

# POPULATION GENETICS OF THE CRITICALLY ENDANGERED SPOON-BILLED SANDPIPER

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Nov 26, 2019



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

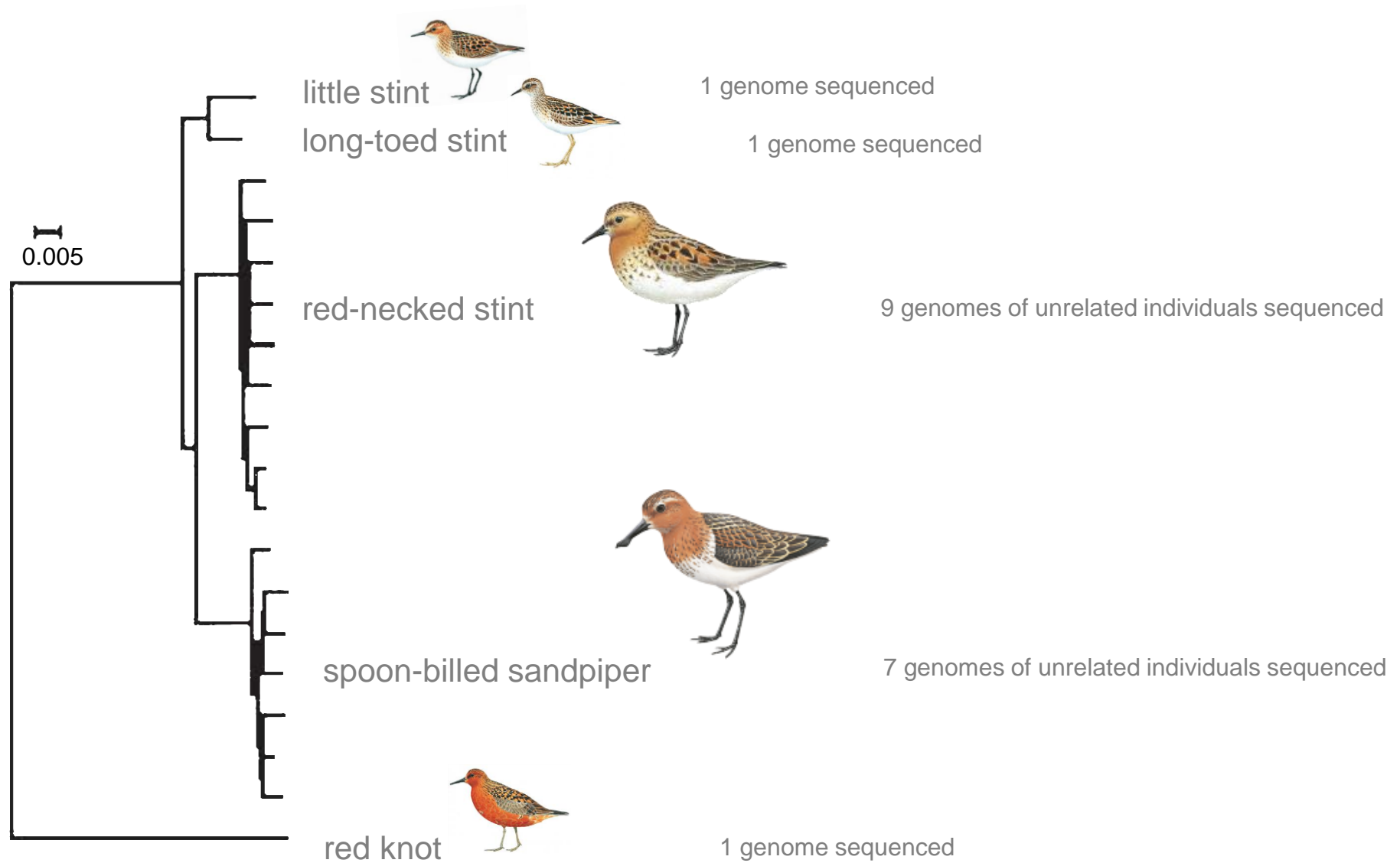
