

Afsplitsen of
samenvoegen

wat verklaart de
variatie in
populatiestructuur
in steltlopers?



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ondersoorten in steltlopers: “habitat dichotomie”

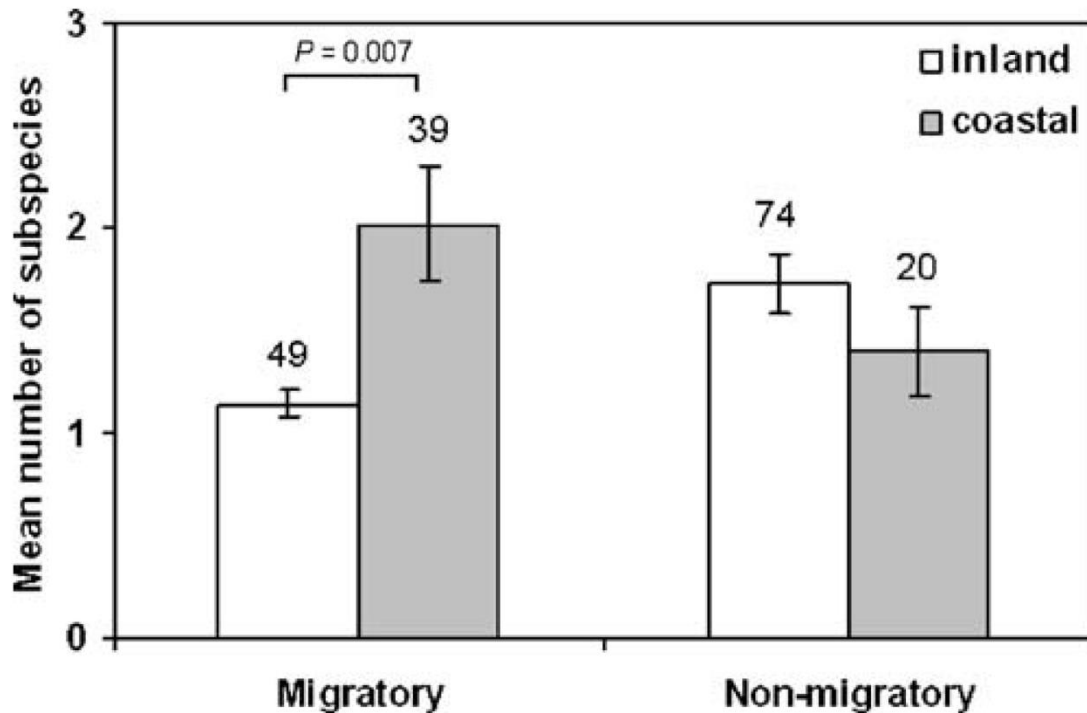
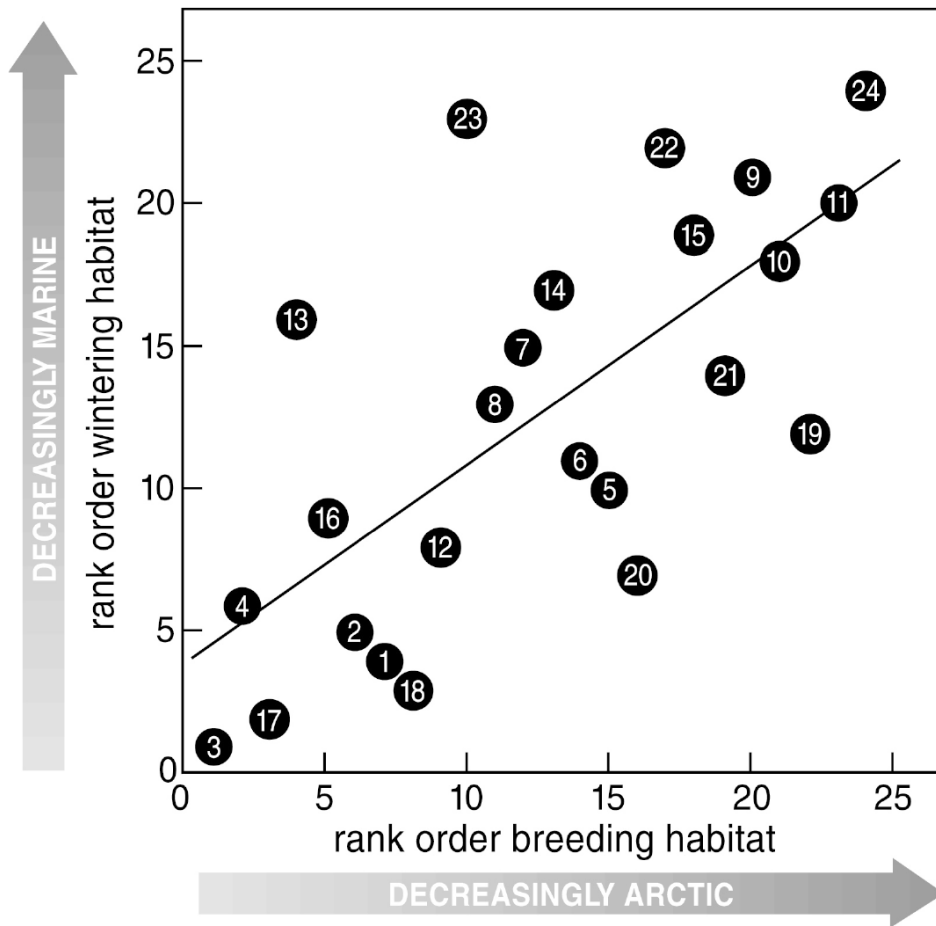


Fig. 1 Mean number of sub-species per species for migratory and non-migratory waders. Pelagic wintering species ($N=2$) and partial migrants ($N=31$) not shown. *Error bars* represent the Poisson standard errors

trekkende
steltlopers die
's winters
kustgebonden
zijn hebben
meer
ondersoorten

“habitat dichotomie”: jaarrond correlatie leefgebieden



kustgebonden
steltlopers broeden
meestal in Arctische
gebieden

- *weinig leefgebied*
- *populaties kunnen snel afnemen: 'bottlenecks'*

is habitat inderdaad belangrijke factor in
populatievorming in steltlopers?

“terugkijken is vooruitkijken”

het genoom is ons gereedschap omdat het evolutionaire
veranderingen vastlegt

genoom geeft inzicht in ontstaan en bestendigen van
ecologische en morfologische verschillen

twee hypotheses

- a. **kustgebonden steltlopers**: veel ondersoorten, dus sterke genetische populatiestructuur
- b. **binnenlandse steltlopers**: geen 'bottlenecks' dus veel genetische variatie (binnen populaties)



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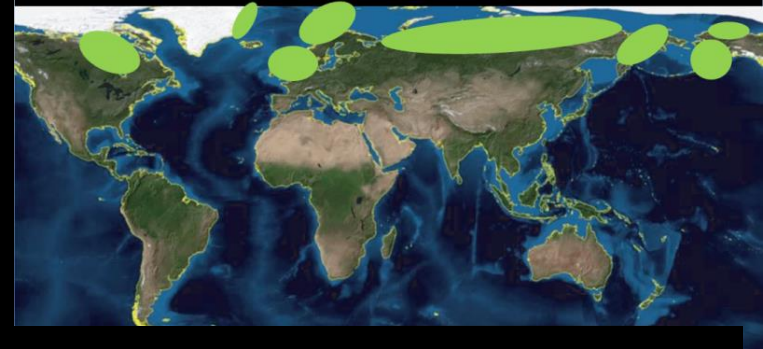
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a. sterke **genetische populatiestructuur** in kustgebonden steltlopers

