Line 52: “Alga” should be in lowercase (“alga”).

line 53: that is not entirely correct as you forgot to mention that a carbon source (acetate) would be required in the dark. Another way of stating the same idea would be by mentioning that “photosynthetic machinery in Chlamy is not required as long as they have access to acetate, which make this organism an ideal system to study photosynthesis via classic forward genetic approaches.”

The reference “1” is not entirely correct. The chlamy genome was published in 2007 and not in 2010.

line 60: please, note that prokaryotic organisms also produces sRNAs.

line 62: PTGS also plays a crucial role as an antiviral barrier in higher plants (as well as in insects).

line 73: “mainly” from coding regions.

line 73: a “feature” more typical of the animal miRNA “system”.

line 75: I do not understand this sentence. Please, note that THERE ARE CLEAR evidence of endonucleolytic cleavage; however, these cleavages do not affect the mRNA steady-state levels of miRNA targets. This argue in favour of either translational repression or fine-tuning mRNA levels as main mechanisms of miRNA action.

line 83: based on my comment above, it is more than a decade since the first draft of the Chlamydomonas genome was published.

line 85. I would say “it is a pertinent time to study the whole population of sRNAs in Chlamydomonas”.

line 114: Figure “9” cannot be the first figure. Renaming figures and/or change the order is required.

line 121: it is not correct to say that loci were 0-30 nt in length. Loci with 0-15 nt should not be considered unless you define them as “tinny” sRNAs.

line 132: it might be a good idea to compare 5’ nucleotide preferences for different sizes. Is it the same preference for 20-nt sRNAs than for 21-nt sRNAs. What about the other sizes?

line 160. Do you mean across different wild type strains? In line with the comments just below (line 163), I wonder how many of “specific” loci correspond to transposons. In fact I think it is very important to define the origin of these 89% of loci that you define as “specific”.

I am very surprised for this huge amount of specific loci. Is it the same between Arabidopsis ecotypes? or this is a specific feature of Chlamydomonas? If that is the case, then it would be nice to describe this feature more both in the result section and during discussion.

line 171. I do not know whether the cluster 1 makes any biological sense. The main reason that I have to state this is that the median size is too short. 24-39 nucleotides means they produce very few (only 1?) sRNAs. Might be better to think more about this cluster and, if this cluster is in fact a good one, then discuss about the above mentioned feature.

Comment added later: I have seen that you already mention these things in the discussion section. Great.

line 196. Cluster 4 seems to include most miRNAs. Then, it is weird that this cluster has only a slight DCL3 dependency because all miRNAs in Chlamy depend on DCL3 to be produced. It suggest to me that cluster 4 actually comprises two subgroups: DCL3 dependent loci (only miRNAs?) and DCL3 indedependent loci (I do not know how to name them). Is my interpretation true? Given our expertise in miRNAs and my previous paper about the dcl3 mutant, I think we should be very precise with the description of the cluster that contains all miRNAs.

REFERENCE TO BE INCLUDED:

- Lou S, Sun T, Li H, Hu Z. Mechanisms of microRNA-mediated gene regulation in unicellular model alga *Chlamydomonas reinhardtii*. *Biotechnol Biofuels*. 2018;11:244. Published 2018 Sep 8. doi:10.1186/s13068-018-1249-y

This is a very recent review to be referenced at some point during the introduction. In fact, it nicely describes all what is know about RNA silencing in Chlamydomonas!