Erratum

The F1-ATP synthase complex in bloodstream stage trypanosomes has an unusual and essential function

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Owing to a typesetting error, Figures 1C and 3C of the above article were published incorrectly in print. The correct Figures 1 and 3 are reproduced below in their entirety.

The Publisher would like to apologize for any inconvenience this may have caused.

Figure 1 For Figure Caption see next page.

Figure 3 Knockdown of ATP synthase subunit α expression is lethal to *Dk T. evansi* Antat 3/3. (A) Culture growth shown as cumulative cell numbers after normalization for dilution during cultivation. Expression of subunit α was silenced using tet-inducible RNAi (solid squares), and uninduced cells were maintained in parallel (open squares). Growth curves for two individual clones are shown. (B) Determination of mRNA levels for ATP synthase subunits α and β and for the mitochondrial transcript ND4 as described for Figure 1B. Total RNA was isolated from induced cells after 24 h and from uninduced control cells. Indicated are relative changes in mRNA levels with respect to *LS T. brucei*. Average numbers for four real-time PCR experiments are shown, using RNA preparations from two independent RNAi experiments. (C) Western blot analysis of crude cytosolic (C), soluble mitochondrial (M), and insoluble (I) fractions prepared from RNAi-induced cells after 31 h and from uninduced control cells. The blots were probed with reagents detecting the indicated proteins. Coomassie staining (bottom panel) revealed the protein loading. (D) Analysis of ATP hydrolytic activity in crude mitochondrial fractions, generated as in (C) and assayed by measuring release of free phosphate. Average numbers for four assays are shown, using extract preparations from two independent RNAi experiments. See Figure 1D for abbreviations.

Figure 1 Knockdown of ATP synthase subunit α expression is lethal to LS stage *T. brucei*. (A) Culture growth shown as cumulative cell numbers after normalization for dilution during cultivation. Expression of subunit α was silenced using tet-inducible RNAi (solid squares); uninduced cells were maintained in parallel (open squares). (B) Determination of mRNA levels for ATP synthase subunits α and β and for the mitochondrial transcript ND4 by real-time RT-PCR ($\Delta\Delta Ct$ method). Total RNA was isolated from induced cells after 43 h as well as from uninduced control cells. Primers for subunit α were located outside the region targeted by RNAi. Relative changes in mRNA levels with respect to the parental cell line are indicated, using β -tubulin mRNA or 18S rRNA for normalization. Average numbers for four amplifications are shown, using RNA preparations from two independent RNAi experiments. (C) Western blot analysis of crude cytosolic (C), soluble mitochondrial (M), and insoluble (I) fractions prepared from RNAi-induced cells after 45 h and from uninduced control cells. The blots were probed with reagents detecting the indicated proteins. Coomassie staining (bottom panel) revealed the protein loading. (D) Analysis of ATPase activity in crude mitochondrial fractions, generated as in (C) and assayed by measuring release of free phosphate. ATP synthase inhibitors oligomycin (OM; 2.5 μ g/ml) and azide (A; 1 mM) were added where indicated. Average numbers for four assays are shown, using extract preparations from two independent RNAi experiments.