Kanoet *Calidris canutus*



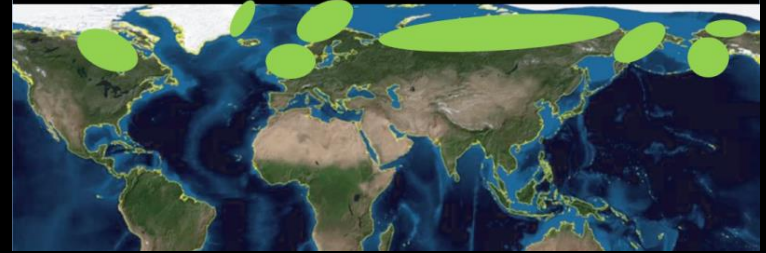
Bontje *Calidris alpina*



Kanoet *Calidris canutus*

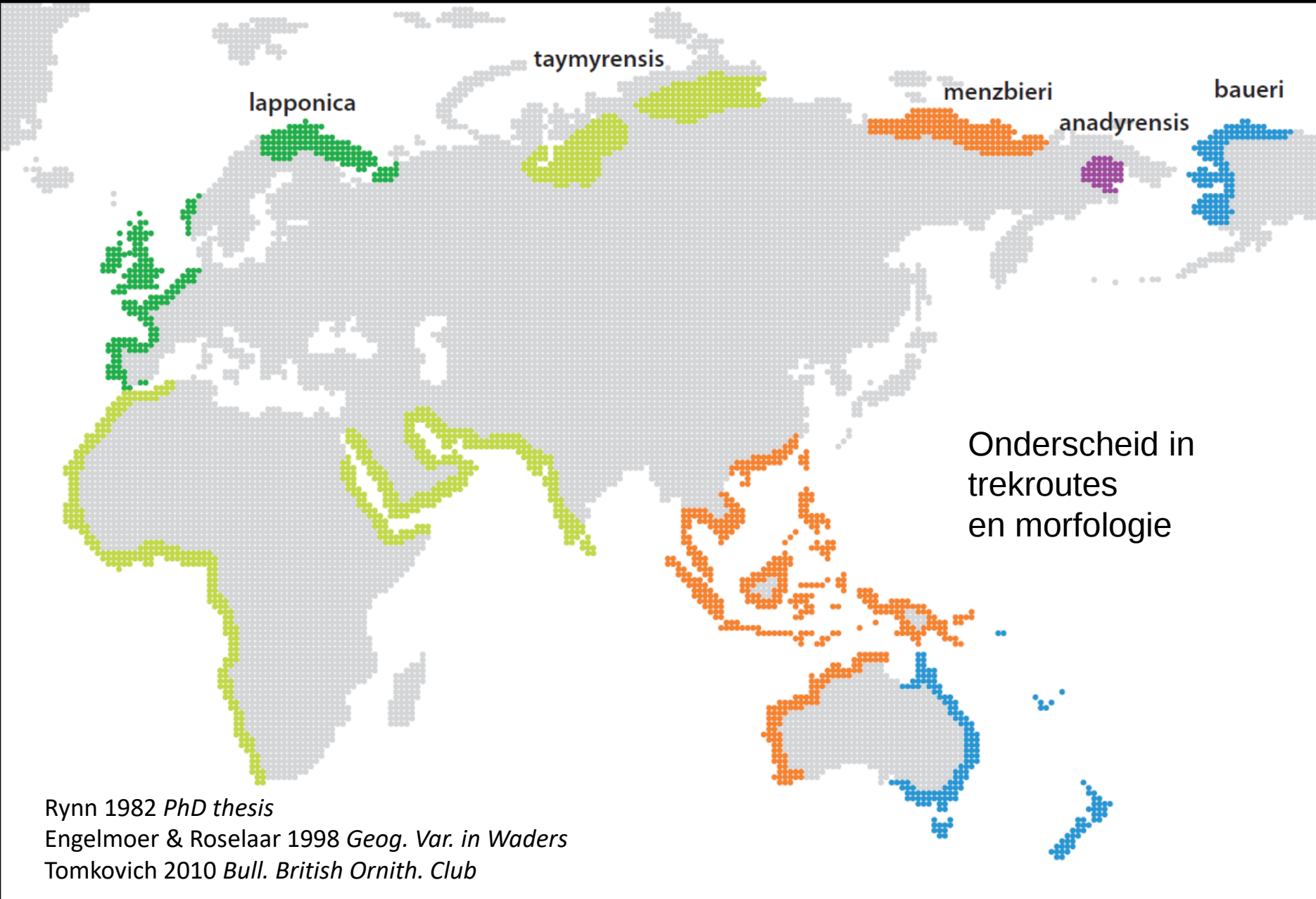


Bontje *Calidris alpina*