of least concern



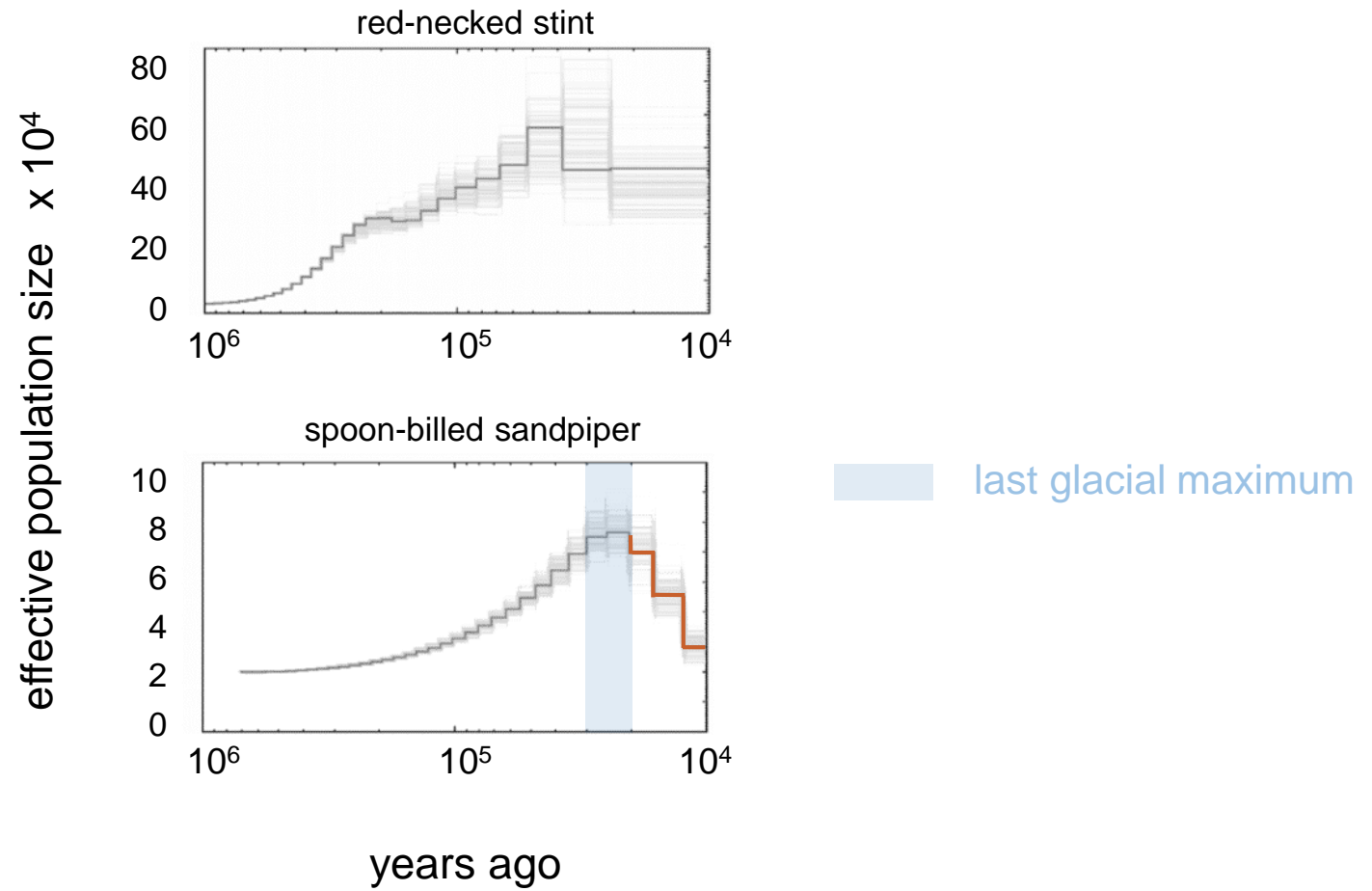
photo by Ekaterina Maksimova



## Phylogeny of sequenced *Calidris* species

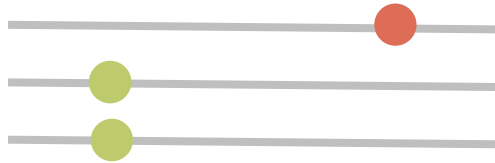


## Demographic history reconstructed with PSMC

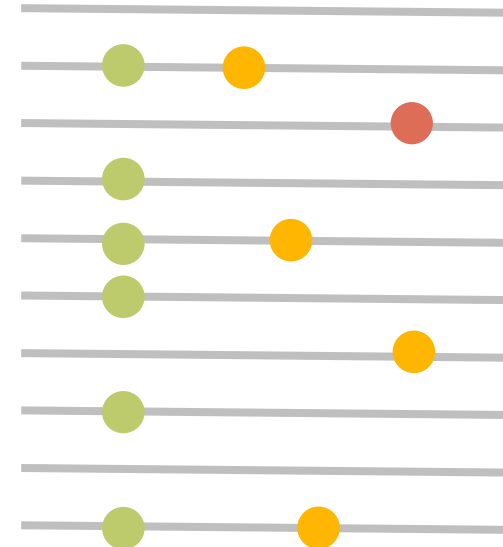


