Collection and identification of fecal samples

Mix and store in 95% ethanol

Keep tubes at 4°C

Freeze-Drying

Sifting

Weighing

Methanol extraction

Solid Phase Extraction (SPE)

Hormones RIA (Estrogens, Progestogens, Glucocorticoids, Testosterone metabolites)
FECAL SAMPLE COLLECTION

Samples are collected ad libidum from free-living baboons living in the Amboseli basin of Kenya. When a known animal is observed defecating, we collect the freshly-dropped sample within minutes of its deposit. The sample is well-mixed in a small waxed paper cup with a wooden stirrer and an aliquot is placed in a plastic 20ml vial (Evergreen Scientific 220-3519-080; caps 300-3532-G20) prefilled with 95% ethanol. We add feces until we get a 2.5:1 ratio of ethanol to feces. The vial is identified with the baboon’s name (ID), the sample date, and time of collection. Samples are stored at 4°C until shipped to University of Nairobi for further processing. A list of all samples, including the baboon id, the date and time of collection, and any additional notes about the sample, accompanies the samples to Nairobi.

FREEZE-DRYING

Samples are sent to the University of Nairobi every two weeks, where they are freeze-dried immediately.

Write the sample ID on the cap of each vial. Prepare and send to Princeton an excel sheet containing the sample ID, baboon’s name (ID), collection date and time, freeze dried date and notes about the texture, quantity, or composition of the sample.

Evaporate ethanol:
Allow all ethanol to evaporate by removing the caps and placing the opened vials under a fume hood. Stir the samples regularly as the ethanol evaporates (about every 2 hours), as regular stirring facilitates complete and uniform drying of the sample. Continue with the hood drying until samples are completely dry (dry samples will be “crunchy” when stirred). Stir the vial thoroughly, especially at the bottom, to make sure that the whole sample is completely dry. It takes 24-40 hrs (depending primarily on the water content of the feces) for the ethanol to completely evaporate. Recap the vials and store samples at -20°C until ready for freeze drying.

Freeze dry samples:
Cut cotton gauze into squares (about 7 cm per side). Remove the cap from the sample and fasten the cotton gauze over the vials using a rubber band. Place the tubes in the freeze-drying flasks. Place the flasks in the freezer to cool them down (30 min, -20°C). Once samples are cold, place them into the freeze-drier.

- Temperature should be below -50°C
- Vacuum should be around 30 millitorrs
- Oil in pump must be checked before every use

Once samples are completely freeze-dried, cap the vials and store samples at -20°C until ready for sifting.
SIFTING

Note: Sifting should be done in a humid area to keep airborne fecal dust to a minimum. If necessary, run a humidifier to make the area locally humid.

1. Fold a piece of weighing paper (4” x 4”) diagonally.
2. Sift the dried fecal sample through a mesh tea strainer (~40 mesh) onto the weighing paper.
   NOTE: Use the end of a metal spatula to break-up and sift feces through strainer. The first particles that come through look like very dry, fine, dirt. Stop sifting when vegetative matter begins to come through. The purpose of sifting is to separate the feces from the vegetation, not to mash up the vegetation into fine pieces.
3. Transfer the fecal powder back into the collection plastic tube, and discard the vegetative matter.
4. Clean strainer and spatula with ethanol between each sample.
5. Store samples at −20°C until shipment to Duke University and upon arrival in Durham place samples back in the −20°C freezer.

WEIGHING

Note: As for the sifting step, we recommend that sifting be done in a humid area to keep airborne fecal dust to a minimum.

We use a high precision balance Denver Instruments Co. A-250.

1. Label 16x100 mm test tubes with sample ID by using an alcohol resistant marker.
2. Crease weighing paper diagonally, place on balance, and press TARE.
3. Weigh 0.20 grams (between 0.2000 and 0.2050 grams) of fecal powder. If there is not enough sample to attain 0.20 g, then record the exact weight on the data sheet. Cap tubes and place in rack.
4. Save the remaining fecal powder in a tube labeled with sample number and date.
5. Discard the vial and weighing paper into the biohazard waste. Rinse the tea strainer and spatula with ethanol between each sample.
6. Store tubes and fecal powder at −20°C until ready for methanol extraction.

