

# POPULATION GENETICS OF THE CRITICALLY ENDANGERED SPOON-BILLED SANDPIPER

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photo by Gerrit Vyn



Wildlife is experiencing a global decline in population size, possibly on a way to a massive extinction event. Birds are not an exception, especially migratory birds.



spoon-billed sandpiper

**100 – 200**  
breeding pairs



red-necked stint

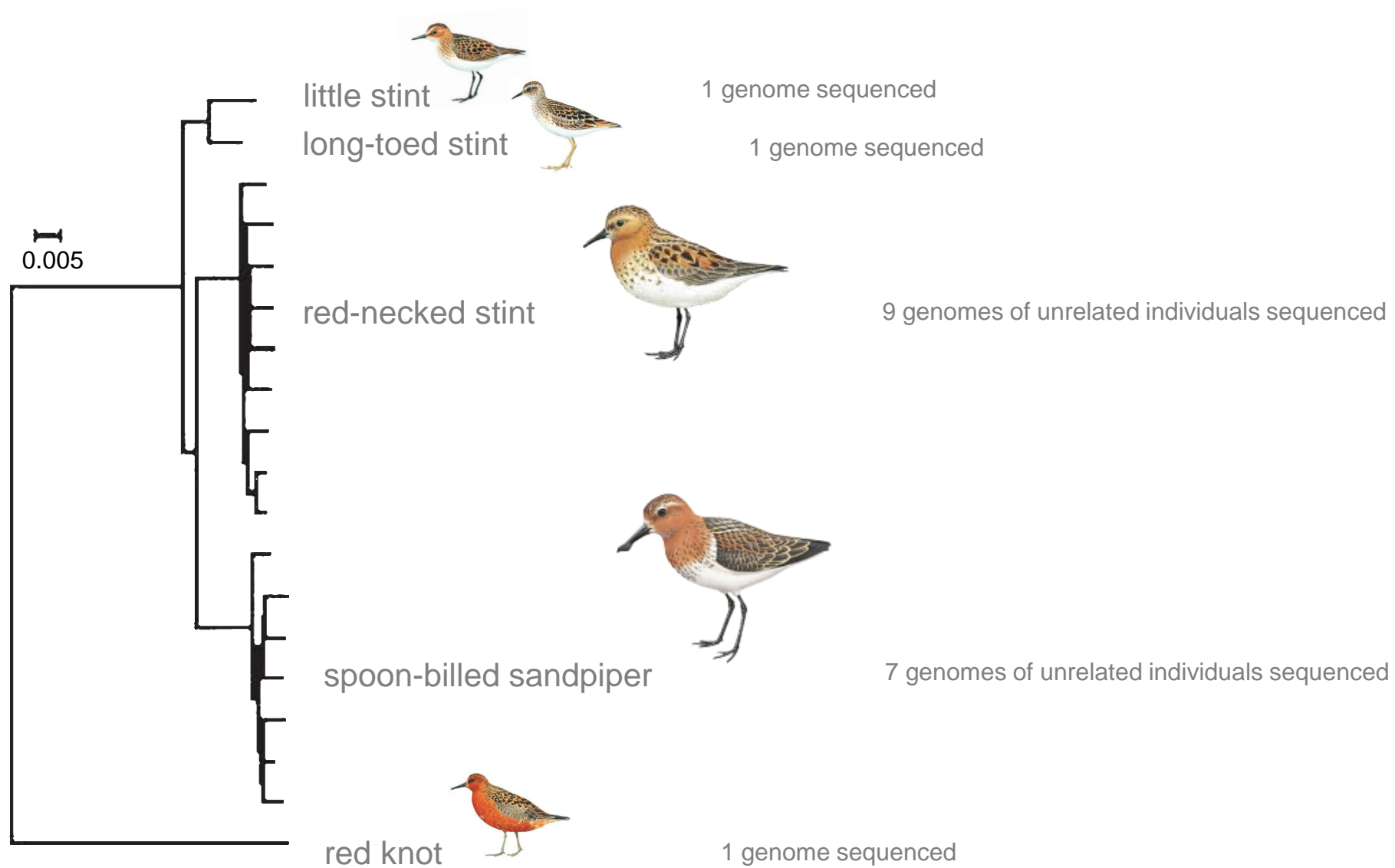