# What happens when a population grows?

gain of rare alleles,  
common ones are not affected

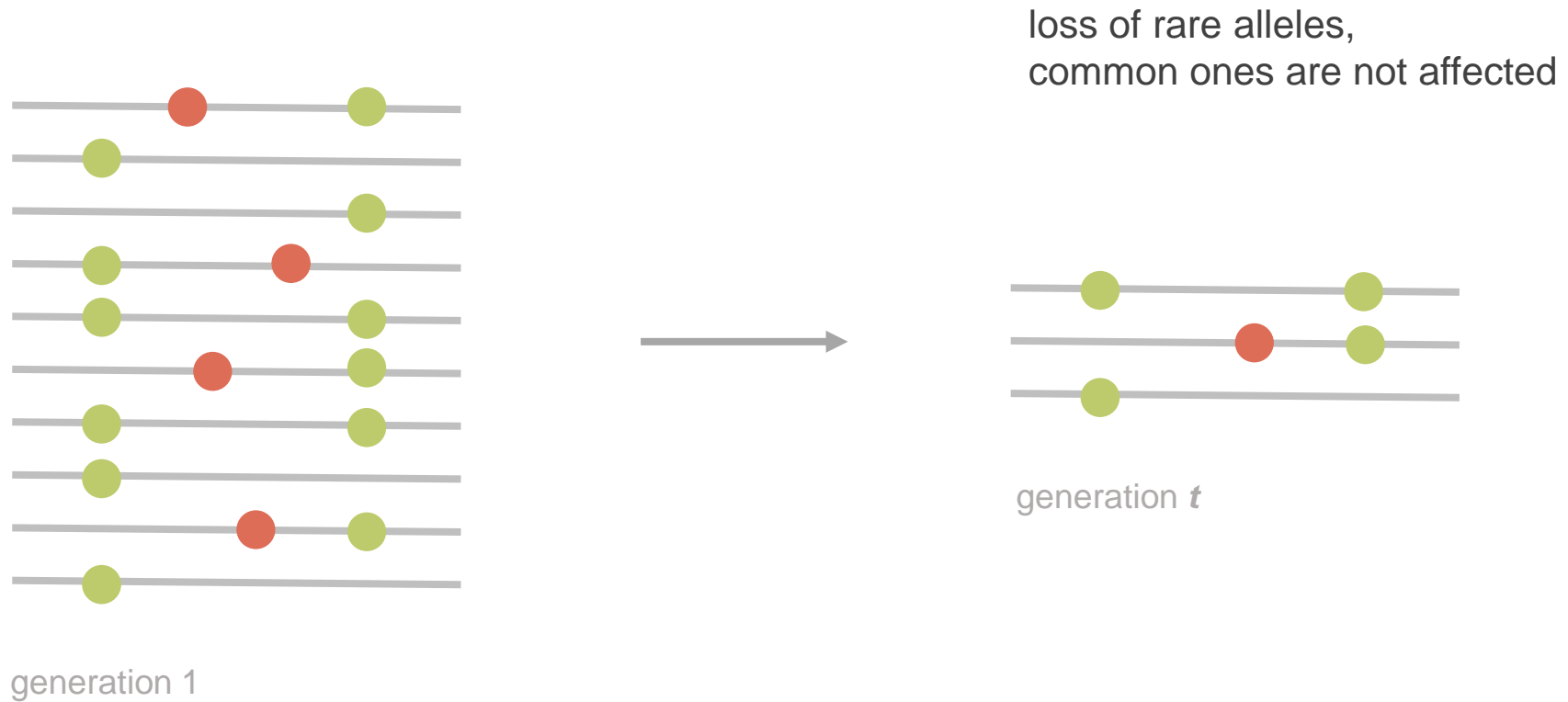


generation 1



generation  $t$

What happens when a population goes through a bottleneck?



