Electronic supplementary material

1. Sediment coring, dating and processing

The short cores (NC91-1S, NC01-1S) were taken with a single-drive piston corer (Wright 1980) and extruded upright in the field with a fixed-interval sectioning device (Verschuren 1993). The long core was recovered in 1m-segments with a square-rod piston corer (Wright 1967), extruded in the field and wrapped in polyethylene and aluminium foil for transport. In the lab, cores were cut longitudinally for detailed stratigraphic analysis. Cores were finally sliced in 2 cm segments. The outermost 2 mm of each core slice was removed to overcome any contamination which may have occurred during extrusion. In the laboratory, water content, dry weight and organic-matter content of all sediment samples were determined by loss-on-ignition methods (Bengtsson & Enell 1986). Sediment chronology of core NC01-1S is based on a series of stratigraphic marker horizons corresponding to known historical events and stratigraphic correlation with the Pb^{210} dated core NC93-1S (Verschuren 2001, Mergeay et al. 2004). Core NC01-D was dated using lithostratigraphic correlation between NC01-D and the ^{14}C-dated core NC93-2L, combined with patterns of loss-on-ignition (Mergeay 2005). Age at depth for each individual core increment was estimated by linear interpolation between identified time-marker horizons.

2. DNA extraction and amplification

DNA was extracted by placing dormant eggs in 10 µl proteinase K buffer (16 mM $(NH_4)_2SO_4$, 67 mM Tris-HCl pH 8.8, 0.01% Tween-20, 10% dithiotreitol and 0.5 mM proteinase K). *Daphnia* from zooplankton samples were treated similarly, in 100 µl proteinase K buffer. Samples were incubated for 1 h at 56°C followed by 10 min at

96°C, and 2 min centrifugation (13 000 rpm, 20 cm diameter), after which the supernatant was transferred to a new UV-sterilized micro-centrifuge tube. Samples were stored at –20°C. PCR preparations were carried out in a separate self-contained laboratory, using UV-sterilized material and pre-sterilized filter tips, always including 6 negative controls. PCR products were separated and visualised on a Li-Cor 4200 system (Li-Cor Biosciences, Lincoln NE, USA) using a 6% Sequagel XR polyacrylamide gel (National Diagnostics, Charlotte NC, USA). PCR products were always run in parallel with a sizing standard (supplied by the manufacturer). Allele sizes were scored with the GeneImagIR 4.03 software (Scanalytics, Billerica MA, USA).

3. DNA sequencing and analyses

DNA sequencing of the 12S rRNA mitochondrial gene followed Mergeay et al. (2005). DNA quality of ancient eggs was frequently inadequate to sequence complete 12S (c. 500 nt) or ND5 (subunit 5 of the mitochondrial NADH gene, c. 880 nt) fragments, consequently a 130 nt fragment was amplified and sequenced using the internal primers 12S_int1F (5' GAGAGTGACGGGCGATATG 3') and 12S_intR (5' ACTTCAGGTCAAGGTGCAG 3'). To maximize phylogenetic resolution DNA isolates from recent samples were subjected to amplification of the more variable ND5 fragment instead of 12S, using primers DpuND5 (forward) and ND5-new (reverse) (Colbourne et al. 1998). ND5 PCR was carried out in 25 µl reactions containing 1x Silverstar PCR buffer (Eurogentec, Seraing, Belgium), 1.5 mM $MgCl_2$, 200 µM of each DNTP, 0.4 µM of each primer, 1µl of template DNA, 1 u *Taq* polymerase and UV-sterilised mQ-H_2O. ND5 PCR amplifications involved a denaturing step of 5 min at 95°C, followed by 5 cycles of 45 s at 95°C, 45 s at 45°C, 90s at 72°C, 35 cycles of 45 s

at 95°C, 45 s at 50°C, 90s at 72°C, and a final elongation of 7 min at 72°C. PCR products were excised from agarose gels and purified using the GFX^{TM} PCR DNA and gel band purification kit (Amersham Biosciences, Buckinghamshire, UK). Approximately 10-50 ng of purified fragment was subjected to sequencing PCR using 3.2 pmol of the forward primer and the ABI Big Dye Terminator Kit (Applied Biosystems, Foster city CA, USA). Sequencing reaction products were analysed using an ABI 3130 capillary DNA sequencer.

4. Table 1: African sampling localities used for ND5 sequencing and population genetic analysis. [1]: only ND5 sequencing. See Mergeay et al. (2005) for similar results on other Kenyan populations.

Toponym	**Geographical coordinates**	**Country**	**Habitat**
Lake Naivasha	S 00° 46.3' E 36° 21.7'	Kenya	eutrophic shallow lake
Lake Limuru	S 01° 06.3' E 36° 37.8'	Kenya	cool vegetated lake
Lake Baringo	N 00° 31.9' E 36° 03.6'	Kenya	warm turbid lake
Korir Dam	N 13° 44.9' E 39° 36.8'	Ethiopia	turbid reservoir
Laelay Wukro Dam	N 13° 48.3' E 39° 36.7'	Ethiopia	turbid reservoir
Lake Chivero	S 17° 54.2' E 30° 47.3'	Zimbabwe	deep eutrophic lake
Cape Flats Death road	S 33° 58.8' E 18° 39.4'	South Africa	intermittent pond
Langebaan Malmesbury[1]	S 33° 29.4' E 18° 27.3'	South Africa	vegetated pond
Gaborone Phakalane	S 24° 34' E 25° 58'	Botswana	sewage lagoon
Gaborone Galis1	S 24° 40' E 25° 57'	Botswana	sewage pond
Gaborone Galis2	S 24° 40' E 25° 57'	Botswana	sewage pond

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