Appendix 1. Multistate mark-recapture model used in the integrated population model to analyze capture-mark-recapture and recovery data.

True states:

1: juvenile alive, aluminum ring
2: adult alive, aluminum ring
3: adult alive physically captured and alphanumeric ring fixed,
4: adult alive resighted with alphanumeric ring
5: recently dead
6: long time dead

Transition matrix

\[
\begin{pmatrix}
0 & S_1(1-a) & S_1a & 0 & 1 - S_1 & 0 \\
0 & S_2(1-a) & S_2a & 0 & 1 - S_2 & 0 \\
0 & 0 & 0 & S_2 & 1 - S_2 & 0 \\
0 & 0 & 0 & S_2 & 1 - S_2 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 \\
0 & 0 & 0 & 0 & 0 & 1 \\
\end{pmatrix}
\]

Vector with state-specific recapture probabilities

\[
\begin{pmatrix}
0 \\
p \\
l \\
c \\
r \\
0 \\
\end{pmatrix}
\]

Parameters:

\(S_1\): Juvenile survival
\(S_2\): Adult survival
\(a\): Probability that an alphanumeric ring is fixed on an individual
\(p\): Recapture probability of an adult with aluminum ring only
\(c\): Resighting probability of an adult with both aluminum and an alphanumeric ring
\(r\): Dead recovery probability
Appendix 2. JAGS code to fit the integrated population model for the Swiss Eurasian kestrel (*Falco tinnunculus*) population breeding in nest-boxes.

cat(file = "ipm.jags", "
model {

### Priors and constraints

# Demographic traits
for (t in 1:(n.occasions-1)){
  sj[t] <- 1/(1+exp(-logit.sj[t]))
  logit.sj[t] ~ dnorm(l.mean.sj, tau.sj)
  sa[t] <- 1/(1+exp(-logit.sa[t]))
  logit.sa[t] ~ dnorm(l.mean.sa, tau.sa)
  a[t] <- 1/(1+exp(-logit.a[t]))
  logit.a[t] ~ dnorm(l.mean.a, tau.a)
  p[t] <- 1/(1+exp(-logit.p[t]))
  logit.p[t] ~ dnorm(l.mean.p, tau.p)
  c[t] <- 1/(1+exp(-logit.c[t]))
  logit.c[t] ~ dnorm(l.mean.c, tau.c)
  r[t] <- 1/(1+exp(-logit.r[t]))
  logit.r[t] ~ dnorm(l.mean.r, tau.r)
  p.success[t] <- 1/(1+exp(-logit.p.success[t]))
  prod[t] ~ dnorm(mean.prod, tau.prod)
  I[t] ~ dnorm(mean.I, tau.I)
}

l.mean.sj <- log(mean.sj / (1-mean.sj))
mean.sj ~ dunif(0, 1)

l.mean.sa <- log(mean.sa / (1-mean.sa))
mean.sa ~ dunif(0, 1)

l.mean.a <- log(mean.a / (1-mean.a))
mean.a ~ dunif(0, 1)

l.mean.p <- log(mean.p / (1-mean.p))
mean.p ~ dunif(0, 1)

l.mean.c <- log(mean.c / (1-mean.c))
mean.c ~ dunif(0, 1)

l.mean.r <- log(mean.r / (1-mean.r))
mean.r ~ dunif(0, 1)

mean.p.success ~ dunif(0, 1)

mean.prod ~ dunif(0, 10)
mean.I ~ dunif(-5, 5)

tau.sj <- pow(sigma.sj, -2)
sigma.sj ~ dunif(0.001, 10)
tau.sa <- pow(sigma.sa, -2)
sigma.sa ~ dunif(0.001, 10)
tau.a <- pow(sigma.a, -2)
sigma.a ~ dunif(0.001, 10)
tau.p <- pow(sigma.p, -2)
sigma.p ~ dunif(0.001, 10)
tau.c <- pow(sigma.c, -2)
sigma.c ~ dunif(0.001, 10)
tau.r <- pow(sigma.r, -2)
sigma.r ~ dunif(0.001, 10)
tau.prod <- pow(sigma.prod, -2)
sigma.prod ~ dunif(0.001, 20)
tau.p.success <- pow(sigma.p.success, -2)
sigma.p.success ~ dunif(0.001, 3)
tau.I <- pow(sigma.I, -2)
sigma.I ~ dunif(0.001, 5)