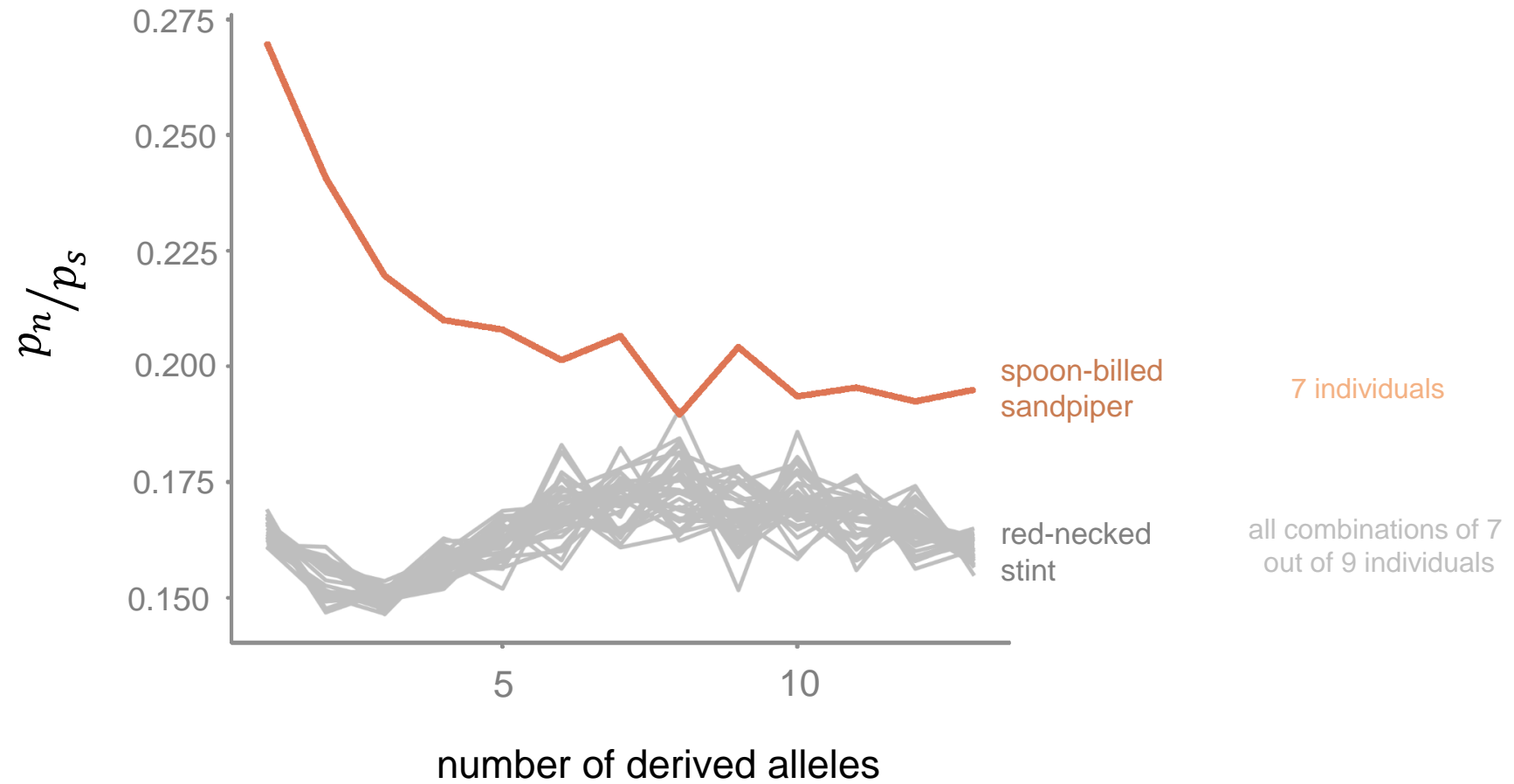
What do we see from the data?