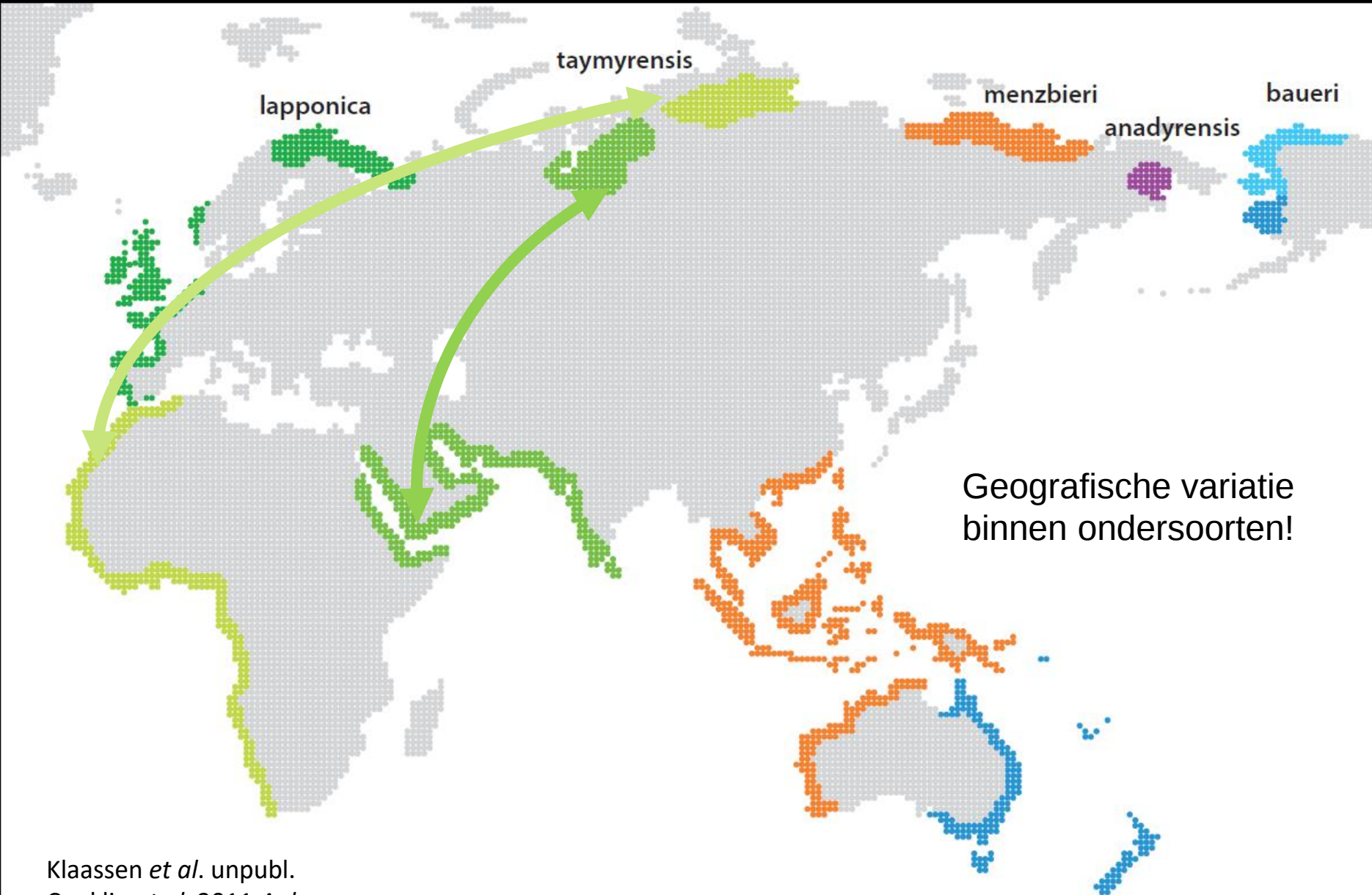




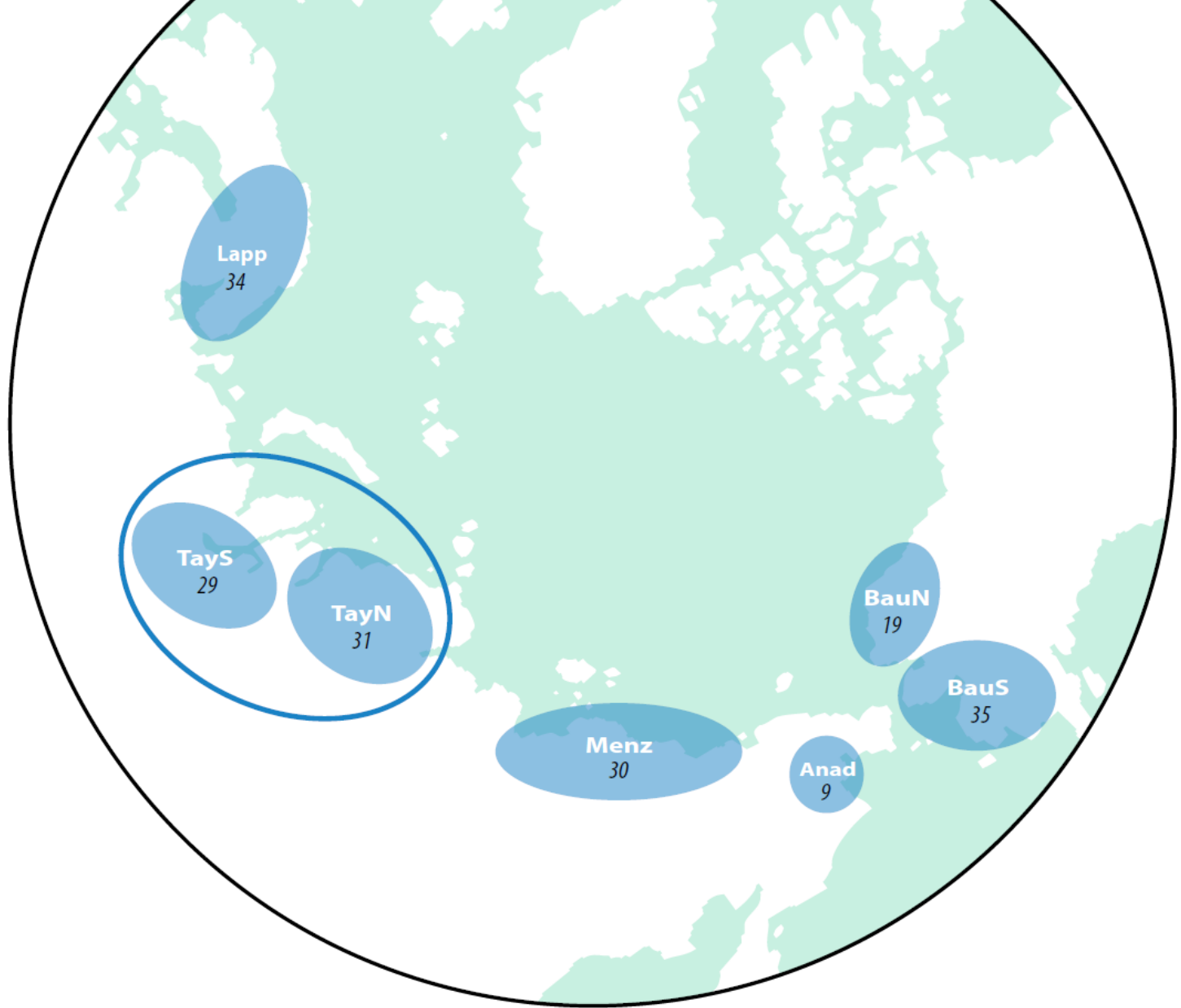
erkende ondersoorten



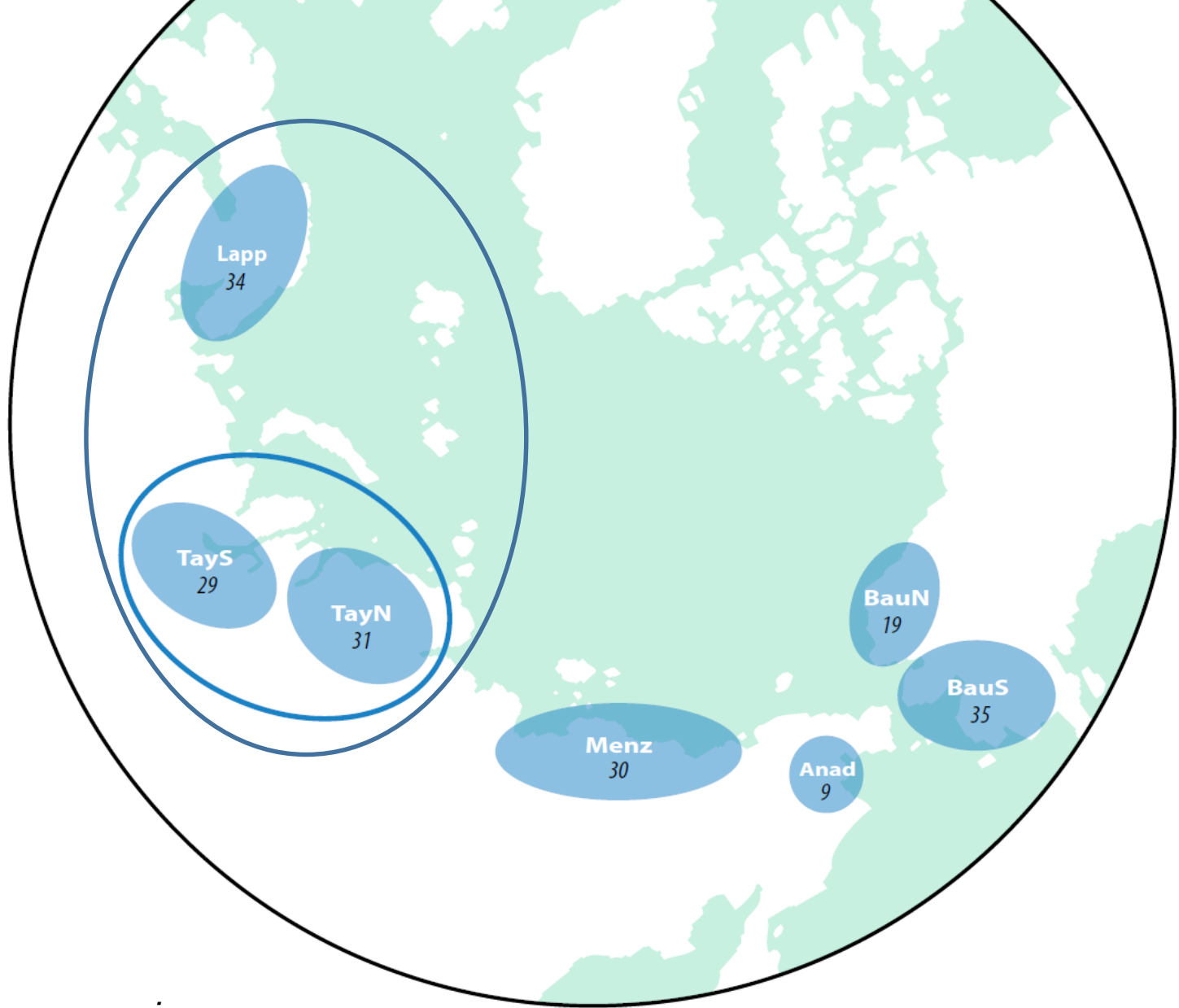
hypothetische ondersoorten



Klaassen *et al.* unpubl.