of least concern



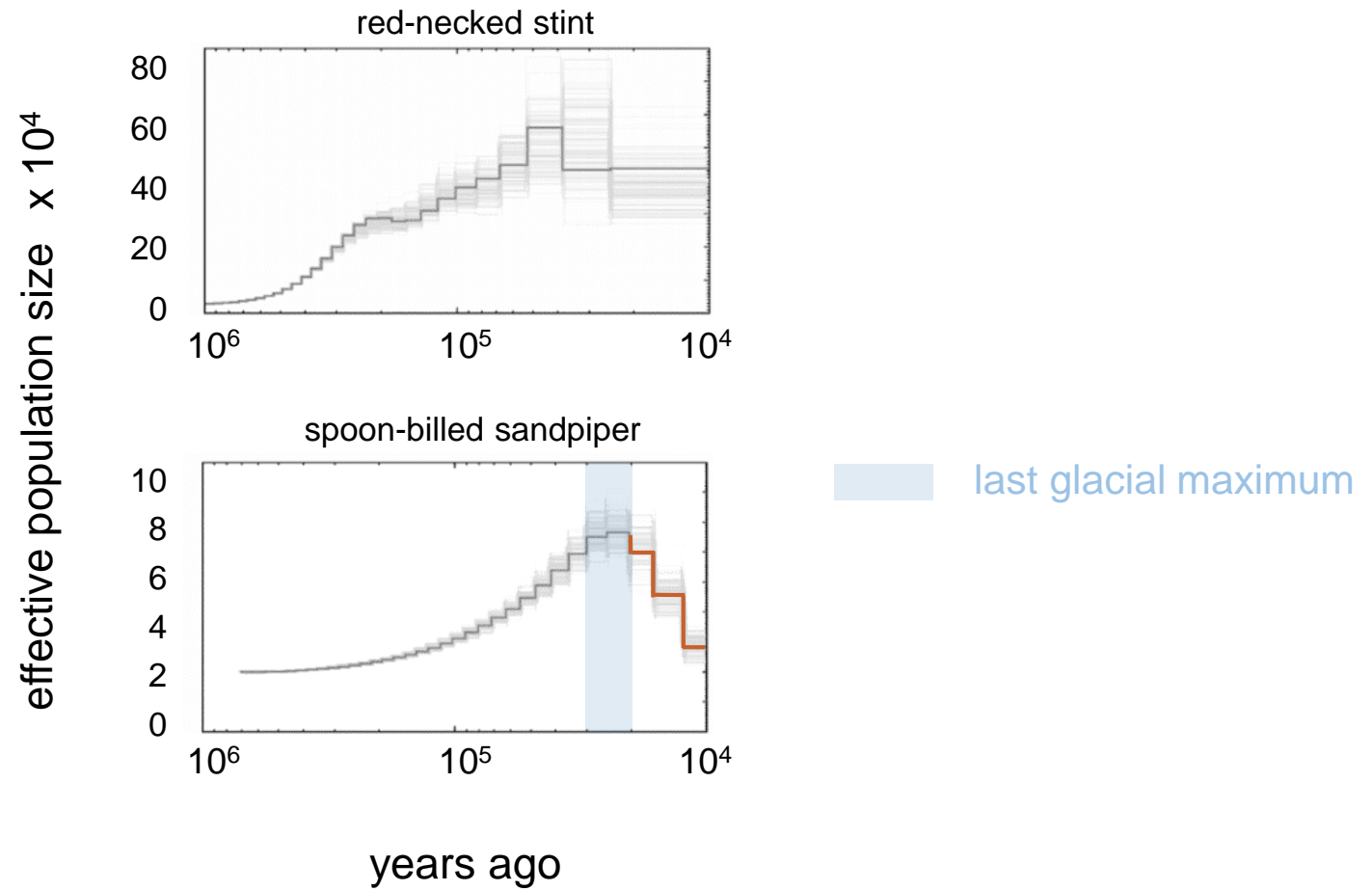


photo by Ekaterina Maksimova

## Phylogeny of sequenced *Calidris* species



## Demographic history reconstructed with PSMC

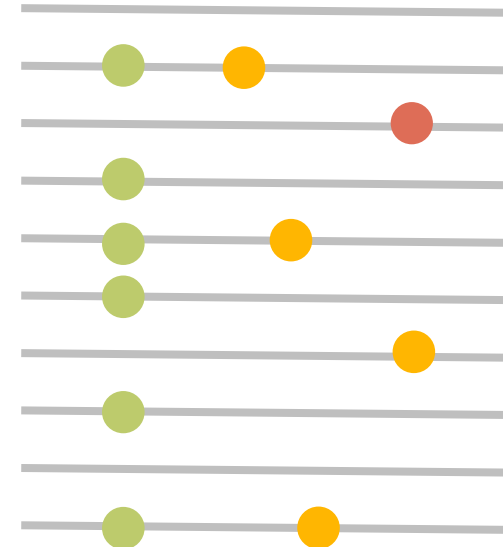


# What happens when a population grows?

gain of rare alleles,  
common ones are not affected



generation 1



generation  $t$

What happens when a population goes through a bottleneck?