The overall level of nucleotide diversity indeed did not change much

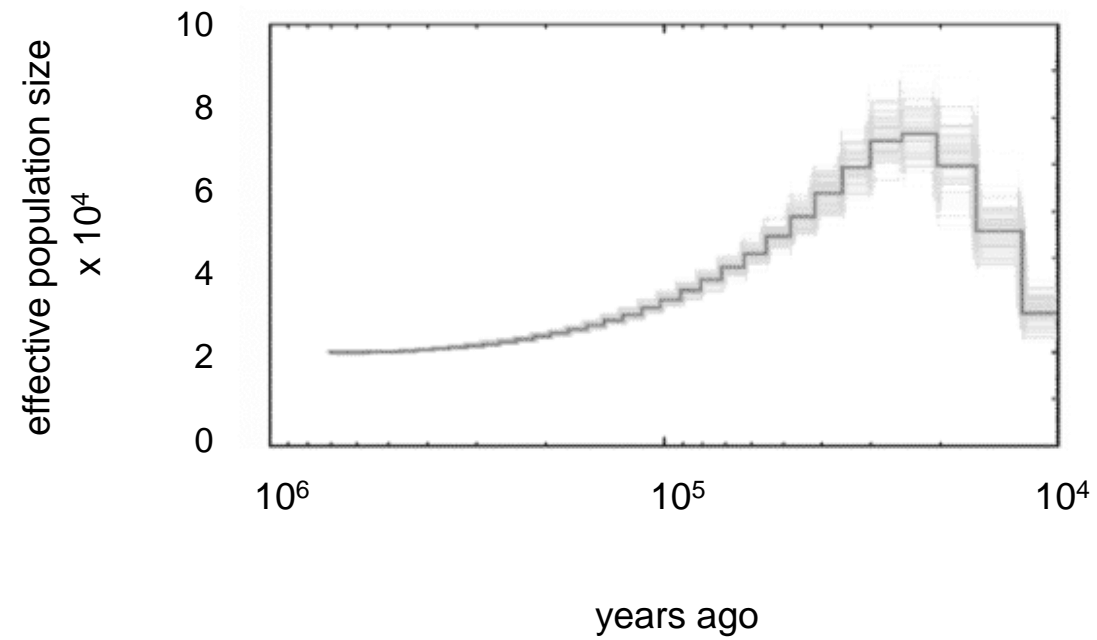


But the proportion of deleterious polymorphisms increased

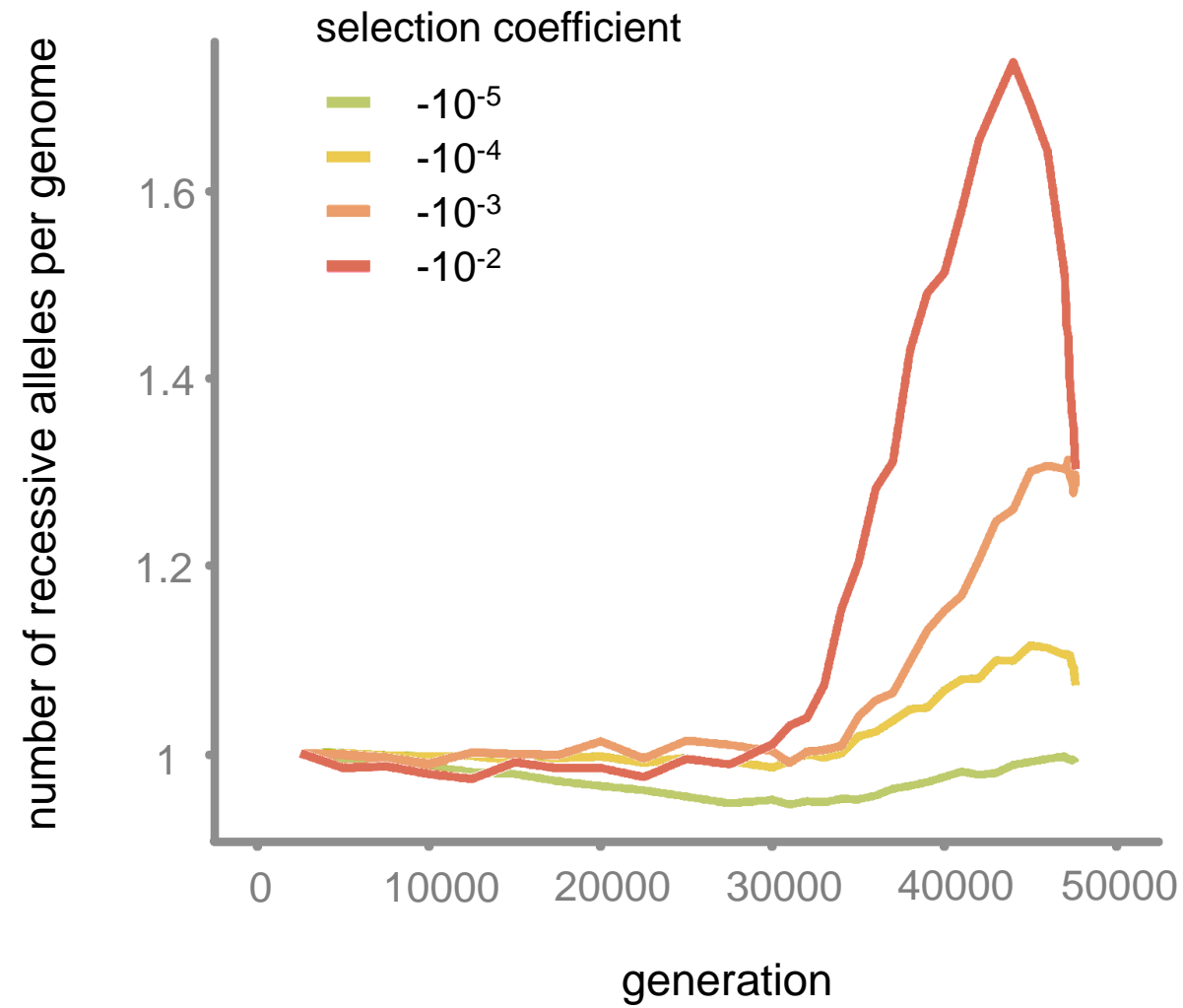


What happened with the spoon-billed sandpiper?