# Population count
sigma.fit ~ dunif(0, 50)
tau.fit <- pow(sigma.fit, -2)

# Derived and other quantities
mean.fec <- mean(fec)
mean.lambda <- mean(lambda)

# Define state-transition and observation probabilities for the mark-recapture-recovery model
for (t in 1:(n.occasions-1)){
  ps[1,t,1] <- 0
  ps[1,t,2] <- sj[t]*(1-a[t])
  ps[1,t,3] <- sj[t]*a[t]
  ps[1,t,4] <- 0
  ps[1,t,5] <- 1-sj[t]
  ps[1,t,6] <- 0

  ps[2,t,1] <- 0
  ps[2,t,2] <- sa[t]*(1-a[t])
  ps[2,t,3] <- sa[t]*a[t]
  ps[2,t,4] <- 0
  ps[2,t,5] <- 1-sa[t]
  ps[2,t,6] <- 0

  ps[3,t,1] <- 0
  ps[3,t,2] <- 0
  ps[3,t,3] <- 0
  ps[3,t,4] <- sa[t]
  ps[3,t,5] <- 1-sa[t]
  ps[3,t,6] <- 0

  ps[4,t,1] <- 0
  ps[4,t,2] <- 0
  ps[4,t,3] <- 0
  ps[4,t,4] <- sa[t]
for (s in 2:ns) {
  for (u in 1:ns) {
    po[s,t,u] <- po[1,t,u]
  }
}

for (s in 1:ns) {
  for (u in 1:ns) {
    qo[s,t,u] <- 1-po[s,t,u]
  }
}

### Define the multinomial likelihood for the mark-recapture-recovery model (data in m-array format)
for (t in 1:((n.occasions-1)*ns)) {
  marr[t,1:(n.occasions*ns-(ns-1))] ~ dmulti(pr[t,], rel[t])
}

## Define the cell probabilities of the m-array
# Define matrix Q: product of probabilities of survival and non-capture
for (t in 1:(n.occasions-2)) {
  Q[(t-1)*ns+(1:ns), (t-1)*ns+(1:ns)] <- ones
for (j in (t+1):(n.occasions-1)) {
    Q[(t-1)*ns+(1:ns), (j-1)*ns+(1:ns)] <- Q[(t-1)*ns+(1:ns), (j-2)*ns+(1:ns)] %*% (ps[,t] * qo[,t])
}

Q[(n.occasions-2)*ns+(1:ns), (n.occasions-2)*ns+(1:ns)] <- ones

# Define the cell probabilities of the multistate m-array
# The main diagonal
for (t in 1:(n.occasions-2)) {
    pr[(t-1)*ns+(1:ns), (t-1)*ns+(1:ns)] <- Q[(t-1)*ns+(1:ns), (t-1)*ns+(1:ns)] %*% (ps[,t] * po[,t])
}

# Above main diagonal
for (j in (t+1):(n.occasions-1)) {
    pr[(t-1)*ns+(1:ns), (j-1)*ns+(1:ns)] <- Q[(t-1)*ns+(1:ns), (j-1)*ns+(1:ns)] %*% (ps[,j] * po[,j])
}

pr[(n.occasions-2)*ns+(1:ns), (n.occasions-2)*ns+(1:ns)] <-
    ps[,n.occasions-1] * po[,n.occasions-1,]

