), ST2 (4 samples, 3 patients), ST3 (2 samples, 2 patients), ST4 (7 samples, 4 patients), and ST6 (1 samples, 1 patients). ST4 was the most prevalent and diverse subtype. Though it was observed in this study, subtype 6 is not commonly found. One patient presented a mixed infection by ST4 and ST6 subtypes. In addition, the presence of multiple peaks in the sequences suggests the presence of mixed intra-subtype infections. It seems to prove the heterogeneity of *Blastocystis* spp.

Conclusions: The results obtained suggest the presence of mixed *Blastocystis* infections and the high genetic diversity of the parasite which indicates the necessity to check out the techniques used in epidemiological and parasite population studies.