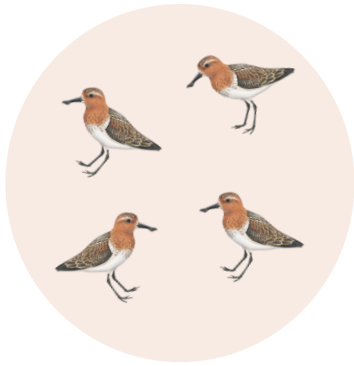
What happened with the spoon-billed sandpiper?



What happened with the spoon-billed sandpiper?



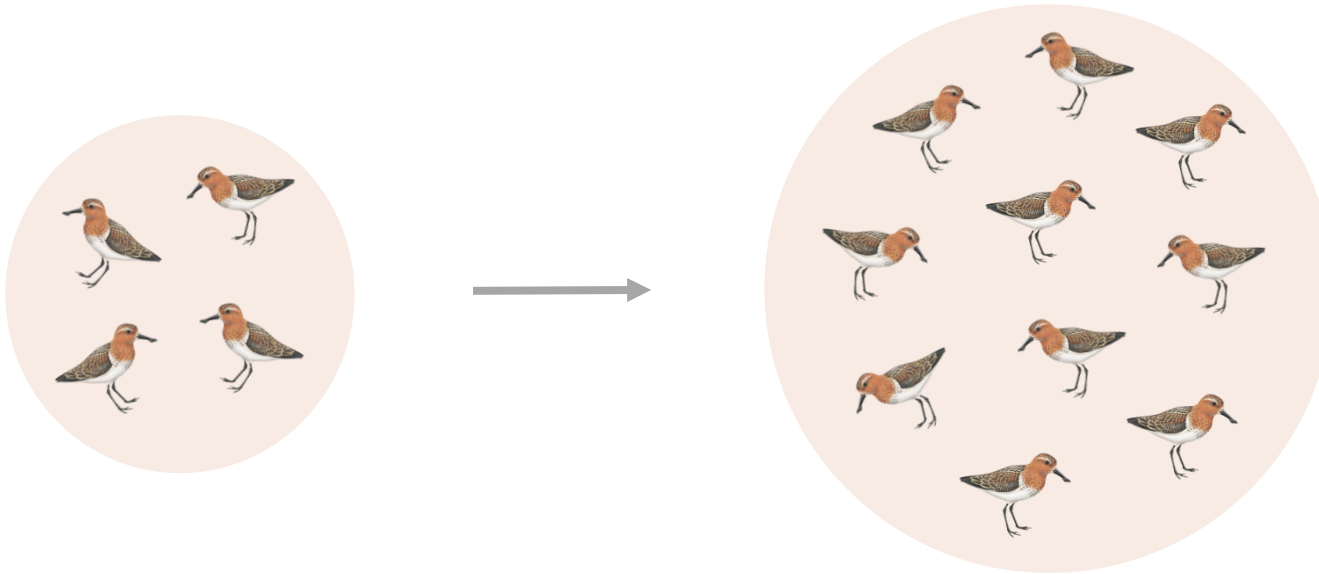
What happened with the spoon-billed sandpiper?