Conklin *et al.* 2011 *Auk*



Het resultaat



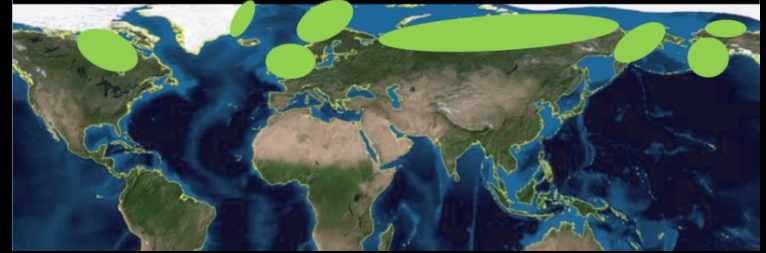
Shocker:

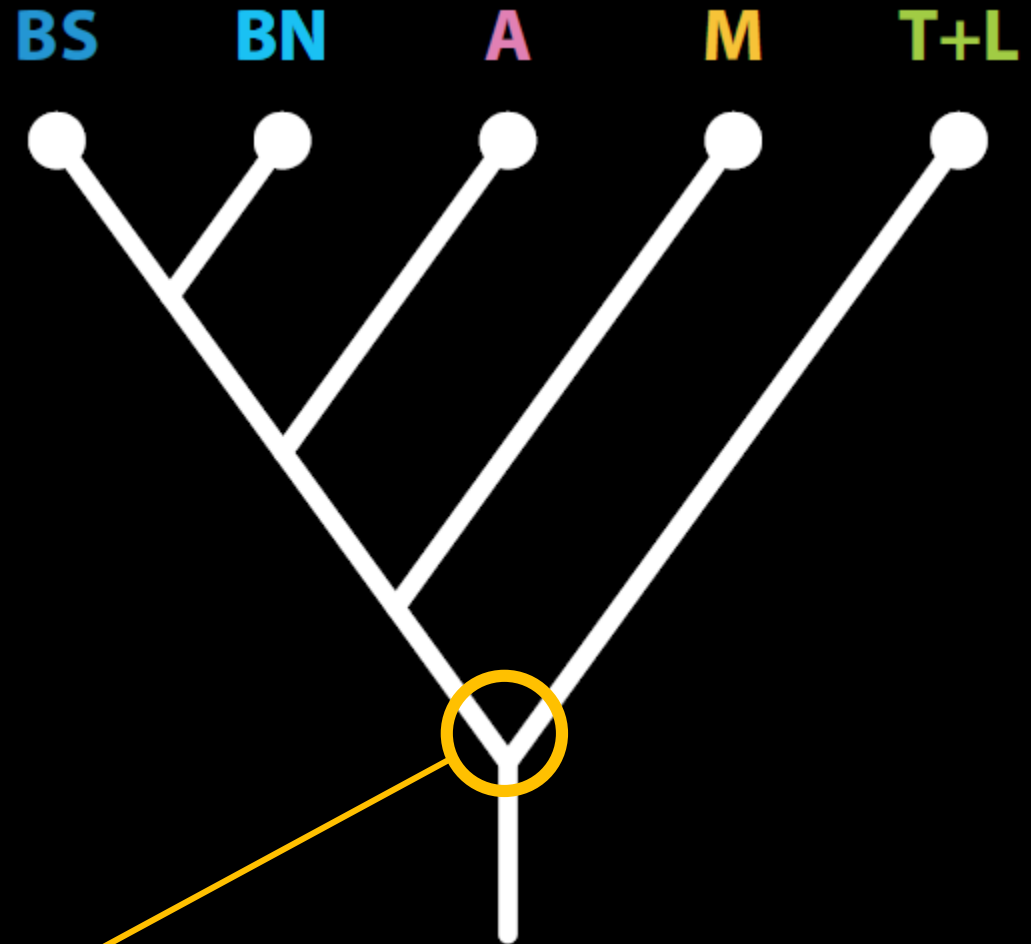
lapponica en *taymyrensis*
zijn genetisch niet te onderscheiden!

