**Electronic Supplementary Material**

**ESM-Methods**

*Telomere length assays*

We used qPCR methods to quantify relative telomere length (TL). DNA was extracted and purified using a DNeasy blood and tissue kit (Qiagen). Following extraction, we used a Nanodrop to check and confirm that all DNA samples were appropriate for qPCR analyses regarding the DNA concentration (always > 60 ng.mL-1) and integrity (260/280 ratios: min: 1.87, max: 1.97; 260/230 ratios: always > 1.9). Telomeric DNA (TEL) and a reference gene (RAG1) were amplified respectively by running 3 plates and standardised to 5 ng of lizard DNA in each well. RAG1 was selected as a control gene because it is known to be a reliable single copy gene, which has been previously used successfully to measure telomere to single copy gene (T/S) ratio and relative TL in lizards (see [19] in the main manuscript). The average cycle threshold (Ct) value and the intra population coefficient of variation (CV) in Ct values were respectively 22.06 cycles and 3.01% for RAG1. Efficiencies averaged respectively 101.00 ± 1.83% (Mean ± SE) and 98.00 ± 3.61% for RAG1 and TEL. For each individual, we assessed the two TL measures at day 0 and at day 96 in the same plates, and we found marginal repeatability in TL between sampling sessions (Intraclass Correlation Coefficient ± 95% confidence interval: 20.0 ± 27.2%, F47,48 = 1.5, p = 0.083). A common sample was run on all plates and the inter-plate CVs were 5.22% and 2.46% respectively for RAG1 and TEL. For each DNA fragment (TEL and RAG1), the melting curves indicate that a single fragment is amplified during the qPCR (Fig. S3).

**Table S1.** Distribution of lizards (57 females and 43 males) from the two hydric treatments amongst the 10 outdoor enclosures (n = 10 lizards / enclosure). All enclosures are identical in length (12.5 m), width (8 m) and composed by 50 cm high vegetation, two permanent watering holes (70L plastic tank), and two piles of stones and logs used as shelters and basking sites by lizards.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Enclosure 1 |  | Enclosure 2 |  | Enclosure 3 |  | Enclosure 4 |  | Enclosure 5 |  | Enclosure 6 |  | Enclosure 7 |  | Enclosure 8 |  | Enclosure 9 |  | Enclosure 10 |
| SexTreatment |  | F | M |  | F | M |  | F | M |  | F | M |  | F | M |  | F | M |  | F | M |  | F | M |  | F | M |  | F | M |
| Control |  | 3 | 2 |  | 2 | 3 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |  | 2 | 3 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |
| Water-restricted |  | 2 | 3 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |  | 3 | 2 |

**Table S2.** Analyses of factors influencing the initial values of two physiological markers of oxidative stress (oxidative damage: ROM-Day0; antioxidant defences: OXY-Day0) and the relative telomere length (TL-Day0). Table reports the construction of linear mixed model and the summary of statistics testing the random effects of mother ID (family effect), and the fixed effects of sex, treatment affiliation and their interaction.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Models |  | Model summary |  |  |  |  |  |  |
| ROM-Day0 ~ Sex + Treatment + Sex\*Treatment + (1|Mother\_ID) |  | Number of individuals  | Mean ROM-Day0 (mgH2O2.dl-1) | Type | Term | Variance |  |  |
|  |  | n = 97 | 2.68 | Random | Mother ID | ~ 0.000 |  |  |
|  |  |  |  |  | Residual | 0.999 |  |  |
|  |  |  |  |  |  | *β* (± SE) | t-stat | P value |
|  |  |  |  | Fixed | Intercept | 0.16 ± 0.19 | -0.8 | 0.418 |
|  |  |  |  |  | Sex (relative to Female) |  |  |  |
|  |  |  |  |  | Male | 0.16 ± 0.29 | 0.6 | 0.576 |
|  |  |  |  |  | Treatment (relative to Control) |  |  |  |
|  |  |  |  |  | Water restriction | 0.07 ± 0.27 | 0.2 | 0.804 |
|  |  |  |  |  | Sex\*treatment | 0.26 ± 0.41 | 0.6 | 0.527 |
| OXY-Day0 ~ Sex + Treatment + Sex\*Treatment + (1|Mother\_ID) |  | Number of individuals | Mean OXY-Day0 (µmol HClO.ml-1) | Type | Term | Variance |  |  |
|  |  | n = 97 | 120.2 | Random | Mother ID | 0.317 |  |  |
|  |  |  |  |  | Residual | 0.720 |  |  |
|  |  |  |  |  |  | *β* (± SE) | t-stat | P value |
|  |  |  |  | Fixed | Intercept | -0.04 ± 0.19 | -0.2 | 0.853 |
|  |  |  |  |  | Sex (relative to Female) |  |  |  |
|  |  |  |  |  | Male | 0.22 ± 0.29 | 0.8 | 0.452 |
|  |  |  |  |  | Treatment (relative to Control) |  |  |  |
|  |  |  |  |  | Water restriction | 0.12 ± 0.27 | 0.5 | 0.650 |
|  |  |  |  |  | Sex\*treatment | -0.41 ± 0.43 | -1.0 | 0.336 |
| TL-Day0 ~ Sex + Treatment + Sex\*Treatment + (1|Mother\_ID) |  | Number of individuals | Mean TL-Day0 (z-score) | Type | Term | Variance |  |  |
|  |  | n = 48 | ~ 0.000 | Random | Mother ID | ~ 0.000 |  |  |
|  |  |  |  |  | Residual | 0.907 |  |  |
|  |  |  |  |  |  | *β* (± SE) | t-stat | P value |
|  |  |  |  | Fixed | Intercept | -0.16 ± 0.27 | -0.6 | 0.553 |
|  |  |  |  |  | Sex (relative to Female) |  |  |  |
|  |  |  |  |  | Male | 0.28 ± 0.40 | 0.7 | 0.477 |
|  |  |  |  |  | Treatment (relative to Control) |  |  |  |
|  |  |  |  |  | Water restriction | 0.11 ± 0.38 | 0.3 | 0.770 |
|  |  |  |  |  | Sex\*treatment | 0.09 ± 0.55 | 0.2 | 0.875 |