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

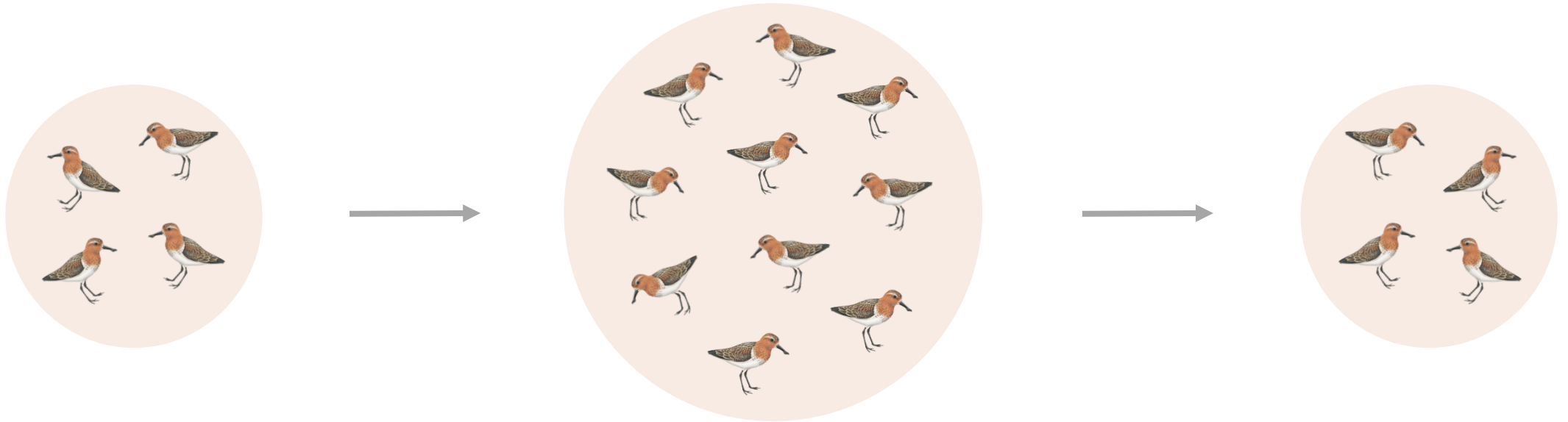


What happened with the spoon-billed sandpiper?



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.

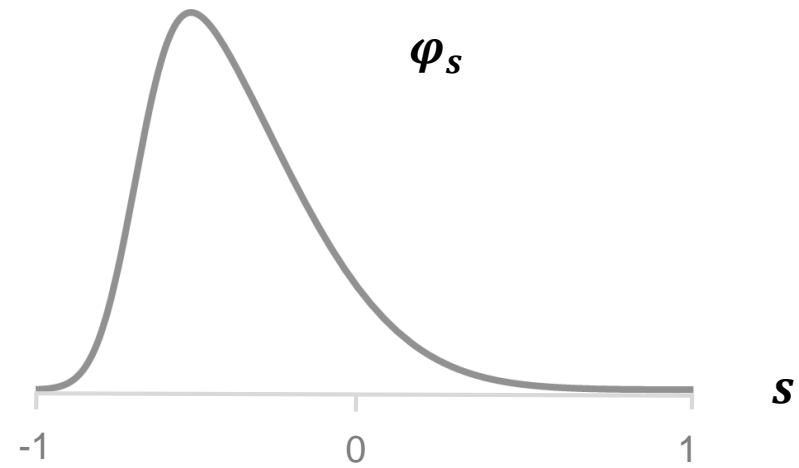
Can we find a distribution of selection coefficients  
that explains what we see?