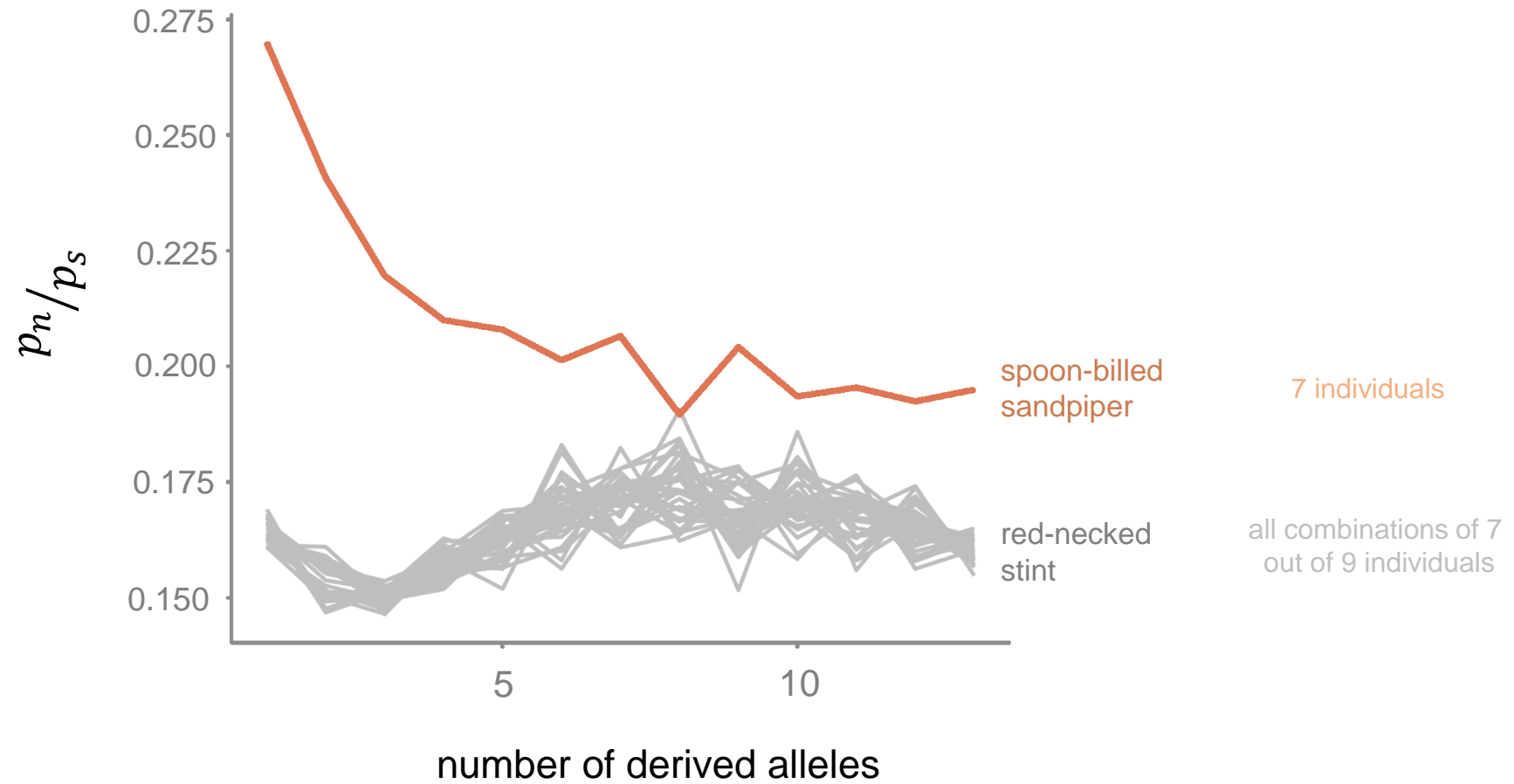


What do we see from the data?

