**Hormone physiology and sleep dynamics among BaYaka foragers of the Congo Basin: gendered associations between nighttime activity, testosterone, and cortisol**

Gettler et al.

\*Codebook

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We used through structural equation modeling via Stata’s “sem” command with option “mlmv,” which prevents casewise omission for missing data, to generate latent variables for nighttime activity (mobile minutes) and total sleep time (TST).

**Variables in file “Gettler Bayaka testosterone sleep data (shared)”**

newid: participant identifier

logt: natural log-transformed testosterone data

men: 0 = women; 1 = men

parent\_infant: 0 = not parent to an infant; 1 = parent to an infant

age = BaYaka age estimates following (Diekmann et al., 2017)

tri\_skinfold = triceps skinfold thickness (mm)

woke\_avg = average wake time on days of cortisol saliva collection

naptime\_avg = average daily naptime

mobileminz = nighttime activity (mobile minutes) during the main sleep period following z-score transformation (SD units) of the latent variable generated through structural equation modeling

tstz = total sleep time (TST) during the main sleep period following z-score transformation (SD units) of the latent variable generated through structural equation modeling

**Table 2**

We used Stata’s mixed command in each of our models, and we used Stata’s margins and dydx command to conduct follow-up analyses following statistically significant interactions.

In each model, “logt” is the dependent variable. We include an example of code for Model 2 in Table 2.

mixed logt i.men##c.mobileminz age parent\_infant tri\_skinfold woke\_avg naptime\_avg || newid:

margins, dydx(mobileminz) at(men=0)

margins, dydx(mobileminz) at(men=1)

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**Variables in file “Gettler Bayaka cortisol sleep data (shared)”**

newid: participant identifier

logcort: natural log-transformed cortisol data

men: 0 = women; 1 = men

parent\_infant: 0 = not parent to an infant; 1 = parent to an infant

age = BaYaka age estimates following (Diekmann et al., 2017)

tri\_skinfold = triceps skinfold thickness (mm)

woke\_avg = average wake time on days of cortisol saliva collection

naptime\_avg = average daily naptime

mobileminz = average nighttime activity (mobile minutes) during the main sleep period following z-score transformation (SD units)

tstz = average total sleep time (TST) during the main sleep period following z-score transformation (SD units)

timecenter = time of day centered according to the first saliva sample timing (near waking)

**Table 3**

We used Stata’s mixed command in each of our models. Following statistically significant interactions, we used Stata’s margins and dydx command to conduct follow-up “spotlight” analyses comparing the slopes for high (+1 SD) and low (-1 SD) values of the sleep-related moderator variables.

In each model, “logcort” is the dependent variable. We include an example of code for Model 2 in Table 3.

mixed logcort c.mobileminz##c.timecenter##i.men c.age##c.timecenter parent\_infant tri\_skinfold woke\_avg naptime\_avg || newid:

margins, dydx(timecenter) at( mobileminz=(-1 1) men=(1)) pwcompare(effects)

margins, dydx(timecenter) at( mobileminz=(-1 1) men=(0)) pwcompare(effects)

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**Variables in file “Gettler Bayaka cortisol sleep sequential days data (shared)”**

newid: participant identifier

logcort: natural log-transformed cortisol data

men: 0 = women; 1 = men

parent\_infant: 0 = not parent to an infant; 1 = parent to an infant

age = BaYaka age estimates following (Diekmann et al., 2017)

tri\_skinfold = triceps skinfold thickness (mm)

wokeup\_time = wake time on the day of cortisol saliva collection

naptime = daily naptime on the day of data collection

mobileminz = average nighttime activity (mobile minutes) during the main sleep period following z-score transformation (SD units)

tstz = average total sleep time (TST) during the main sleep period following z-score transformation (SD units)

timecenter = time of day centered according to the first saliva sample timing (near waking)

percmvpa = daily activity intensity on the day of cortisol saliva collection

**Supp. Table 1**

We used Stata’s mixed command in each of our models. We used Stata’s margins and dydx command to conduct follow-up “spotlight” analyses comparing the slopes for high (+1 SD) and low (-1 SD) values of the sleep-related moderator variables.

In each model, “logcort” is the dependent variable. We include an example of code for the model shown in Supp. Table 1.

mixed logcort c.mobileminz##c.timecenter##i.men c.age##c.timecenter parent\_infant tri\_skinfold wokeup\_time naptime percmvpa || newid:

margins, dydx(timecenter) at( mobileminz=(-1 1) men=(1)) pwcompare(effects)

margins, dydx(timecenter) at( mobileminz=(-1 1) men=(0)) pwcompare(effects)