Kanoet *Calidris canutus*

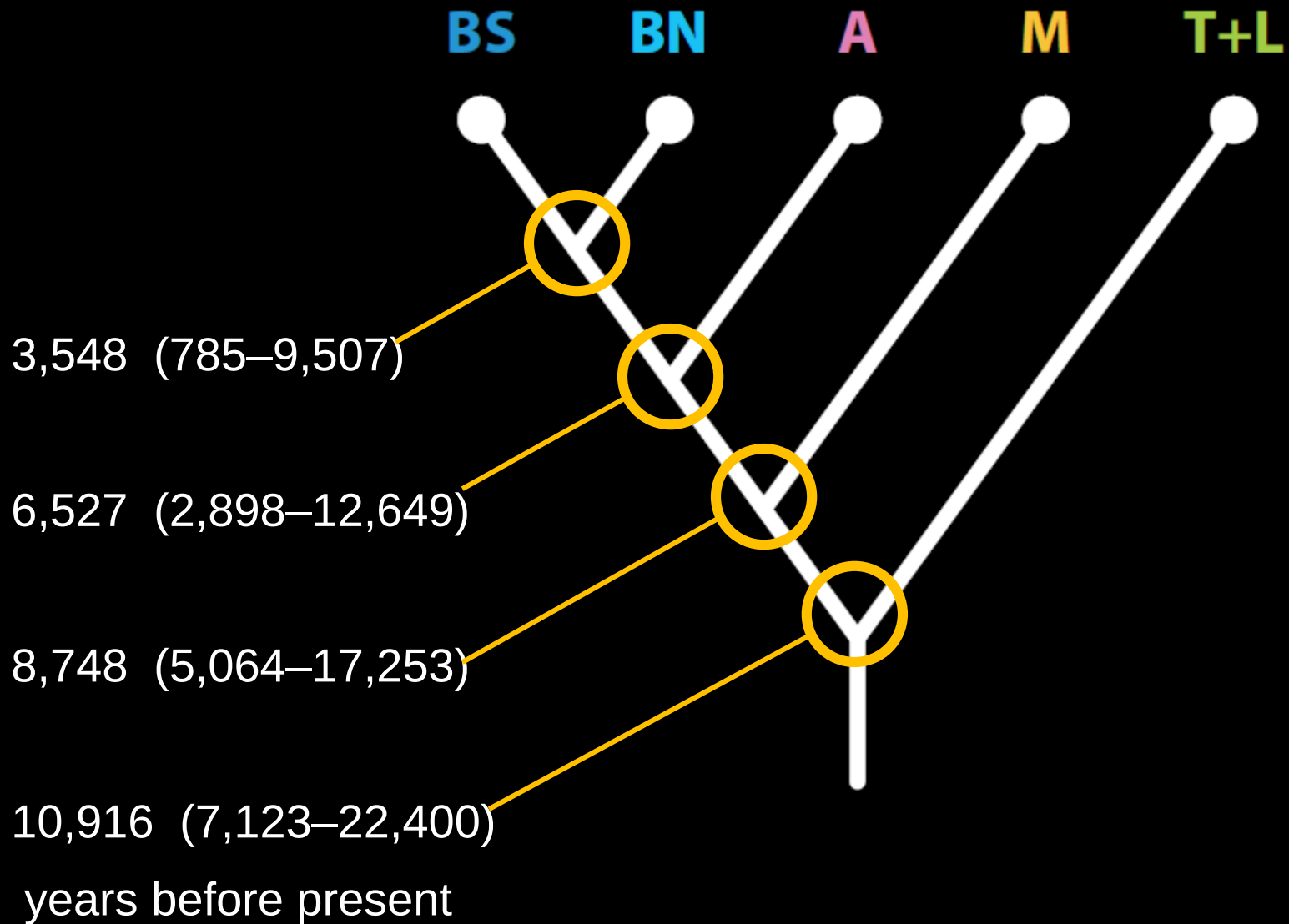


Bontje *Calidris alpina*





10,916 (7,123–22,400)
years before present



conclusie

Rosse Grutto's hebben
duidelijke populaties met
trekwegen die
continenten beslaan

MAAR populaties zijn
genetisch (nog) niet te
onderscheiden (of zelfs
helemaal niet)

implicaties

genetische
populatiestructuur
varieert enorm in
kustgebonden
steltlopers

recente expansie
belangrijk

b. veel **genetische variatie** binnen populaties in binnenlandse steltlopers

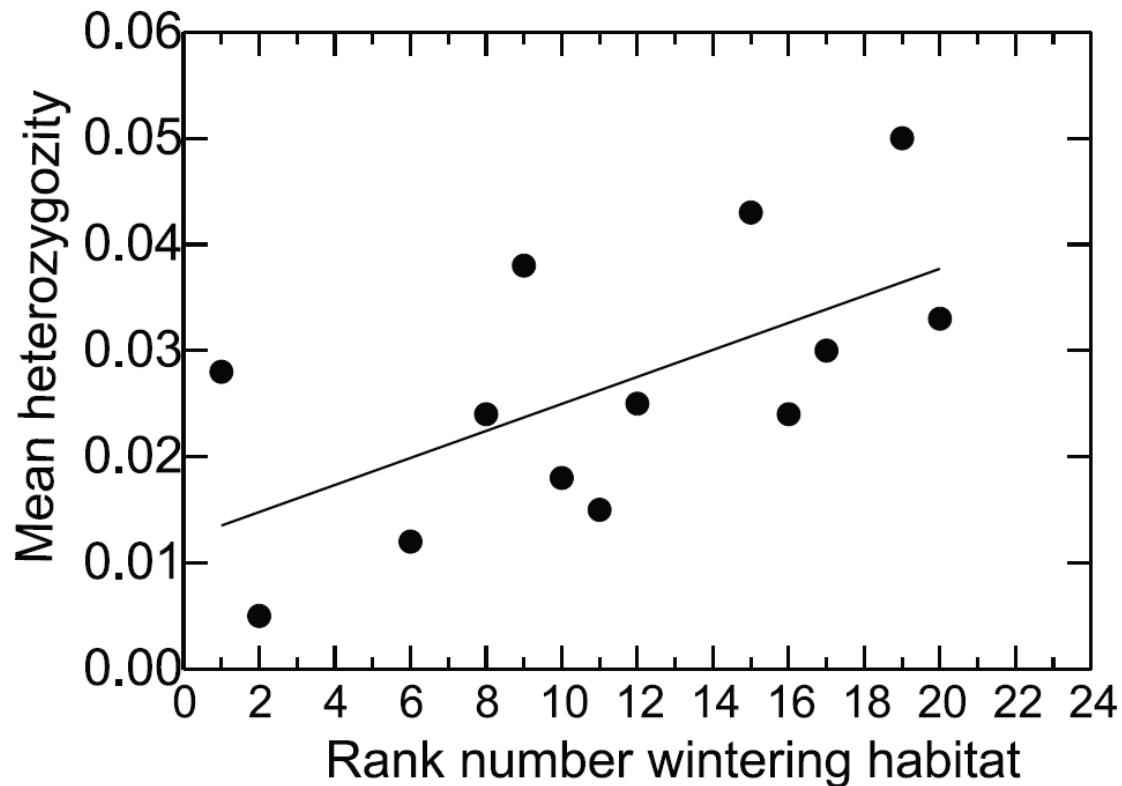


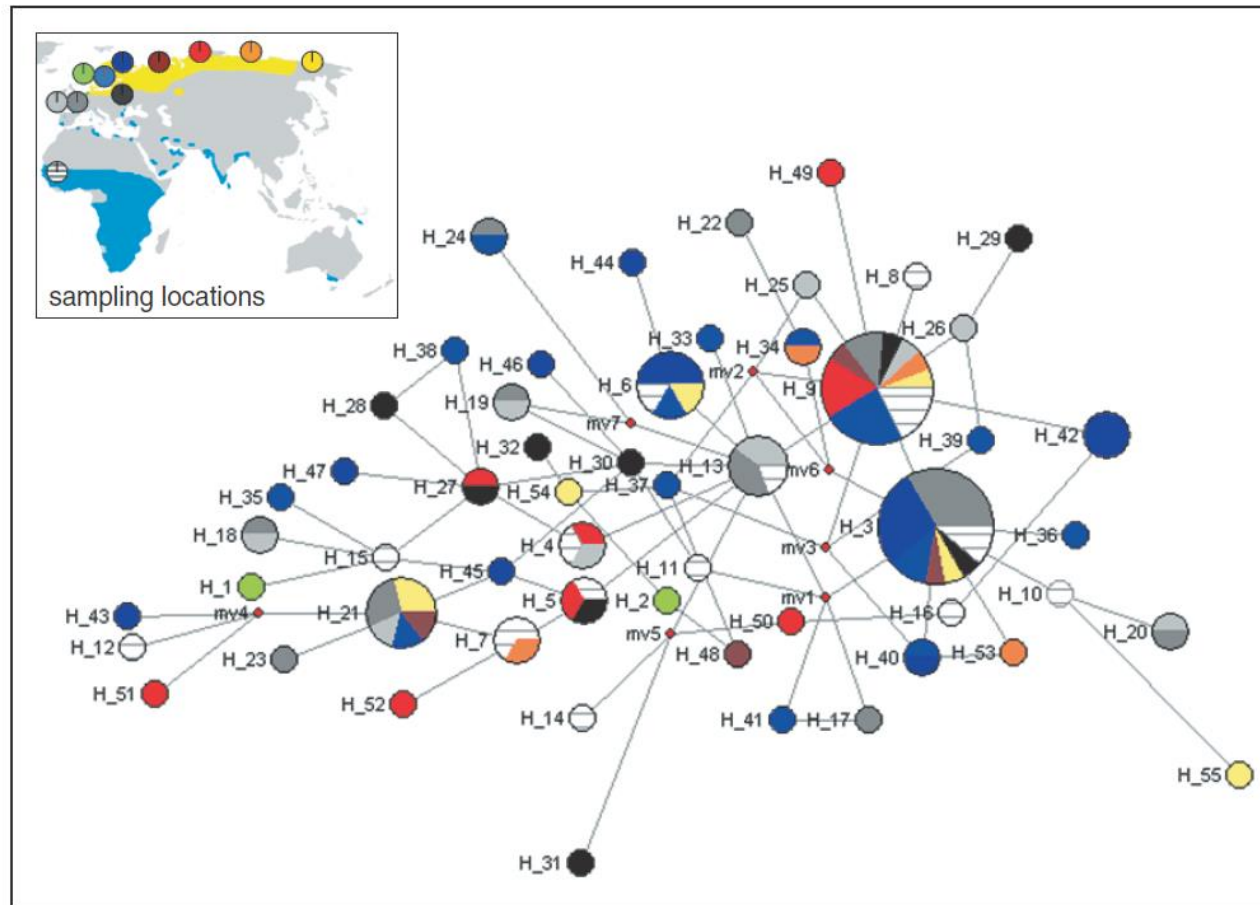
Fig. 2. Relationship between the mean heterozygosity of *Calidris* species (a measure of genetic variability; from Baker 1992: Table 1) and the rank number of the wintering habitat (where the lowest numbers refer to the most marine habitat choice) as the y-axis in Fig. 1 (Spearman rank correlation coefficient is 0.58, $n = 13$, $p < 0.05$). The linear regression line is shown to lead the eye.