On the excel datasheet, record the date the sample was weighed, the sample’s actual weight (particularly important when the sample is less than 0.2 g to correct the hormone concentration that is expressed in ng/g feces). If we have an extra tube of feces for that sample, record the amount of extra fecal powder we have and the location of the extra fecal tube (box # and position in the box).
METHANOL EXTRACTION

1. Add 2 ml of 90% methanol using a repeater pipette to each tube that contains the sifted fecal sample.
2. Cap tightly and place on multi-pulse vortexer, and vortex for 30 minutes.
   - Motor speed =70
   - Pulser =60
3. Centrifuge at 1 g (2300 rpm) for 20 minutes at room temperature (~25°C)
4. Transfer supernatant from 16x100 mm tubes to 1.5 ml eppendorf tubes using Pasteur pipettes.
5. Centrifuge the eppendorf tubes at 2 g (3200 rpm) in the microcentrifuge for 15 minutes.
6. Transfer supernatant to 2 ml microcentrifuge tubes and cap the tube (use a cap with an O-ring to avoid evaporation).
7. Place samples in storage boxes and store at –20°C until ready to assay.
8. Clearly label each box with the sample ID numbers.

SOLID PHASE EXTRACTION (SPE)

We use the Waters Oasis HLB cartridges (catalog # WAT 094226)
Remove samples from freezer and warm them up in 37°C water bath

Sample dilution:
1. Vortex tubes for about 10 sec
2. Place 800 µl of the methanol extract in 12x75 mm test tubes
3. Dry it down with pressurized air in 37°C water bath
4. Add 300 µl of 90% methanol
5. Vortex for about 30 sec
6. Add 700 µl of distilled water
7. Vortex again

Cartridge preparation:
1. Place cartridges (labeled with sample ID) on the cartridge support (a wooden support made in our lab containing 36 holes and a collection tray below it).
2. Wash the Oasis cartridges with 1 ml of 100% methanol (use Eppendorf Repeater pipette). Discard eluate.
3. Wash again with 1 ml of distilled water. Discard eluate.
4. Load diluted samples onto the cartridges. Discard eluate.
5. Rinse with 1 ml of 20% methanol. Discard eluate.

Sample elution:
1. Remove cartridges from wooden support and place into 16x100 mm test tubes.
2. Add 2 ml of 100% methanol. Let run through and collect eluate in tubes.
3. Dry with pressurized air in 37°C water bath.
4. Add 800 µL of 90% methanol. Vortex for 30 sec.
5. Transfer into 1.5 ml conical microcentrifuge tubes with O-ring cap.
6. Store samples at –20°C.
HORMONE ANALYSIS (using RadioImmunoAssay, RIA)

We used I\textsuperscript{125} clinical diagnostic kits from various vendors. We have modified each kit to work with the baboon fecal samples.

MP Biomedicals Corticosterone for Rats and Mice: Catalog #07-120102 (100 tube kit) or #07-120103 (200 tube kit). We use the kit at half the volumes suggested in the kit literature.

MP Biomedicals Total Estrogens: Catalog # 07-140202 (100 tube kit), or #07-140205 (500 tube kit). We use a quarter of the volume suggested in the kit literature for the standards and half the volume for the tracer, first and second antibody. The samples are diluted to a 1:200 dilution in the assay buffer. Sample dilutions are adjusted if the female is pregnant.

Progesterone: The tracer and standards are from MP Biomedicals (catalog # 07-170121 for tracer, catalog # 07-170130 for standards, catalog # 07-170171 for standard 0. The progesterone first antibody is the CL 425 (from C. Munro, UC Davis), diluted to 1:12000. And the second antibody is a Goat Anti-Mouse IgG (from Equitech-Bio catalog #GAMG-0100)

MP Biomedicals Testosterone: Catalog # 07-189102 (100 tube kit) or # 07-189105 (500 tube kit). We use one half of the volume suggested for the standards, tracer, first and second antibody.

