

Interactive comment on “Blastodinium spp. infect copepods in the ultra-oligotrophic marine waters of the Mediterranean Sea” by C. Alves-de-Souza et al.

Anonymous Referee #1

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This paper contributes valuable information on morphotypes of *Blastodinium*, copepod infections, SSU rDNA gene sequence analyses and oligonucleotidic probes to describe abundances of *Blastodinium* dinospores in three stations of a cruise. For me, this represents very valuable data for this manuscript.

When authors infer about dinospore distributions and their ecological relevance in oligotrophic waters, they have to take in mind several points:

-the authors recognise that your work likely underestimates the genetic diversity of *Blastodinium*, since several morphotypes could not be amplified with cluster-specific oligonucleotidic probes. -the parasites presented highly seasonality -there is no data

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on copepod abundance and distribution in the sampling stations since sampling were performed by a net

These points raise some questions: -does dinospores morphology reflect the different clusters defined in this study based upon the SSU RDNA gene analyses? -does the authors expect similar results in winter conditions? -the abundance and distribution of the copepods is not known, so is the paragraph of dinospore-host distribution in oligotrophic waters going beyond to the infections data?

There are good points in this work since results will raise several hypothesis to be tested. For e.g. why high values in one stations and in two groups (Corycaeida and Calanoida Group) were recorded. Other example is about the *Blastodinium* infections, that are supposed to be initiated during the early stages of copepod development however, it seems there is a drastic partitioning between nauplii and dinospores in that cruise. Does the authors have any explanation for the first stage of infection by *Blastodinium*?

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