The overall level of nucleotide diversity indeed did not change much

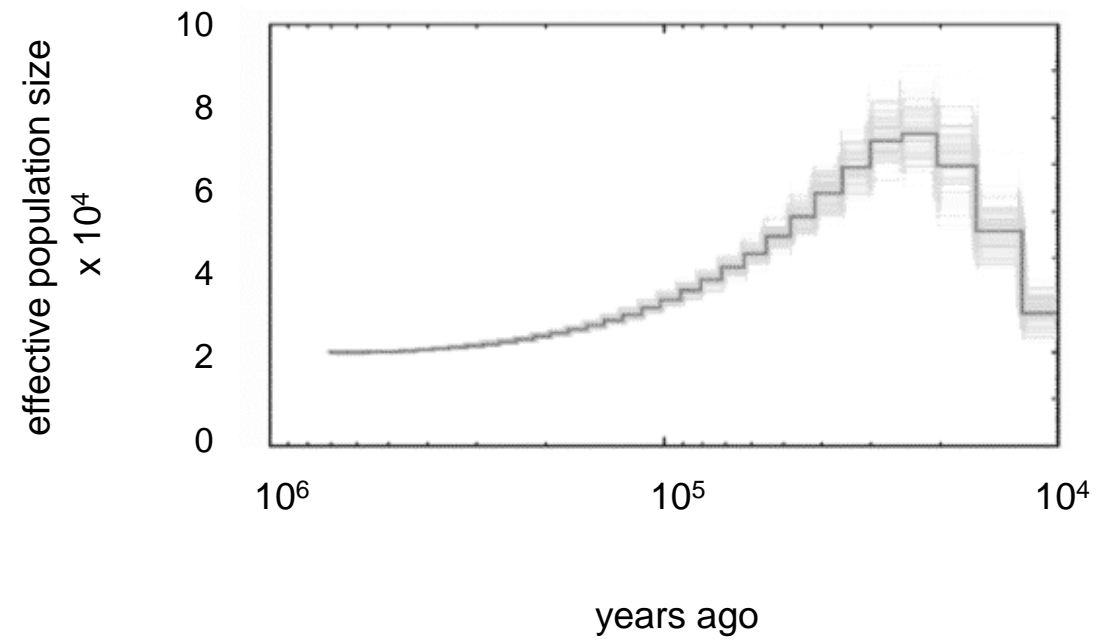


But the proportion of deleterious polymorphisms increased



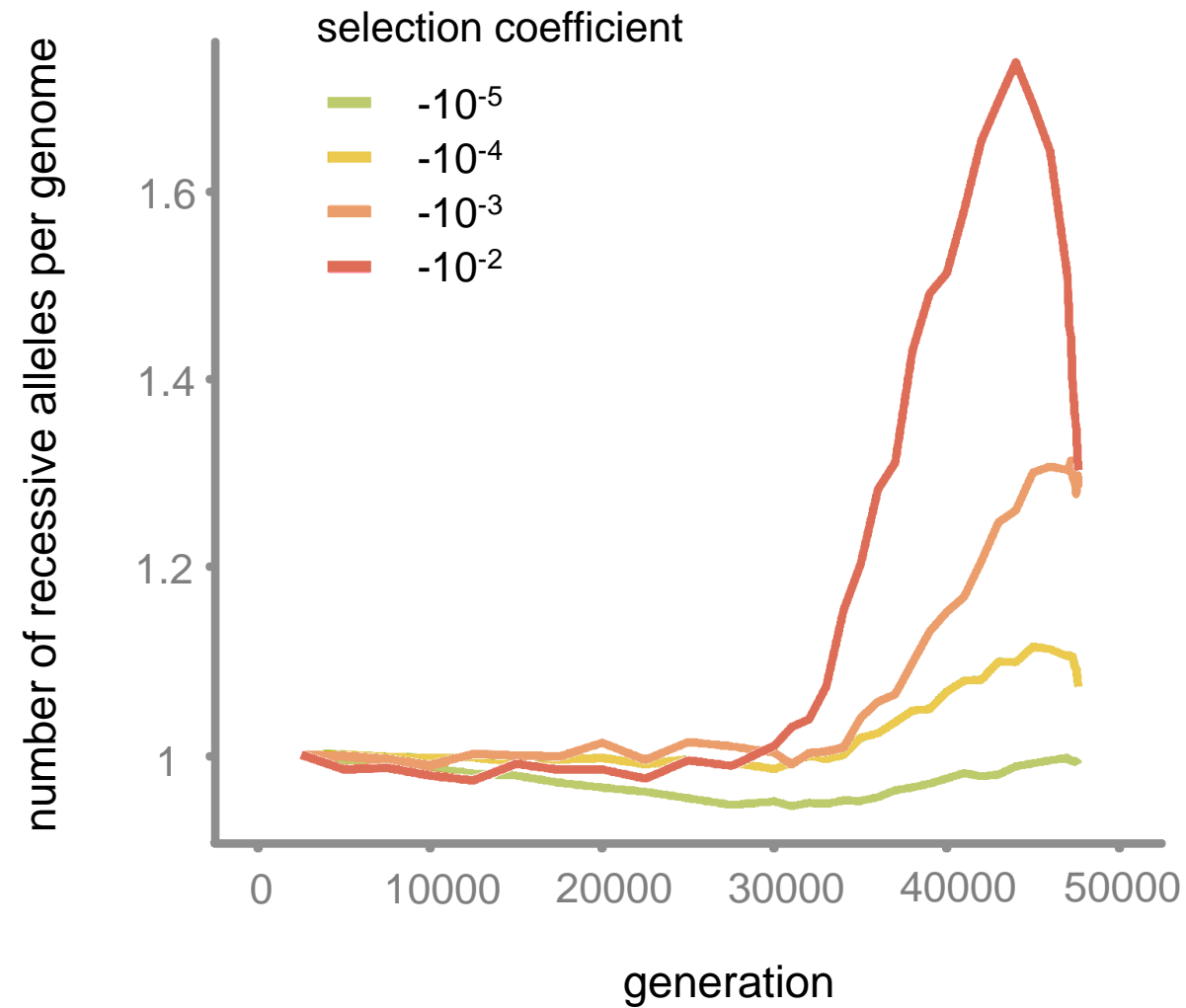
What happened with the spoon-billed sandpiper?