**MP Biomedicals Corticosterone RIA**

1. Add standards and samples as follows:

<table>
<thead>
<tr>
<th>Tube number</th>
<th>Charcoal strip (µl)</th>
<th>Std or sample (µl)</th>
<th>Buffer (µl)</th>
<th>1st AB yellow (µl)</th>
<th>Tracer (blue) (µl)</th>
<th>Vortex, cover with parafilm and incubate at room T°C for 2 hr</th>
<th>2nd AB</th>
<th>Vortex</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC</td>
<td>1-2</td>
<td>-</td>
<td>400</td>
<td>-</td>
<td>100</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NSB</td>
<td>3-4</td>
<td>5, dry</td>
<td>150</td>
<td>-</td>
<td>100</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bo</td>
<td>5-6</td>
<td>5, dry</td>
<td>50</td>
<td>100</td>
<td>100</td>
<td>Vortex</td>
<td></td>
<td>250</td>
</tr>
<tr>
<td>Sdt 1-6</td>
<td>7-18</td>
<td>5, dry</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>Vortex, centrifuge at 4°C for 20 min at 3200 rpm</td>
<td></td>
<td>250</td>
</tr>
<tr>
<td>Ctl Low</td>
<td>19-20</td>
<td>-</td>
<td>50</td>
<td>100</td>
<td>100</td>
<td></td>
<td></td>
<td>250</td>
</tr>
<tr>
<td>Ctl High</td>
<td>21-22</td>
<td>-</td>
<td>50</td>
<td>100</td>
<td>100</td>
<td></td>
<td></td>
<td>250</td>
</tr>
<tr>
<td>Pool Low</td>
<td>23-24</td>
<td>5, dry</td>
<td>50</td>
<td>100</td>
<td>100</td>
<td></td>
<td></td>
<td>250</td>
</tr>
<tr>
<td>Pool Med</td>
<td>25-26</td>
<td>10, dry</td>
<td>50</td>
<td>100</td>
<td>100</td>
<td></td>
<td></td>
<td>250</td>
</tr>
<tr>
<td>Pool High</td>
<td>27-28</td>
<td>15, dry</td>
<td>50</td>
<td>100</td>
<td>100</td>
<td></td>
<td></td>
<td>250</td>
</tr>
<tr>
<td>Samples</td>
<td>29-198</td>
<td>10, dry</td>
<td>50</td>
<td>100</td>
<td>100</td>
<td></td>
<td></td>
<td>250</td>
</tr>
</tbody>
</table>

**NOTE:** “dry” indicates tubes to be dried down first with pressurized air (in water bath) Tubes 1-2 are not centrifuged. Cover samples with parafilm to avoid contamination.

2. After centrifugation place all tubes in a bucket of icy water.
3. Aspirate supernatant.
4. Load samples into gamma counter.
MP Biomedicals Total Estrogens RIA

Sample dilution (1:20)
- Vortex samples (30 secs)
- Add 25 µl of sample
- Add 475 µl of buffer

1. Add standards and samples as follows:

<table>
<thead>
<tr>
<th>Tube number</th>
<th>Std or sample (µl)</th>
<th>1:100 methanol in Buffer (µl)</th>
<th>Buffer (µl)</th>
<th>1st AB (yellow) (µl)</th>
<th>Tracer (blue) (µl)</th>
<th>Vortex, cover with parafilm and incubate at room T°C for 90 min</th>
<th>2nd AB</th>
<th>Vortex and incubate 1 hr at room T°C</th>
<th>Centrifuge at 4°C for 30 min at 3200 rpm</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC 1-2</td>
<td>-</td>
<td>175</td>
<td>175</td>
<td>-</td>
<td>50</td>
<td>Vortex, cover with parafilm and incubate at room T°C for 90 min</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>NSB 3-4</td>
<td>-</td>
<td>150</td>
<td>150</td>
<td>-</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
<tr>
<td>Bo 5-6</td>
<td>-</td>
<td>125</td>
<td>125</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
<tr>
<td>Sdt 1-6</td>
<td>7-18</td>
<td>125</td>
<td>-</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
<tr>
<td>Pool Low</td>
<td>19-20</td>
<td>250</td>
<td>-</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
<tr>
<td>Pool High</td>
<td>21-22</td>
<td>250</td>
<td>-</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
<tr>
<td>SPE Low</td>
<td>23-24</td>
<td>250</td>
<td>-</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
<tr>
<td>SPE Med</td>
<td>25-26</td>
<td>10</td>
<td>240</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
<tr>
<td>SPE High</td>
<td>27-28</td>
<td>20</td>
<td>230</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
<tr>
<td>Samples 29-198</td>
<td>25</td>
<td>225</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Centrifuge at 4°C for 30 min at 3200 rpm</td>
</tr>
</tbody>
</table>