**Table S3**. Analyses of factors impacting the changes in two physiological markers of oxidative stress (oxidative damage: ΔROM; antioxidant defences: ΔOXY) and relative telomere length (ΔTL). Table reports the construction of the best linear mixed models and the summary of statistics testing the random effects of mother ID (family effect), lizard ID (repeated measures) and outdoor enclosure (see distribution of lizard in Table S1), and the fixed effects of initial value as covariates, sex, hydric treatment, time, first and second interaction term. We used a backward procedure and removed the second order interaction term when non-significant (analysis on ΔOXY) to facilitate result interpretation.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Models |  | Model summary |  |  |  |  |  |  |  |
| ΔROM ~ initial ROM + Sex + Treatment + Time + Sex\*Treatment + Sex\*Time + Treatment\*Time + Sex\*Treatment\*Time + (1|Mother\_ID) + (1|Lizard\_ID) + (1|Enclosure) |  | Number of individuals  | Mean ΔROM (mgH2O2.dl-1) | Type | Term | Variance |  |  |  |
|  |  | n = 168 | 0.23 | Random | Mother ID | 0.044 |  |  |  |
|  |  |  |  |  | Lizard ID | ~ 0.000 |  |  |  |
|  |  |  |  |  | Enclosure | 0.025 |  |  |  |
|  |  |  |  |  | Residual | 0.655 |  |  |  |
|  |  |  |  |  |  | *β* (± SE) | t-stat | P value |  |
|  |  |  |  | Fixed | Intercept | -0.22 ± 0.17 | -1.3 | 0.211 |  |
|  |  |  |  |  | initial ROM | -0.73 ± 0.07 | -9.8 | < 0.001 | \*\*\* |
|  |  |  |  |  | Sex (relative to Female) |  |  |  |  |
|  |  |  |  |  | Male | 0.16 ± 0.25 | 0.6 | 0.528 |  |
|  |  |  |  |  | Treatment (relative to Control) |  |  |  |  |
|  |  |  |  |  | Water restriction | 0.05 ± 0.22 | 0.2 | 0.809 |  |
|  |  |  |  |  | Time (relative to Day 36) |  |  |  |  |
|  |  |  |  |  | Day 96 | 0.57 ± 0.25 | 2.3 | 0.025 | \* |
|  |  |  |  |  | Sex\*treatment | -0.65 ± 0.35 | -1.9 | 0.066 | **·** |
|  |  |  |  |  | Sex\*time | -0.64 ± 0.37 | -1.7 | 0.084 | **·** |
|  |  |  |  |  | Treatment\*time | -0.09 ± 0.34 | -0.3 | 0.788 |  |
|  |  |  |  |  | Sex\*treatment\*time | 1.52 ± 0.52 | 2.9 | 0.004 | \*\* |
| ΔOXY ~ initial OXY + Sex + Treatment + Time + Sex\*Treatment + Sex\*Time + Treatment\*Time + (1|Mother\_ID) + (1|Lizard\_ID) + (1|Enclosure) |  | Number of individuals | Mean ΔOXY (µmol HClO.ml-1) | Type | Term | Variance |  |  |  |
|  |  | n = 166 | 76.4 | Random | Mother ID | 0.036 |  |  |  |
|  |  |  |  |  | Lizard ID | ~ 0.000 |  |  |  |
|  |  |  |  |  | Enclosure | ~ 0.000 |  |  |  |
|  |  |  |  |  | Residual | 0.886 |  |  |  |
|  |  |  |  |  |  | *β* (± SE) | t-stat | P value |  |
|  |  |  |  | Fixed | Intercept | 0.18 ± 0.18 | 1.0 | 0.337 |  |
|  |  |  |  |  | initial OXY | -1.06 ± 0.10 | -10.9 | < 0.001 | \*\*\* |
|  |  |  |  |  | Sex (relative to Female) |  |  |  |  |
|  |  |  |  |  | Male | -0.26 ± 0.25 | -1.0 | 0.299 |  |
|  |  |  |  |  | Treatment (relative to Control) |  |  |  |  |
|  |  |  |  |  | Water restriction | -0.23 ± 0.24 | -1.0 | 0.335 |  |
|  |  |  |  |  | Time (relative to Day 36) |  |  |  |  |
|  |  |  |  |  | Day 96 | 0.33 ± 0.27 | 1.2 | 0.228 |  |
|  |  |  |  |  | Sex\*treatment | 0.74 ± 0.31 | 2.4 | 0.019 | \* |
|  |  |  |  |  | Sex\*time | -0.73 ± 0.30 | -2.5 | 0.015 | \* |
|  |  |  |  |  | Treatment\*time | -0.58 ± 0.30 | -2.0 | 0.054 | **·** |
| ΔTL ~ initial TL + Sex + Treatment + Sex\*Treatment + (1|Mother\_ID) + (1|Enclosure) |  | Number of individuals | Mean ΔTL (z-score) | Type | Term | Variance |  |  |  |
|  |  | n = 48 | -0.053 | Random | Mother ID | ~ 0.000 |  |  |  |
|  |  |  |  |  | Enclosure |  ~ 0.000 |  |  |  |
|  |  |  |  |  | Residual | 0.881 |  |  |  |
|  |  |  |  |  |  | *β* (± SE) | t-stat | P value |  |
|  |  |  |  | Fixed | Intercept | -0.30 ± 0.27 | -1.1 | 0.261 |  |
|  |  |  |  |  | initial TL | -0.77 ± 0.15 | -5.2 | < 0.001 | \*\*\* |
|  |  |  |  |  | Sex (relative to Female) |  |  |  |  |
|  |  |  |  |  | Male | 0.87 ± 0.39 | 2.2 | 0.033 | \* |
|  |  |  |  |  | Treatment (relative to Control) |  |  |  |  |
|  |  |  |  |  | Water restriction | 0.43 ± 0.38 | 1.1 | 0.261 |  |
|  |  |  |  |  | Sex\*treatment | -1.42 ± 0.54 | -2.6 | 0.012 | \* |