What happened with the spoon-billed sandpiper?

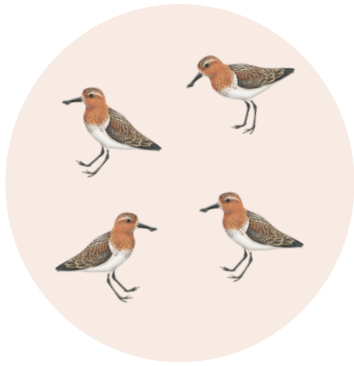




What happened with the spoon-billed sandpiper?

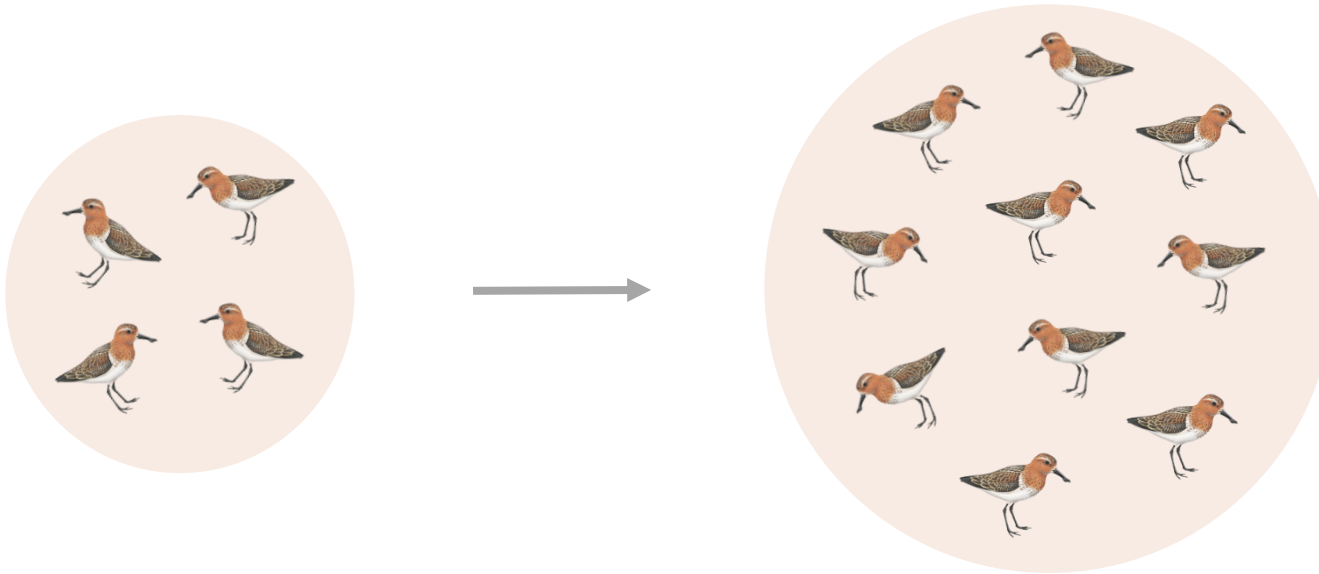


What happened with the spoon-billed sandpiper?