2. Then proceed as indicated for corticosterone RIA.
**Progesterone RIA**

- Standards + tracer (MP Biomedicals)
- 1\textsuperscript{st} AB: CL 425 (C. Munro, UC Davis)
- 2\textsuperscript{nd} AB: Goat Anti-Mouse IgG (Equitech-Bio GAMG-0100)

*Buffer preparation:*

- RIA buffer: PBS/BSA/Tween buffer (1 liter):
  
  \[
  \begin{align*}
  &8\text{g NaCl} \\
  &0.2\text{g KCl} \\
  &1.44\text{g Na}_2\text{HPO}_4 \\
  &0.24\text{g NaH}_2\text{PO}_4
  \end{align*}
  \]

  Stir at low heat (Graduation 2 for heat on plate)
  Once dissolved add:
  \[
  \begin{align*}
  &1\text{g BSA (Bovine Serum Albumin)} \\
  &1\text{g Tween 80}
  \end{align*}
  \]
  After complete dissolution, adjust pH to 7.5 (add NaOH if pH lower than 7.5)

- PEG buffer: 5\% PEG in PBS buffer (1 liter):
  
  \[
  \begin{align*}
  &8\text{g NaCl} \\
  &0.2\text{g KCl} \\
  &1.44\text{g Na}_2\text{HPO}_4 \\
  &0.24\text{g NaH}_2\text{PO}_4
  \end{align*}
  \]

  Stir at low heat (Graduation 2 for heat on plate)
  Once dissolved add:
  \[
  \begin{align*}
  &50\text{ g PEG 8000 (Polyethylene Glycol)}
  \end{align*}
  \]
  After complete dissolution, adjust pH to 7.5 (add NaOH if pH lower than 7.5)

*Antibody and serum preparation:*

- 1\textsuperscript{st} AB (CL425)
  \[
  \begin{align*}
  &\text{d1/12000:} \\
  &40\mu\text{l 1}\text{st AB d1/10} \\
  &48\text{ ml PBS/BSA/Tween Buffer}
  \end{align*}
  \]

- Normal mouse serum 1\% (Sigma)
  \[
  \begin{align*}
  &500\mu\text{l serum} \\
  &49.5\text{ml PEG Buffer}
  \end{align*}
  \]

- 2\textsuperscript{nd} AB: Goat- Anti-Mouse IgG (Equitech-Bio GAMG-0100)
  \[
  \begin{align*}
  &\text{d1/100:} \\
  &10\text{ ml 2}\text{nd AB} \\
  &990\text{ ml PEG Buffer}
  \end{align*}
  \]
  (if only for 1 RIA: 2 ml of 2nd AB in 198 ml PEG Buffer)
1. Add standards and samples as follows:

<table>
<thead>
<tr>
<th>SDT</th>
<th>Tubes #</th>
<th>SPE pool (µl)</th>
<th>Sdt 1 or other (µl)</th>
<th>RIA Buffer (µl)</th>
<th>1st AB 1/12000 (µl)</th>
<th>Tracer (µl)</th>
<th>Mouse serum (µl)</th>
<th>2nd AB 1/100 (ml)</th>
<th>Incubate for 1hr at room T°C</th>
<th>Centrifuge at room T°C for 20mm at 3100 rpm</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC</td>
<td>1-2</td>
<td>-</td>
<td>-</td>
<td>1250</td>
<td>-</td>
<td>100</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>NSB</td>
<td>3-4</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>100</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>B0</td>
<td>5-6</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sdt 2</td>
<td>7-8</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sdt 3</td>
<td>9-10</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sdt 4</td>
<td>11-12</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sdt 5</td>
<td>13-14</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sdt 6</td>
<td>15-16</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sdt 7</td>
<td>17-18</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sdt 8</td>
<td>19-20</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>CTL</td>
<td>21-22</td>
<td>-</td>
<td>-</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>SPE pool</td>
<td>23-24</td>
<td>5, dry</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>SPE pool</td>
<td>25-26</td>
<td>10, dry</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>SPE pool</td>
<td>27-28</td>
<td>20, dry</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Samples</td>
<td>29-198</td>
<td>10, dry</td>
<td>50</td>
<td>-</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
</tbody>
</table>

