Corrigendum

Steady-state levels of imported tRNAs in Chlamydomonas mitochondria are correlated with both cytosolic and mitochondrial codon usages

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Nucleic Acids Research, 2009, 37(5): 1521–1528, https://doi.org/10.1093/nar/gkn1073

The data presented in Figure 3A is the same as that presented partially in Figure 3A of (9).

In (9), we have studied the expression of the cytosolic tRNA population in the green alga *Chlamydomonas* by northern blots. These data are presented in Figure 3A in (9).

The study published in NAR focuses on the import of cytosolic tRNAs into mitochondria of the green alga. Indeed, the expression of the cytosolic tRNAs presented in (9) serves as a support: some of the mitochondrial tRNA samples analyzed in the NAR article have been loaded on the same gels as the cytosolic ones to allow comparison and quantification. Figure 3A is an illustration of the northern blots. The quantification of all results permitted to get the histogram presented on Figure 3B but the data and the results are new as compared to (9). However, we agree that this should have been better mentioned. (9) was only noted in the text and for a matter of clarity, we now include an additional sentence in the legend of Figure 3 where it is clearly stated that the expression of cytosolic tRNAs by northern blots was previously published.

This error does not affect the results and conclusion of the article.

REFERENCE

9. Cognat, V., Deragon, J.M., Vinogradova, E., Salinas, T., Remacle, C. and Maréchal-Drouard, L. (2008) On the evolution and expression of Chlamydomonas reinhardtii nucleus-encoded transfer RNA genes. *Genetics*, **179**, 113–123.

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Figure 3. Expression and sub-localization of the nucleus-encoded tRNAs of *C. reinhardtii.* (**A**) Whole-cell RNA fraction (**T**) and mitochondrial RNA fraction (**M**) separated on polyacrylamide gel and hybridized against probes specific to cytosolic tRNA genes (see Table 1 and supporting information Table S1). Note that the expression of the cytosolic tRNAs by northern blots in whole-cell extract has previously been described (9) and was used as a support to illustrate the differences between cytosolic and mitochondrial fractions. Reproduced by permission of the Genetics Society of America. Name of probes is given below each Northern experiment. (**B**) Extent of mitochondrial import for each cytosolic tRNA in percentage. For each tRNA, two to four independent Northern blot experiments were performed. Three and four independent total and mitochondrial RNA preparations were used for the whole set of Northern experiments. For each probe, a typical experiment is presented in (**A**) but the percentages of extent of mitochondrial import given in (**B**) are the mean values obtained with two to four independent Northern blot experiment were used for the scale, they will not be visible for most tRNAs. The standard deviations observed are usually less than 5%. Only for two probes, Y and Me, a higher deviation of around 10% was observed.