voorspellingen voor Kemphanen

- weinig populatiestructuur
- veel genetische variatie in grote wereldpopulatie



weinig populatiestructuur in binnenlandse soorten



ja,
geen
genetische
populatie-
structuur in
Kemphanen

veel genetische variatie in binnenlandse steltlopers

nee, juist zeer weinig **genetische** variatie



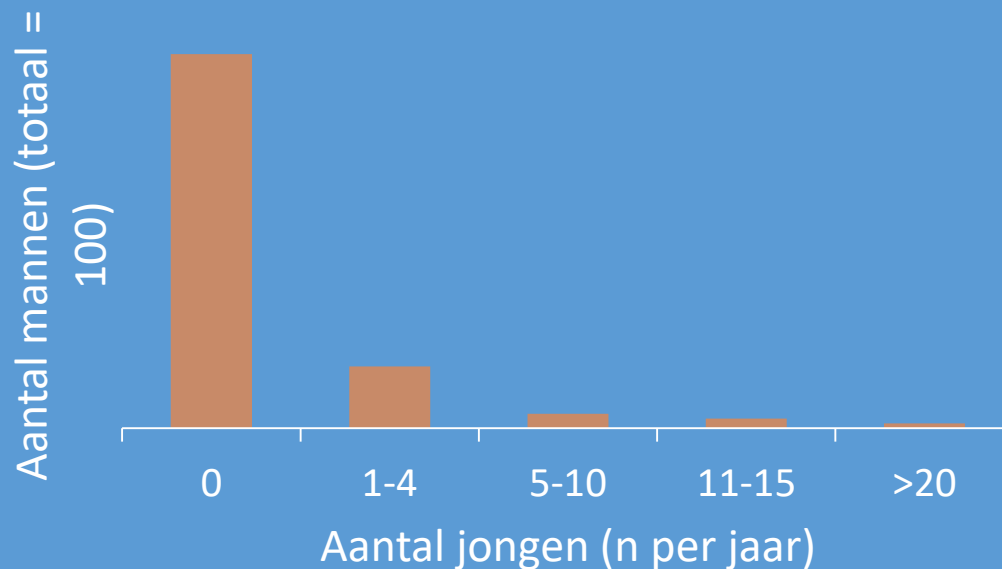
verlies genetische variatie

weinig genetische variatie door verlies langs de mannelijke
lijn! Geschatte reductie = 79 – 97 %



verlies genetische variatie door voortplantingssysteem?

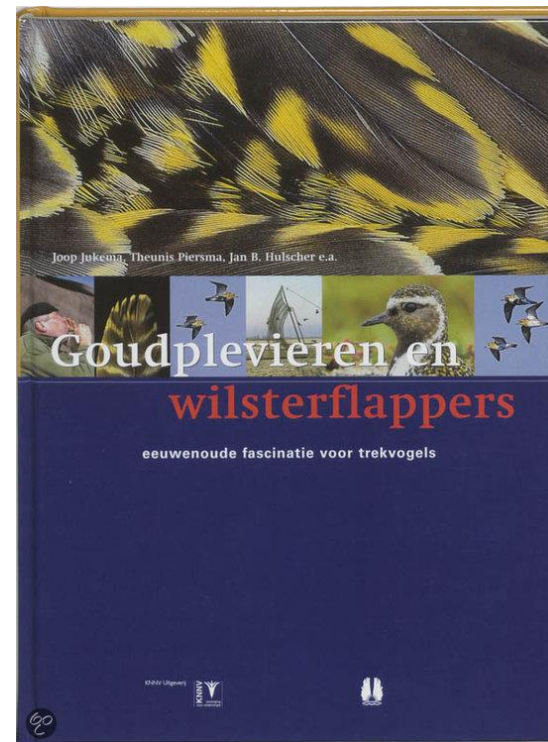
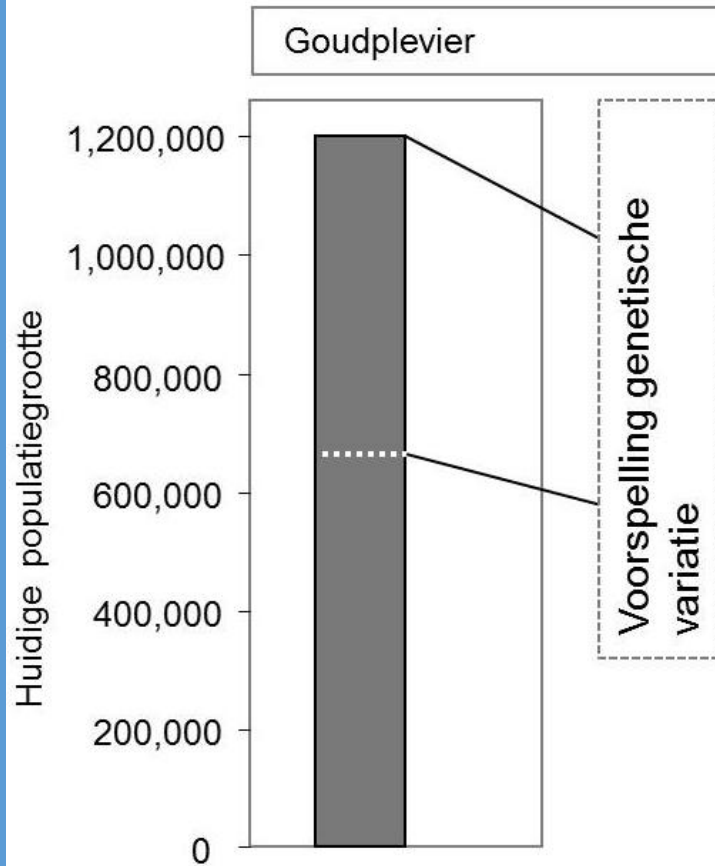
elke generatie wordt maar een klein deel van de genetische variatie doorgegeven > eerste bewijs dat veel mannen zich niet voortplanten