# Below main diagonal
for (t in 2:(n.occasions-1)) {
    for (j in 1:(t-1)) {
        pr[(t-1)*ns+(1:ns), (j-1)*ns+(1:ns)] <- zero
    }  # j
}

# Last column: probability of non-recapture
for (t in 1:((n.occasions-1)*ns)) {
    pr[t,(n.occasions*ns-(ns-1))] <- 1-sum(pr[t,((n.occasions-
    1)*ns)])
}  # t

## Likelihood for logistic and normal regression models for
# reproductive success and productivity data
for (t in 1:(n.occasions-1)) {
    n.success[t] ~ dbin(p.success[t], n.brood[t])
    for (i in 1: n.product[t]) {
        n.chick[i,t] ~ dnorm(prod[t], tau.prod)
    }
    fec[t] <- p.success[t] * prod[t]
}

## Likelihood for the state-space model
# Initial state
N[1,1] ~ dunif(5, 25)
N[2,1] ~ dunif(5, 25)
# Population projection (state process)
for (t in 1:(n.occasions-1)){
    N[1,t+1] <- fec[t]/2 * sj[t] * (0.35*N[1,t] + N[2,t]) + (N[1,t] +
    N[2,t]) * I[t]
    N[2,t+1] <- sa[t] * (N[1,t] + N[2,t])

    # Growth rate
    lambda[t] <- Ntot[t+1]/Ntot[t]
}

# Observation model
for (t in 1:n.occasions){
    C[t] ~ dnorm(Ntot[t], tau.fit)
    count[t] ~ dnorm(C[t], sd.count[t])

    # Total population size
    Ntot[t] <- N[1,t] + N[2,t]
}

# Total population size
Ntot[t] <- N[1,t] + N[2,t]

# Bundle data
# Number of states
ns <- length(unique(as.numeric(ch.new))) + 1
jags.data <- list(marr = ms.arr, n.occasions = ncol(ch.new), rel =
    rowSums(ms.arr), ns = ns, zero = matrix(0, ncol = ns, nrow = ns), ones
    = diag(ns), n.chick = n.chick, n.success = n.success, n.brood =
    n.brood, n.product = n.product, count = count, sd.count = sd.count)

# Initial values
inits <- function(){list()

    parameters <- c("l.mean.sj", "l.mean.sa", "mean.sj", "mean.sa",
    "mean.fec", "mean.p.success", "mean.prod", "mean.I", "mean.lambda",
    "sigma.sj", "sigma.sa", "sigma.p.success", "sigma.prod", "sigma.fit",
    "lambda")

# MCMC settings
ni <- 100000
nt <- 10
nb <- 40000
nc <- 3

# Call JAGS from R (BRT 1 min)
IPM <- jags(jags.data, inits, parameters, "ipm.jags", n.chains = nc,
             n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)
Appendix 3. Goodness-of-Fit tests for the different model components of the IPM.

We assessed the goodness-of-fit (GOF) for all model components of Bayesian IPM. For the capture-recapture-recovery model we performed GOF tests using the program U-CARE (v.2.3.2, Choquet et al. 2009b). For the other models (logistic regression for breeding success, normal regression for productivity and population index) we conducted posterior predictive checks using the Freeman-Tukey statistic. We performed a graphical assessment and computed Bayesian p-values for the discrepancy statistics (Gelman et al. 2004).

The GOF tests ($\chi^2 = 48.5, P = 0.61$) provided no indication of lack of fit for the capture-recapture-recovery model. We found neither support for transience ($\chi^2 = 16.93, P = 0.08$) nor for trap dependence ($\chi^2 = 10.47, P = 0.40$).

The next figure shows the posterior predictive check of a logistic regression to the breeding success data. The solid line represents the 1:1 line. The test suggested no lack of fit between observed and replicated data (Bayesian $P$-value = 0.53).