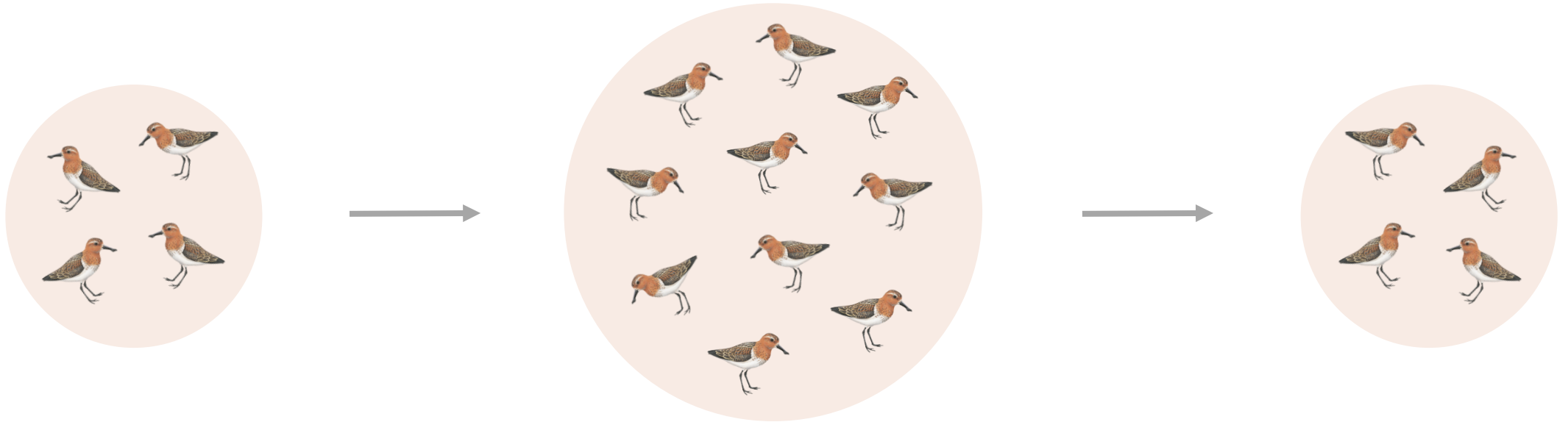
In a small population, genetic drift helps remove bad recessive variants.

What happened with the spoon-billed sandpiper?



When a population is growing, genetic drift stops, allowing to accumulate new deleterious variants.

What happened with the spoon-billed sandpiper?



When a population declines immediately after a population growth, it maintains some of the new recessive deleterious variants.

Can we find a distribution of selection coefficients  
that explains what we see?

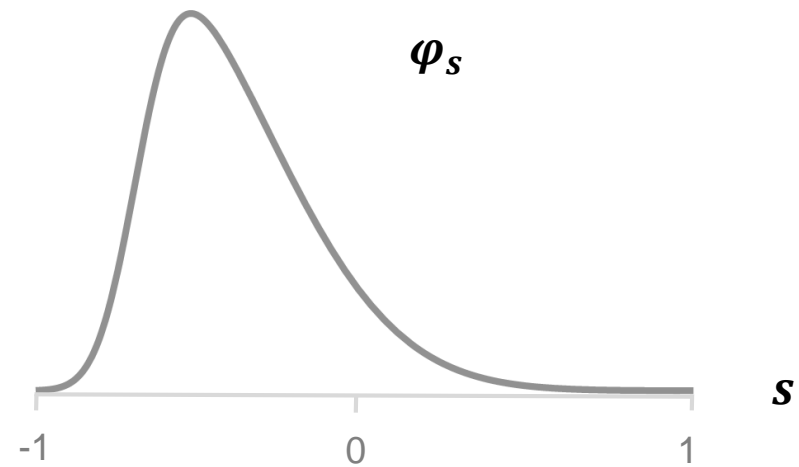




spoon-billed sandpiper



red-necked stint



probability density function of the distribution of  
selection coefficients on new mutations