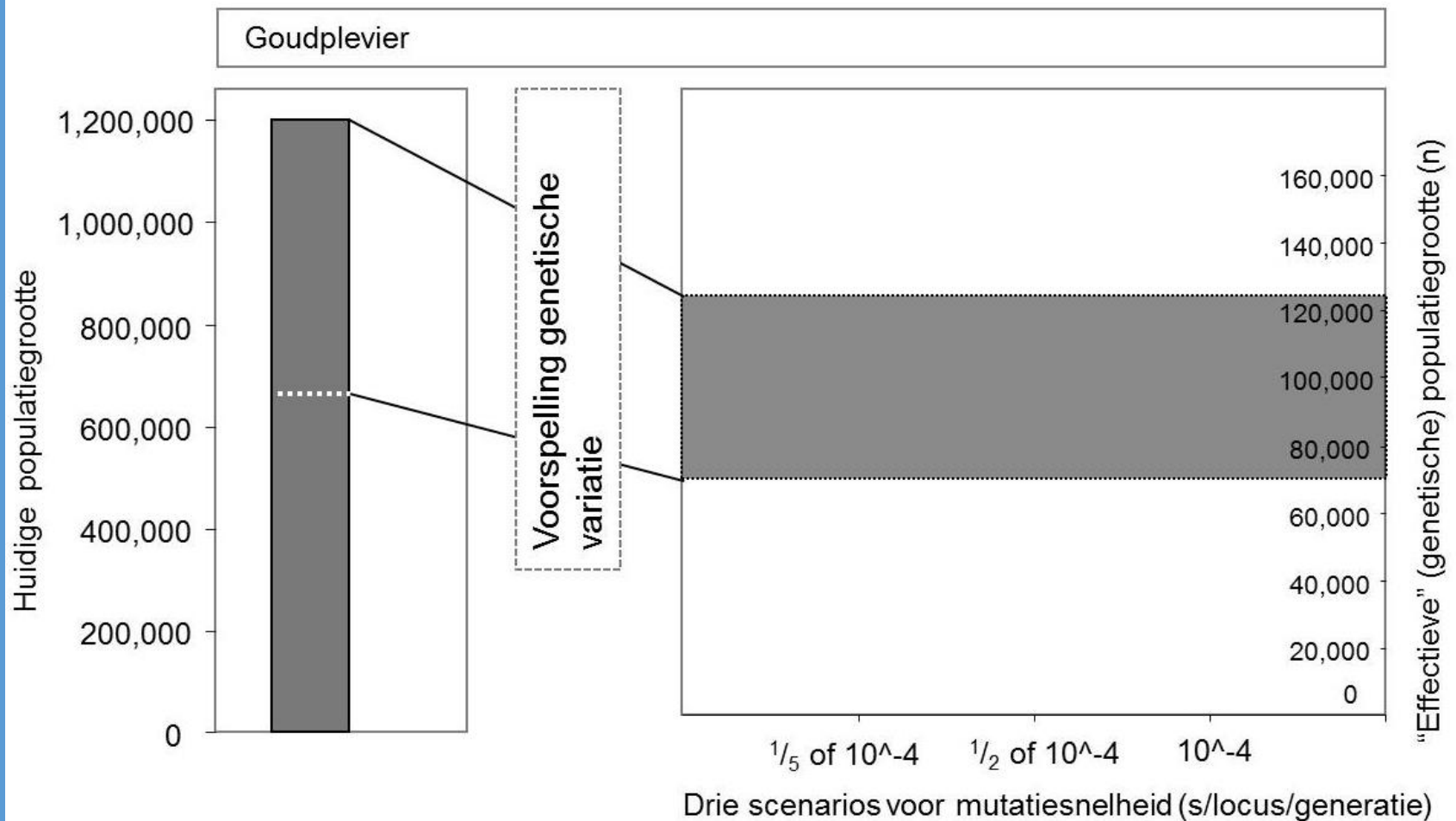
uitstapje naar Goudplevieren



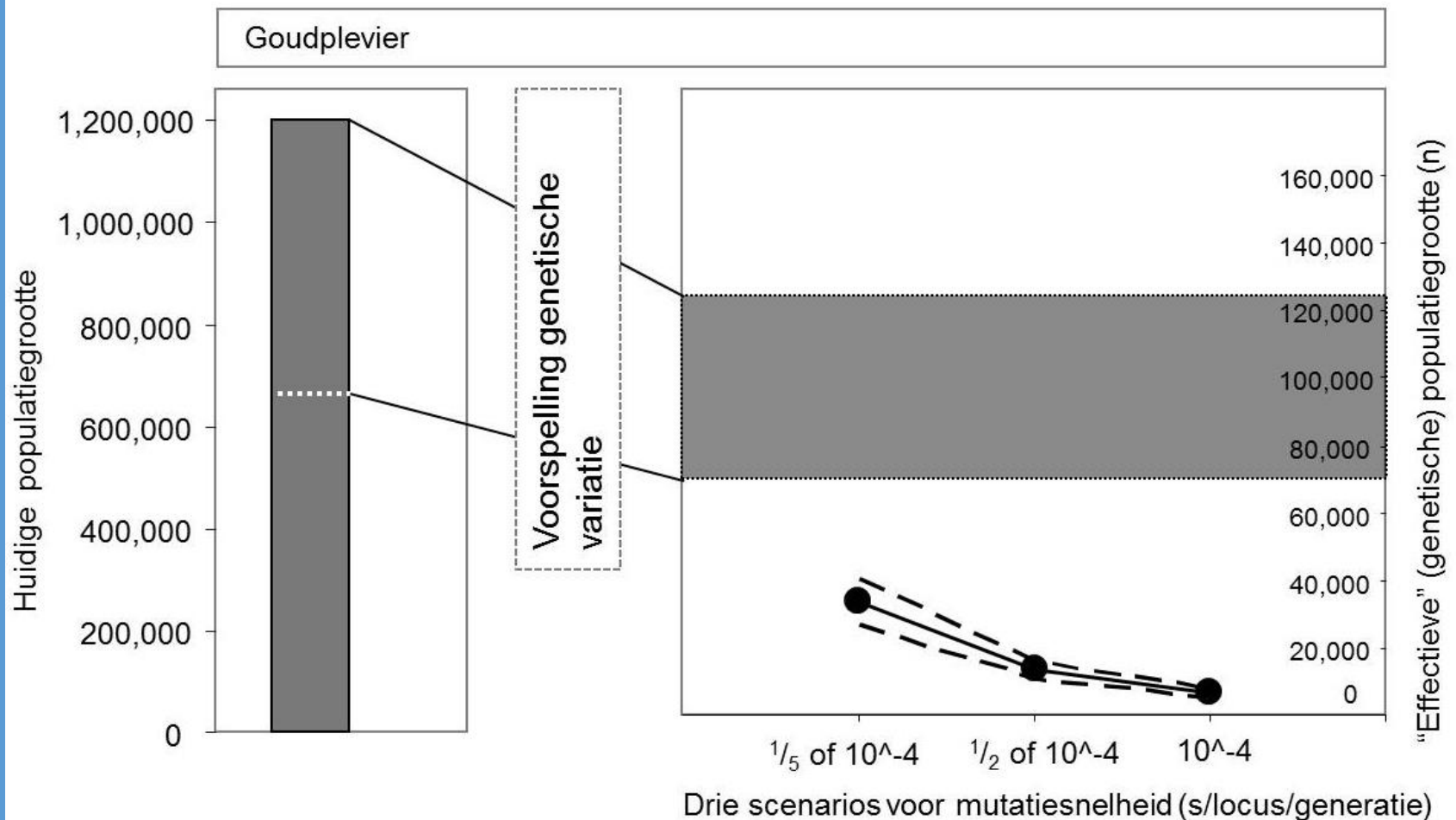
veel genetische variatie in binnenlandse steltlopers?



veel genetische variatie in binnenlandse steltlopers?



weinig genetische variatie door populatiefluctuaties?



conclusie

Kemphanen en
Goudplevieren hebben
opvallend weinig
genetische variatie

implicatie

habitat is geen
betrouwbare voorspeller
van genetische variatie
in steltlopers

voortschrijdende inzichten

evolutionaire verschillen die bijgedragen aan de verschillen in populatiestructuur en genetische variatie

“habitat dichotomie” is generalisatie; verschaduwd door:

- recente expansie: *oud of nieuw?*
- voortplantingssysteem: *andere polygame soorten?*
- recente fluctuaties in populatiegrootte