**Figure S1.** Principal component analysis of the variance-covariance patterns for oxidative stress (OS) and telomere length (TL).We assessed OS using three markers of oxidative damages (ROM-Day0, ΔROM-Day36, ΔROM-Day96), and three markers of antioxidant defences (OXY-Day0, ΔOXY-Day36, ΔOXY-Day96) each of them being measured at three sampling times. We measured TL at Day0 and Day96 (ΔTL-Day96). The major axis PC1 explained 32.0% of the global variance and was most correlated with OXY-Day0, ΔOXY-Day36, ΔOXY-Day96, TL-Day0, and ΔTL-Day96. The second major axis PC2 explained 20.9% of the global variance and was mostly correlated with ROM-Day0, ΔROM-Day36, ΔROM-Day96, and ΔOXY-Day96.This illustrates that OS markers are relatively uncorrelated, whereas initial TL or TL shortening are inversely correlated with initial or changes in antioxidant capacity, respectively.

**Figure S2.** Graphical representation of the relationship between telomere length at the onset of the experiment (TL-Day0) and the longevity of lizards using annual survival curves (mean and confidence intervals).TL-Day0 was considered either long $[TL>\overbar{TL}$, blue lines (means) and shade (95% confidence interval)] or short $[TL<\overbar{TL}$, yellow lines (means) and shade (95% confidence interval)]. Short TL-Day0 are associated with shorter longevity, and the differences in mortality risk between long and short TL-Day0 occurred over the next two years following the experiments (year 2-3), in both sexes (interaction between sex and TL-Day0: z = -0.2, p = 0.805).

**Figure S3**. Validation of the qPCR primers obtained with single peak of melting curves obtained for both A) TEL and B) RAG1, suggesting that those were the only amplicons. Curves illustrate the changes in fluorescence over time [d(RFU/d(T)] during an incremental increase in temperature.

