**Objectives:** To evaluate the association between the cerebrospinal fluid (CSF) expression of miR-21, miR-155, miR-146a and miR-142-3p and different MR parameters in MS patients.

**Methods:** An observational cross-sectional study was designed. Circulating RNAs were extracted, retrotranscribed and preamplified from CSF, and miRNAs were quantified in a real-time PCR. MR parameters analysed were: number of lesions in T2, number of gadolinium enhancing lesions (Gd+) in T1, presence of hipointense T1 lesions (hipoT1), and brain parenchymal fraction (BPF).

**Results:** 29 patients (79.30% were female) with a mean age of 40 (± 10.22) years old were analysed. Positive correlations were observed between Gd+ and miR-21 expression (r=0.418, p=0.030) and BPF with both miR-155 and miR-142-3p expression (r=0.541, p=0.021 and r=0.602, p=0.010 respectively). A downregulation of miR-142-3p in patients with hipoT1 compared with those without (0.016 vs. 0.067; p=0.017) and an upregulation of miR-146a in patients with ≥9 lesions in T2 compared with those with < 9 lesions (0.325 vs. 0.197; p=0.021) were also found.

**Conclusions:** miR-21 and miR-146a upregulation were found related to MR activity. miR-155 and miR-142-3p, which are related to inflammation, were found associated to less brain atrophy. The differential expression of miRNAs involved in the immune system regulation in CSF of MS patients is associated to different MR parameters.