Supplementary Material for:

Playing evolution in the laboratory: from the first major evolutionary transition to global warming

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Table of Contents:

| Fig. S1A, B | Page 2 |
| Chromosomal inversion polymorphism | Page 3 |
| Fig. S2 | Page 3 |
| Thermal performance curves | Page 4 |
| Fig. S3 | Page 4 |
| Fig. S4 | Page 5 |
| References | Page 5 |
Fig. S1: A) The Stochastic Corrector Model. Different genes (closed and open circles) contribute to the fitness of the compartments (protocells) in that they catalyse steps of metabolism, for example. During protocell growth, the templates are free to compete and can replicate at different rates (first-level or within-cell selection). During protocell fission, there is random assortment of templates into offspring protocells, which generates variation in protocells’ gene composition on which natural selection at the compartment level (second-level or group selection) can act and oppose to (correct) internal deterioration owing to within-cell competition. Thus, protocells with an optimal ratio of genes (say 1:1, in white) will have a higher fitness than those with suboptimal ratios. B) Trait-group model. A population of replicators (genes) at time $t$ is transiently subdivided into different groups (compartments). Within these groups, replicators are free to compete and the different genes contribute to the well-being (fitness) of the compartment. The contribution of each compartment to the pool of replicators at time $t+1$ will depend on group’s fitness (e.g., compartments with an initial 1:1 ratio of functional genes could grow faster and deliver more replicators to the next pool).
Chromosomal inversion polymorphism. An old and long ago solved issue in population genetics was to quantify how much genetic variation is hosted by populations. A satisfactory answer was given after the introduction of molecular techniques in population genetics — protein gel electrophoresis in the 1960s, restriction fragment length polymorphisms in the 1970s, and DNA sequencing in the 1980s. Richard Lewontin’s book *The Genetic Basis of Evolutionary Change* [1] offers a lucid account of the struggle to measure genetic variation in the early days of population genetics. An exception was chromosomal inversion polymorphism in some Diptera (flies, mosquitoes, etc.). The reason is that these insects host cells that undergo endomitosis; the replication of chromosomes without further cell division. This generates polytene chromosomes with thousands of DNA strands that can be observed under the light microscope (fig. S2). From 1932 to the mid-1940s Theodosius Dobzhansky and his colleagues collected samples from natural populations of *Drosophila pseudoobscura* and some related species, and observed that their populations were usually polymorphic for inversions [2,3].

An inversion is a structural variation in a chromosome in which a fragment involving several genes rotates 180°, resulting in a region where the positions of these genes are inverted relative to the original sequence (fig. S2). The main reason why inversions are evolutionarily important is because they inhibit recombination in heterokaryotypes (heterozygous individuals for different gene arrangements) and can maintain supergene (i.e., a group of neighbouring genes on a chromosome which are inherited together and are functionally related in an evolutionary sense) architectures. Following Dobzhansky’s pioneering studies, many biologists gathered an extensive historical record of the distribution of different inversions in *Drosophila* species worldwide, including *D. subobscura*. This historical record has been an invaluable source of information to provide suggestive evidence that climate change is driving genetic adaptive evolution, as discussed in the paper.

![Image](https://example.com/fig_s2)

**Fig. S2:** The pictures on the left show individuals that are homozygous (*A*<sub>ST</sub>/*A*<sub>ST</sub>) or heterozygous (*A*<sub>ST</sub>/*A*<sub>2</sub>) for chromosomal gene arrangements on the A (sex) chromosome of *D. subobscura* (light microscope). The schematic diagram on the right illustrates how the pairing of homologous chromosomes in heterozygous individuals with different gene arrangements forms a chromosomal loop.
**Thermal performance curves.** A fitness performance curve plots (e.g.) the intrinsic population growth rate against temperature. Fitness increases exponentially with temperature from a critical thermal minimum ($CT_{\text{min}}$) up to a maximum fitness ($r_{\text{max}}$) at the optimum temperature ($T_{\text{opt}}$), and then drops swiftly to the critical thermal maximum ($CT_{\text{max}}$). The dependence of fitness on temperature can be modelled as a Gaussian function for the increasing portion of the curve up to $T_{\text{opt}}$, and a quadratic decline to zero fitness at $CT_{\text{max}}$ as follows [4]:

\[
W(T) = \begin{cases} 
  r_{\text{max}} \left( 1 + \frac{1}{2} \left( \frac{T - T_{\text{opt}}}{CT_{\text{max}} - T_{\text{opt}}} \right)^2 \right) & \text{for } T \leq T_{\text{opt}} \\
  r_{\text{max}} \left( \exp \left( 1 - \left( \frac{T - T_{\text{opt}}}{CT_{\text{max}} - T_{\text{opt}}} \right)^2 \right) \right) & \text{for } T > T_{\text{opt}}
\end{cases}
\]

where $\sigma_p$ is the phenotypic standard deviation.

Fig. S3: Hypothetical performance curves (from eqn. 1) for two genotypes (blue: cold-adapted; red: warm-adapted) under a constant thermal regime ($T_{\text{sel}}$) in the laboratory. In keeping with laboratory results, we assume that ‘warmer is better’ (warm-adapted $r_{\text{max}} >$ cold-adapted $r_{\text{max}}$) and cold-adapted genotypes prefer lower temperatures (warm-adapted $T_{\text{opt}} >$ cold-adapted $T_{\text{opt}}$). Although the temperature (‘cold’) imposed by the selective regime is closer to $T_{\text{opt}}$ of cold-adapted genotypes, the fitness ($r$) of warm-adapted genotypes is higher.
Fig. S4: Multivariate evolutionary trajectories of Adraga, Groningen and Montpellier populations founded in 2010 for five phenotypic traits using Principal Component Analysis.

REFERENCES