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Kristen Choffe – genetic marker design

Marco van der Velde – general lab support

Anneke Bol – extractions for Mauritania samples

Students:

Aija Lehikoinen – PCRs for sequencing

Martijn Weemeijer – help with primer development

Samples (all species)

Burke Museum, U of Washington

Royal Ontario Museum

Pavel Tomkovich

Pavel Tomkovich

Zoological Museum, Moscow State U

Burke Museum,
U of Washington

Job ten Horn
NIOZ

Joop Jukema &
Wilsterflappers

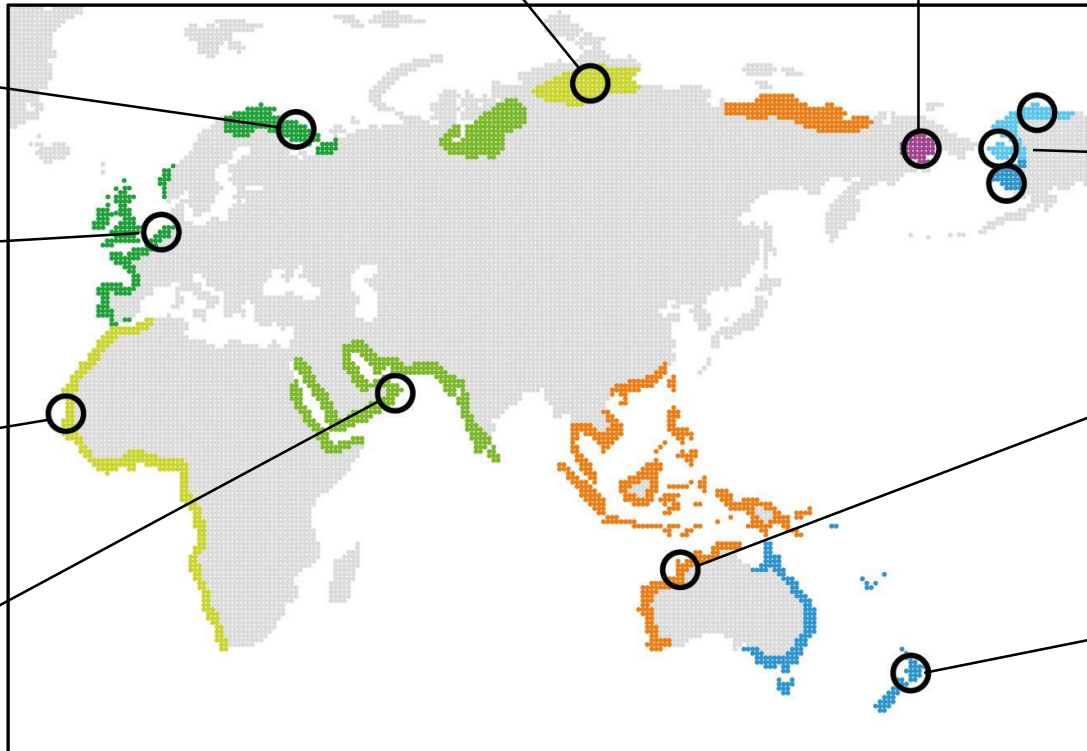
Anneke Bol
NIOZ

Jim de Fouw
NIOZ

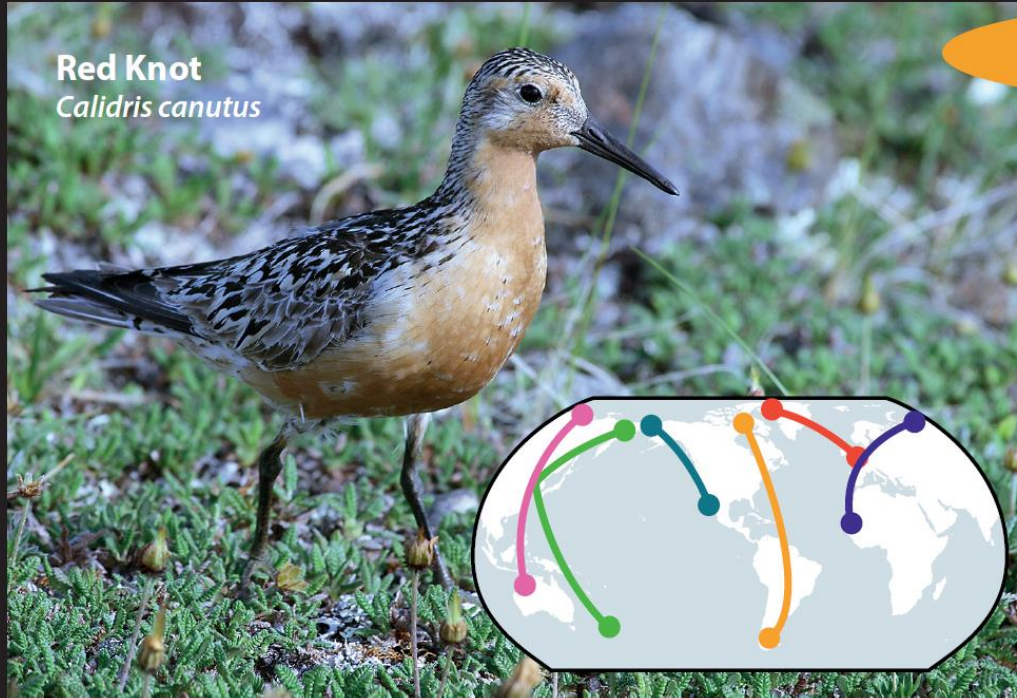
Robert Gill
Dan Ruthrauff
Lee Tibbitts
USGS Alaska

Chris Hassell
GFN
USGS Alaska

Phil Battley
Andrew Fidler
Angela Merino
Massey University
USGS Alaska



Red Knot
Calidris canutus



MSc Opportunity

Are you an ecologist who thinks about evolution?

This MSc project will focus on differentiation among Red Knot populations in mitochondrial DNA, a fast-evolving and selectively neutral genetic marker with well-established utility to detect very recent population processes. Using samples collected globally, we will characterize genetic diversity within and among populations, estimate timelines of divergence, and explore scenarios of gene flow, to uncover clues to the evolutionary history of Red Knots.

Interested?

The candidate will learn to perform standard laboratory techniques (e.g., PCR, gel electrophoresis, Sanger sequencing) and calculate standard population genetic parameters (e.g., F_{st} , effective population size, divergence time). Beyond that, there is great latitude to explore the vast array of ever-evolving genetic analytical tools, according to the candidate's interests. We are particularly interested in students willing to discover and experiment independently with new statistical genetic methods (e.g., Bayesian coalescent analysis). Experience with labwork is very helpful, and a positive attitude toward problem-solving in unfamiliar computer programs is essential.

Supervisors: Jesse Conklin, Yvonne Verkuil, Theunis Piersma

Starting date: September 2016 or later

If this sounds exciting to you, contact:

Jesse at j.r.conklin@rug.nl

or

Yvonne at y.i.verkuil@rug.nl

Unraveling the evolutionary history of a long-distance migratory bird

Red Knots (*Calidris canutus*) are among the longest-migrating and most intensively-studied of all shorebirds, providing famous examples of the physiological adaptations, phenotypic flexibility, and perilous conservation status of migratory birds. Based on their high-arctic breeding distribution and previous genetic work, Red Knots are thought to have diversified into six morphologically and behaviorally distinct flyway populations just since the Last Glacial Maximum (<20,000 years). Broadly, we are interested in how rapidly these changes occurred, how they reflect historical geographic and climatic changes, and to what extent future adaptation and gene flow among populations may be hindered by flyway-specific selection for migratory phenotypes.