The next figure shows the posterior predictive check of a normal regression to the productivity data. The solid line represents the 1:1 line. The test suggested no lack of fit between observed and replicated data (Bayesian $P$-value = 0.51).
Posterior predictive check of model adequacy of a normal regression to the population index. The solid line represents the 1:1 line. The test suggested no lack of fit between observed and replicated data (Bayesian $P$-value = 0.50).
Literature Cited


Appendix 4. Parameter uncertainty and sensitivity analysis

Breeding probability of one year-old (i.e. recruitment probability) and adult individuals could not be estimated from our dataset since we lack information on the breeding state of individuals that were recaptured alive. Kestrels may recruit at the age of one year but an unknown proportion of individuals is likely to delay their first reproduction. We found no estimates of recruitment probability for kestrels in the literature, but several studies reported the proportion of 1-year old breeders in the breeding population. This value ranges from 0.15 to 0.39 (Dijkstra et al., 1990; Laaksonen, Lyytinen, & Korpimäki, 2004; Schifferli, 1964; Village, 1990). A preliminary analysis showed that a recruitment probability of 0.35 results in a proportion of 0.15 of 1-year old breeders (CRI = [0.13, 0.17]) in our integrated population model. Thus we used 0.35 as recruitment probability in our IPM. As we investigated the sink-source state of this population, we preferred a conservative estimate that underestimates rather than overestimates the recruitment probability.

We also needed to deal with the adult breeding probability. Although non-breeding individuals may be pervasive in populations (Newton, 1998), they are poorly studied. For the kestrel, there is to our knowledge only a single estimate of the adult non-breeding component that originates from Village (1990). Based on an intense monitoring of a breeding population, Village estimated that the percentage of unpaired adult females reaches 21% (average over 6 years, Village 1990 Table 67). In addition, (Village, 1990) reported that around 10% of the pairs failed to lay eggs. To assess the sensitivity of our model to this uncertainty, we ran integrated population models using a range of different adult breeding probabilities. We considered values ranging from 1 to 0.70 assuming that this range includes the true unknown value for our population.

Literature Cited


Appendix 5. Effects of nest types on fecundity

We reviewed the literature on reproduction of kestrels to investigate the effects of nest types on fecundity. We only included studies reporting the fecundity as the average number of fledglings per reproductive attempt and the type of nest used. From each study we recorded sample size (number of clutches monitored) and study duration. We defined three categories of nest types that reflect their openness. First, nest boxes that gather all types of nest boxes designed to fit the requirements of kestrels. Second, natural cavities that include tree cavities, cavities in buildings, more generally all nests on man-made structures and cliffs. This category includes both closed and semi-closed nests, but nest descriptions were generally not precise enough to define more accurate classes. Finally, open nests include old stick nests of birds, often of corvid species. When available, we recorded clutch size, hatching success (number of chicks hatched against clutch size) and chick survival (number of chicks reaching the ringing age against the number of chicks hatched). A statistical meta-analysis was performed to test the effect of nest types on fecundity. We fitted a Gaussian mixed model in a Bayesian framework. Fecundity was modeled as a function of nest type and the variance of the population random effect was inversely proportional to the sample size and the length of the study. The code of the model implemented in JAGS is available in the appendix.

To quantify the effect of nest boxes in the observed population dynamics, we ran a second time the integrated population model assuming absence of nest boxes by removing the effect of nest-box on fecundity. We subtracted from the observed fecundity the difference of the average number of fledglings between nest boxes and natural cavity and open nests, respectively. We compared the resulting changes in net dispersal rate between the models. In the absence of nest boxes, kestrels breed mainly in open nests in Switzerland. In a local study, Jeanmonod & Broch (2001) reported that around 80% of kestrels were breeding on trees in disused nests of other species. To assess the potential role of nest boxes on the population dynamics we therefore first compared fecundity obtained in nest boxes and fecundity obtained in open nests. We also assessed a scenario under which 80% of kestrels breed in open nests and 20% in natural cavities. These simulations all assume that survival is not affected by the nest type. We discuss in appendix 7 the effect of a violation of this assumption on the results.