***s***



***sh***



**0**

genotype

relative fitness

$$subs(\varphi_s, N_e, h) = \underbrace{2N_e ut}_{\text{number of mutations}} \cdot \underbrace{\int_s \frac{\int_0^1 e^{2N_e s((2h-1)x^2 - 2hx)} dx}{\int_0^1 e^{2N_e s((2h-1)x^2 - 2hx)} dx}}_{\text{fixation probability}} \cdot \varphi_s ds$$

$x$	allele frequency
$s$	selection coefficient
$N_e$	effective population size
$h$	dominance coefficient
$u$	mutation rate
$t$	number of generations

$\varphi_s (\mu, \sigma, \alpha)$  probability density function of the distribution of selection coefficients which we model as a skew normal distribution with location parameter  $\mu$ , scale parameter  $\sigma$ , and shape parameter  $\alpha$

$$pols(\varphi_s, N_e, h) = \int_s \int_0^1 2x(1-x) \cdot \frac{1}{c_s} e^{2N_e s(x^2 + 2hx(1-x))} x^{4N_e v - 1} (1-x)^{4N_e u - 1} \cdot \varphi_s dx ds$$

frequency of  
heterozygotes

probability density function  
of the distribution  
of allele frequency  $x$

probability density function  
of the distribution  
of selection coefficients  $s$

$x$  allele frequency

$s$  selection coefficient

$N_e$  effective population size

$h$  dominance coefficient

$u, v$  forward and backward mutation rates

$c_s$  normalizing constant

$\varphi_s(\mu, \sigma, \alpha)$  probability density function of the distribution of selection coefficients  
which we model as a skew normal distribution  
with location parameter  $\mu$ , scale parameter  $\sigma$ , and shape parameter  $\alpha$

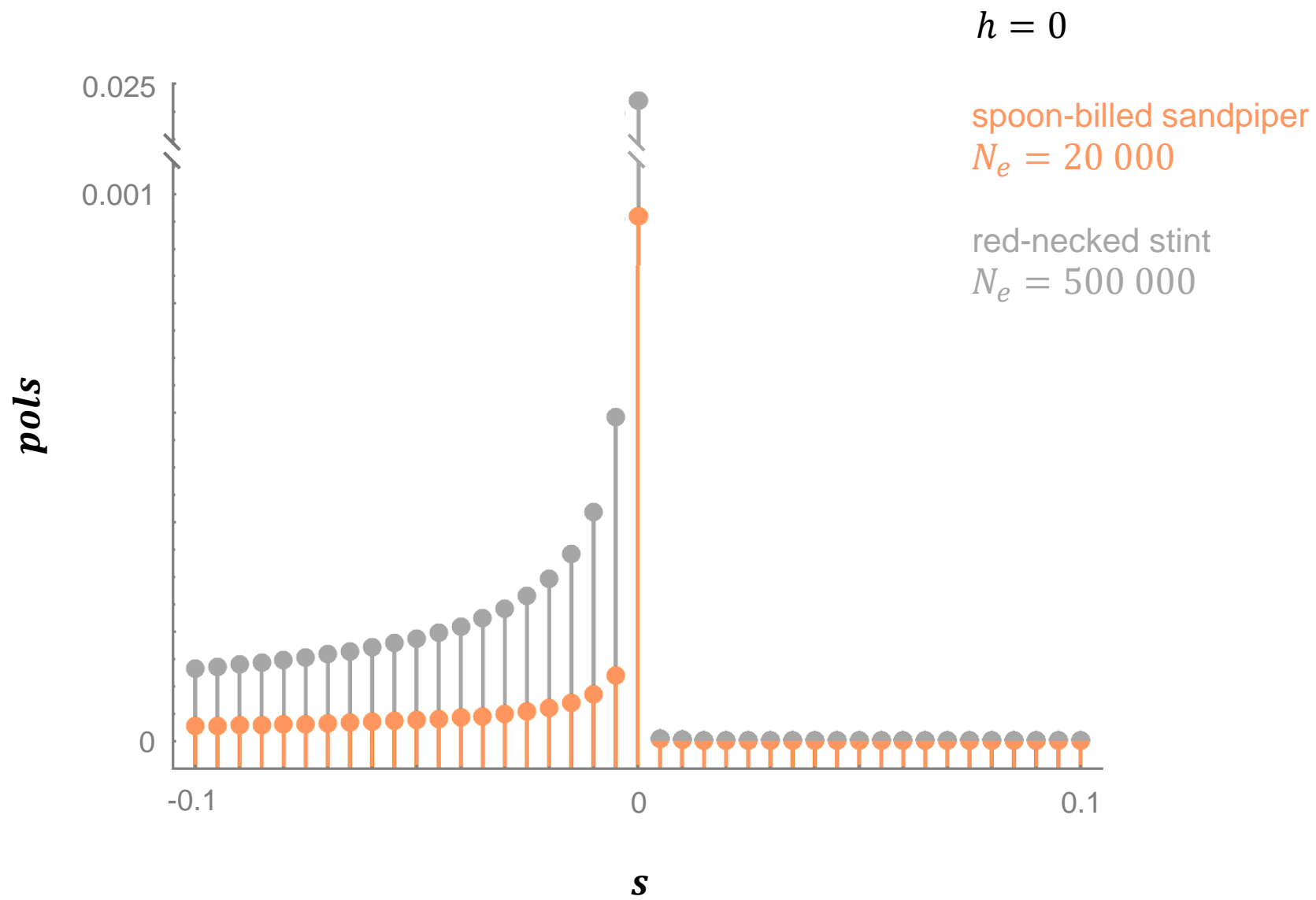
$$pols(\varphi_s, N_e, h) = \int_s \int_0^1 2x(1-x) \cdot \frac{1}{c_s} e^{2N_es(x^2+2hx(1-x))} x^{4N_ev-1} (1-x)^{4N_eu-1} \cdot \varphi_s dx ds$$