2. Then proceed as indicated for corticosterone RIA.
# MP Biomedicals testosterone RIA

1. Add standards and samples as follows:

<table>
<thead>
<tr>
<th>Tubes number</th>
<th>Std or sample (µl)</th>
<th>Sdt 1 (µl)</th>
<th>Diluent</th>
<th>Tracer (µl)</th>
<th>1st AB (µl)</th>
<th>2nd AB (µl)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC</td>
<td>1-2</td>
<td></td>
<td>325</td>
<td>250</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>NSB</td>
<td>3-4</td>
<td>25</td>
<td>250</td>
<td>250</td>
<td>50</td>
<td>50</td>
</tr>
<tr>
<td>Bo Sdt1</td>
<td>5-6</td>
<td>25</td>
<td>-</td>
<td>-</td>
<td>250</td>
<td>250</td>
</tr>
<tr>
<td>Sdt 2</td>
<td>7-8</td>
<td>25</td>
<td>-</td>
<td>-</td>
<td>250</td>
<td>250</td>
</tr>
<tr>
<td>Sdt 3</td>
<td>9-10</td>
<td>25</td>
<td>-</td>
<td>-</td>
<td>250</td>
<td>250</td>
</tr>
<tr>
<td>Sdt 4</td>
<td>11-12</td>
<td>25</td>
<td>-</td>
<td>-</td>
<td>250</td>
<td>250</td>
</tr>
<tr>
<td>Sdt 5</td>
<td>13-14</td>
<td>25</td>
<td>-</td>
<td>-</td>
<td>250</td>
<td>250</td>
</tr>
<tr>
<td>Sdt 6</td>
<td>15-16</td>
<td>25</td>
<td>-</td>
<td>-</td>
<td>250</td>
<td>250</td>
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</table>

Vortex, cover with parafilm and incubate at room T°C overnight 12-24hrs

Centrifuge at 4°C for 30 min at 3200 rpm

2. Then proceed as indicated for corticosterone RIA.
Charcoal: Carbon decoloring alkalin Norit A, Fisher # C176

Wash charcoal:
1. Put charcoal in beaker, then add distilled water.
2. Let the charcoal settle for a few hours or longer, then pipette off the charcoal that floats to the top and pour off and discard most of the liquid.
3. Then pour the charcoal into an aluminum foil-lined box and spread the charcoal out under the hood to dry.

To charcoal strip:
1. Take 10 ml of pool fecal extract in 90% methanol. Add 250 mg of washed charcoal (the ratio should be 50 mg charcoal/2 ml suspension).
2. Stir slowly with stir bar for 1 hr at room temperature.
3. Centrifuge at 2 g for 10 minutes.
4. Pipette off liquid and push through a 0.2 µm filter with a syringe; discard charcoal. The resultant liquid should be clear.
5. To double charcoal strip: Repeat steps 2 through 5.

Preparation of the SPE pool
1. Place 0.2 g of the fecal pool in 16x100 mm test tubes.
2. Do a methanol extraction (Follow the usual protocol)
3. Then conduct SPE (Follow the usual protocol)
4. Pool all the tubes together. Vortex again.
5. Place aliquots of 2 ml in microcentrifuge tubes and store at –20°C.

¹Thanks to Emanuel Wango, in whose Nairobi laboratory some preparatory and storage stages are conducted; to Michela Hau, Samuel Wasser, Patricia Whitten, Coralie Munro and especially Toni Ziegler for advice as we developed procedures; to the lab members in Nairobi and Princeton who provided feedback as users; and to the National Science Foundation, the National Institutes of Health, and Princeton University for laboratory support.