Literature Cited

Appendix 6. JAGS code for the meta-analysis investigating the effect of the nest type on fecundity in the Eurasian kestrel (*Falco tinnunculus*).

cat(file = "weighted_regression.jags", "

model {
  # Priors and constraints
  beta01 ~ dunif(-5, 5)
  beta02 ~ dunif(-5, 5)
  tau.eps <- pow(sigma.eps, -2)
  sigma.eps ~ dunif(0.001, 10)

  for (i in 1:3){
    alpha[i] ~ dunif(0, 5)
  }

  #Likelihood
  for (i in 1:n){
    BS[i] ~ dnorm(mu[i], tau[i])
    mu[i] <- alpha[Nest_type[i]]
    tau[i] <- pow(sigma[i], -2)
    sigma[i] <- exp(beta01 * Study_duration[i] + beta02 * Sample_size[i] + eps[i])
    eps[i] ~ dnorm(0, tau.eps)
  }
}
Appendix 7. Discussion of the modelling assumptions and of the effect of their violation on the results.

The dispersal rates are highly challenging to estimate (Abadi et al., 2010) and not surprisingly most of the studies assessing the source/sink state of a population do not estimate these parameters (Furrer and Pasinelli, 2016). Because our data were analysed with an integrated population model, it was possible to estimate the net dispersal rate. The IPM relies on assumptions and it is important to assess whether the potential violation of these assumptions compromise the inference. Some of the assumptions can be assessed by goodness-of-fit tests (see appendix 3) but for others this is not possible. Here we discuss these latter assumptions and the potential effects of their violations.

The IPM assumed that dispersal occurs only at age 1 year. We made this assumption because it is not possible to estimate both natal and breeding dispersal given the available data. If the IPM is formulated with both processes, the parameters would not be separately identifiable. This assumption is reasonable given the large scale of our study area and the stronger propensity of juveniles to disperse relatively to adults. Terraube et al. 2015 found that the average breeding dispersal distance is 17.8 km for female and Paradis et al. (1998) reported an average breeding dispersal of 14.8 km. Thus breeding dispersal occurs in average over relatively short distance compared to our study area. In kestrels like in birds in general, juveniles disperse over longer distance than adult (Greenwood 1980). Paradis et al. (1998) found that natal dispersal distances in kestrels were roughly 3 times higher than breeding dispersal distances. Because natal dispersal is much more important than breeding dispersal, we preferred to assume that only natal dispersal occurs. However, the violation of this assumption has minor consequences in our case because the IPM only included two age classes (1 year old and >1 year old) with equal survival rates. Thus, whatever the age of the dispersers, they will move from population pools where all individuals have fairly similar vital rates. Pooling all individuals older than 1 year into the same age class is itself a simplifying assumption. This simplification is seen frequently in models for short lived birds (i.e. Robinson et al. 2014) like kestrels (breeding may start at one year, clutch size of 5 eggs, life expectancy less than 10 years). Consistently with this assumption, survival stabilizes after the first year of life in kestrels (Village 1990). Ignoring senescence has a minor effect in our case because we sampled adults of unknown age meaning that we estimated averaged productivity and survival rates relatively to the age rather than extrapolating vital rates of young adult to all age classes (Robert et al. 2015). A further assumption was that the vital rates did not differ among sexes. If adult survival is strongly affected by sex, the IPM may produce biased estimates. However, survival of kestrels is expected to be little affected by the sex (Newton 2016) and field observations are consistent with an equilibrate sex-ratio.