$$c_s = \int_0^1 e^{2N_es(x^2+2hx(1-x))} x^{4N_ev-1} (1-x)^{4N_eu-1} dx$$

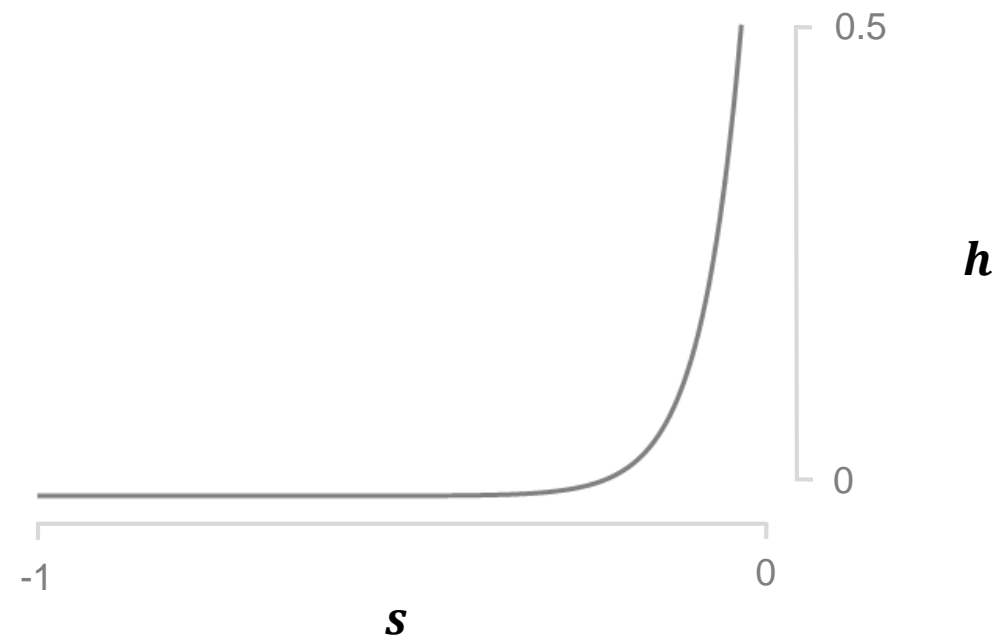
$$h = 0 : \quad \int_0^1 e^{2N_esx^2} x^{4N_ev-1} (1-x)^{4N_eu-1} dx$$

$$h = \frac{1}{2} : \quad \int_0^1 e^{2N_esx} x^{4N_ev-1} (1-x)^{4N_eu-1} dx$$





$$h = \frac{e^{\beta s}}{2}$$



Deng H.W. and Lynch M. Genetics 1996  
Balick D.J. et al. PLOS Genetics 2015



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