The IPM included two demographic parameters that were not estimated from our datasets, i.e. the recruitment probability at one year of age and the adult breeding frequency. Values for these parameters were therefore fixed in the IPM. For the recruitment probability, we used the lowest known values in order to be conservative regarding the assessment of a source status. Higher
values of recruitment probability would result in lower values of the net dispersal rate i.e. stronger emigration, corroborating inference that the population is a source. For the adult breeding probability we have run a sensitivity analysis to assess how much the main results were affected by the uncertainty regarding this parameter. We used different values reflecting values reported in the literature (0.7, 0.8, 0.9 and 1) showing that this uncertainty did not affect the main conclusion of this study (Fig. 3, A3). The lowest value that we used originated from a population that is limited by nest site availability (Village 1990) which is currently not the case in our study area. Thus, again we considered conservative values regarding the assessment of a source status.

Finally, we used simulations to investigate the effect of nest type on kestrel population dynamics. In these simulations we assumed that only fecundity but not the survival of adults was affected by the nest type, i.e. we assumed no covariation between survival and reproduction. Yet nest type may affect both reproduction and survival. In particular nest boxes may positively affect survival for the same reason they increase breeding success (i.e. lower predation risk and less exposure to adverse weather events, Libois et al. 2012). To quantify the potential impact of positive covariation of survival and breeding success, we ran an integrated population model under the assumption that individuals breeding in natural nests suffered not only lower fecundity, but also a 3% and a 10% lower adult survival rate compared to individuals breeding in nest boxes. Results show that the advantage of using nest boxes becomes stronger (Fig. A4). Thus our assessment regarding the advantage of nest boxes on kestrel population dynamics is conservative.
Appendix 8. Additional figures and tables.

Figure A1. Posterior distribution of the average fecundity according to the nest type. Dashed lines show the modes. Estimates are obtained from the meta-analysis on the studies presented in the table A1.

The probability that the fecundity in nest-boxes was higher than in natural cavities and open nests was 0.96 and 1, respectively. The probability that the fecundity is higher in a natural cavity compared to an open nest is 0.95.
Figure A2. Distribution of the average clutch size, hatching success and chick survival according to nest type in the Eurasian kestrel (*Falco tinnunculus*). Estimates are obtained from the meta-analysis on the studies presented in the table A1. The sample size, i.e. the number of populations monitored for each distribution, is provided by n.
Figure A3. Posterior means with 95% credible intervals of the average net dispersal rate over the study period (2002-2016) obtained from the integrated population model according to different values of adult breeding probability. Results are given considering the fecundity estimate from our studied population breeding in nest boxes (filled point) and with a simulated fecundity corresponding to 80% of birds breeding in open nest and 20% in natural cavity nest (appendix 5).
Figure A4. Posterior means with 95% credible intervals of the average net dispersal rate over the study period (2002-2016) obtained from integrated population models with different values of adult breeding probability. Results are given considering the fecundity estimate from our studied population breeding in nest boxes (closed dots) and with simulated fecundities assuming that all kestrels either breed in natural cavities (closed triangles) or in open nests (open dots). We investigated the effect of a positive covariation between reproduction and adult survival by simulation. We assumed that adult survival was either 3% ($S_2=0.70$, panel A) or 10% ($S_2 = 0.65$, panel B) lower when the birds used open nests for breeding compered to when they used nest boxes (see Fig. 3).
**Figure A5.** Locations of recovered adult kestrels that have been ringed as nestling within the study area (gray). Black dots show recoveries within the study area and red dots recoveries outside the study area.

To ensure that migratory movements are excluded as much as possible, we included only recoveries that were obtained during the breeding period (from the 1 April to 15 August). From the total number of 221 recoveries, 88 (40%) originated from outside the study area.
**Table A1.** Review of studies investigating reproductive parameters of Eurasian kestrels (*Falco tinnunculus*).

We only included studies reporting estimates of fecundity (defined as the average number of fledglings per reproductive attempt) and the type of nest used (NB: nest-box, NC: natural cavity, ON: open nest). When available, we considered hatching success (number of chicks hatched against clutch size) and chick survival (number of chicks reaching the ringing age against the number of chicks hatched). Sample sizes for clutch size, hatching success, chick survival and fecundity are given in brackets. For some studies sample size was not provided explicitly for each reproductive parameter. In this case we provided an estimated sample size and those are indicated by “*”.

<table>
<thead>
<tr>
<th>Nest type</th>
<th>Location</th>
<th>Study duration</th>
<th>Clutch size</th>
<th>Hatching success</th>
<th>Chick survival</th>
<th>Fecundity</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>NB</td>
<td>Spain (Extremadura)</td>
<td>1 (1989)</td>
<td>4.2 (136)</td>
<td>0.79 (131)</td>
<td>NA</td>
<td>3.7 (124)</td>
<td>Avilès et al. 2001</td>
</tr>
<tr>
<td>NB</td>
<td>Germany (Berlin)</td>
<td>3 (2002-2004)</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>4.7 (30)</td>
<td>Kübler et al. 2005</td>
</tr>
<tr>
<td>NB</td>
<td>Italy (Parma)</td>
<td>4 (2007, 2009-2011)</td>
<td>5.25 (109)</td>
<td>0.81 (107)</td>
<td>0.96 (106)</td>
<td>4.2 (113)</td>
<td>Costantini et al. 2014</td>
</tr>
<tr>
<td>NB</td>
<td>Germany (Bielefeld)</td>
<td>15 (1972-1987)</td>
<td>5.3 (23)</td>
<td>0.80 (122)</td>
<td>0.93 (98)</td>
<td>4.0 (23)</td>
<td>Hasenclever et al. 1989</td>
</tr>
<tr>
<td>NB</td>
<td>Spain (Avila, Segovia)</td>
<td>6 (1993-1998)</td>
<td>5.0 (84)</td>
<td>NA</td>
<td>NA</td>
<td>3.7 (79)</td>
<td>Fargallo et al. 2001</td>
</tr>
<tr>
<td>NB</td>
<td>Israel</td>
<td>4 (2003-2006)</td>
<td>5.0 (101)</td>
<td>0.71 (103)</td>
<td>0.89 (91)</td>
<td>3.2 (124)</td>
<td>Charter et al. 2007a</td>
</tr>
<tr>
<td>NB</td>
<td>Israel (Jordan Rift Valley)</td>
<td>8 (1999-2006)</td>
<td>4.9 (31)</td>
<td>0.65 (32)</td>
<td>0.90 (26)</td>
<td>3.0 (37)</td>
<td>Charter et al. 2007b</td>
</tr>
<tr>
<td>NB</td>
<td>Finland (Ostrobothnia)</td>
<td>11 (1985-1995)</td>
<td>5.6 (178)</td>
<td>NA</td>
<td>NA</td>
<td>3.8 (180)</td>
<td>Valkama &amp; Korpimäki 1999</td>
</tr>
<tr>
<td>NB</td>
<td>France (Côte d'or)</td>
<td>21 (1992-2012)</td>
<td>4.5 (54)</td>
<td>0.72 (49)</td>
<td>0.98 (49)</td>
<td>2.9 (49)</td>
<td>Sternna &amp; Boileau 2013</td>
</tr>
<tr>
<td>NB</td>
<td>Czech Republic (Hradec Králové)</td>
<td>4 (1986-1989)</td>
<td>4.9 (224)</td>
<td>NA</td>
<td>NA</td>
<td>4.3 (224)</td>
<td>Plesník &amp; Dvůr 1994</td>
</tr>
<tr>
<td>NB</td>
<td>Germany (Berlin)</td>
<td>5 (1989)</td>
<td>5.1 (50)</td>
<td>0.86 (169)</td>
<td>0.95 (141)</td>
<td>4.2 (141)</td>
<td>Schmid 1990</td>
</tr>
<tr>
<td>NC</td>
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<td>Carrillo &amp; González-Dávila 2005</td>
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