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

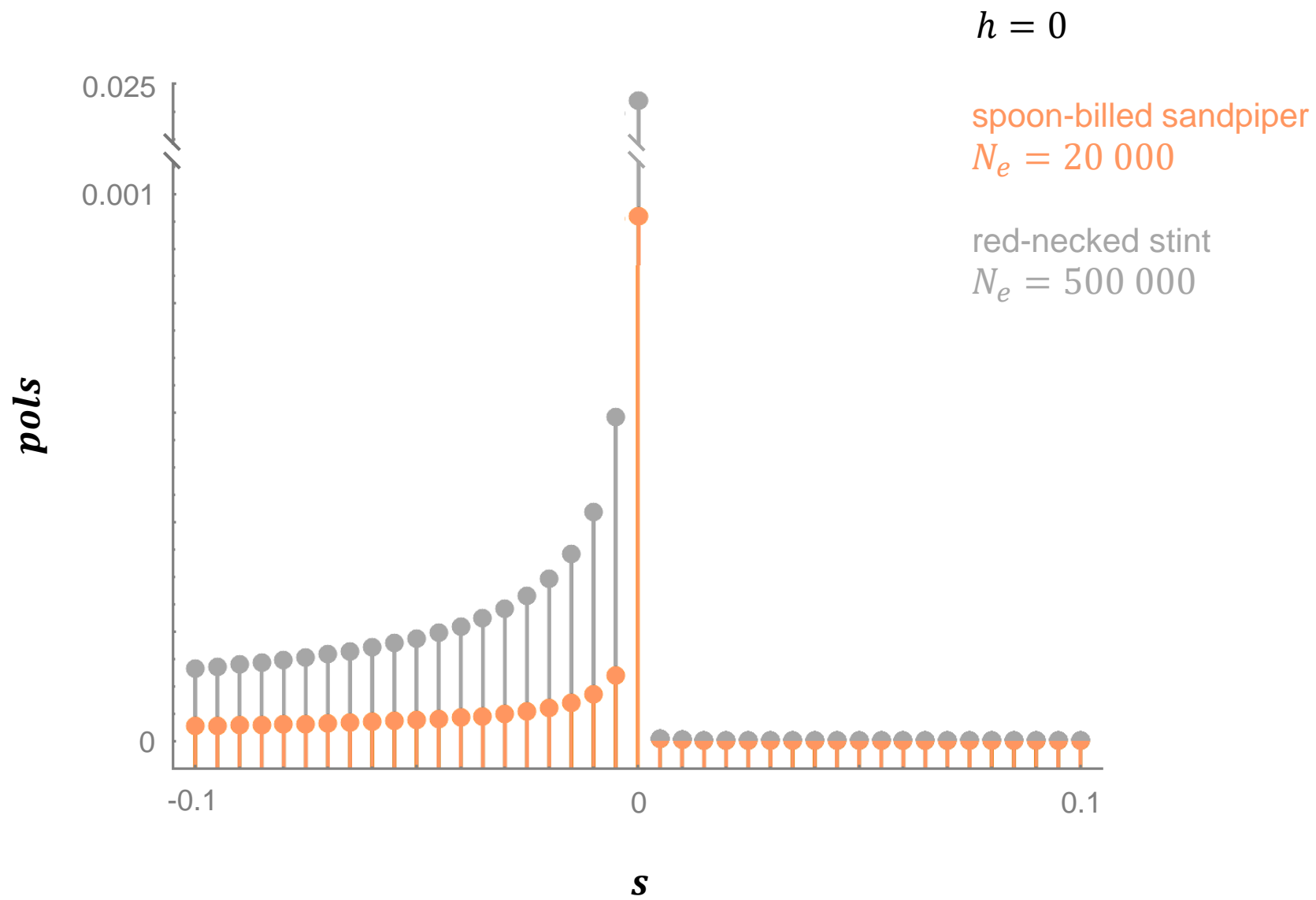
$\varphi_s(\mu, \sigma, \alpha)$  probability density function of the distribution of selection coefficients  
which we model as a skew normal distribution  
with location parameter  $\mu$ , scale parameter  $\sigma$ , and shape parameter  $\alpha$

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

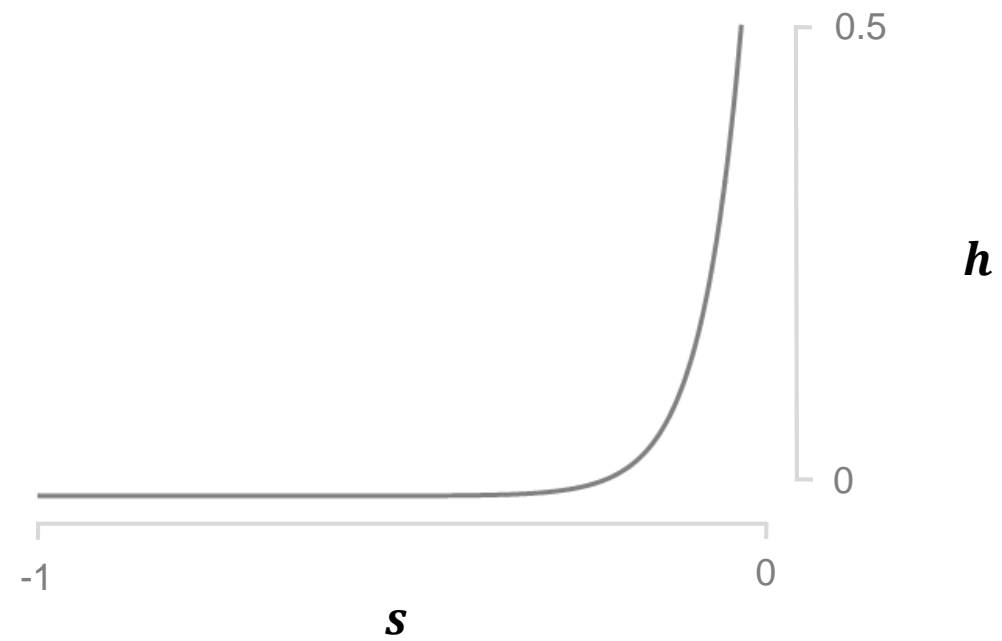
$$c_s = \int_0^1 e^{2N_es(x^2+2hx(1-x))} x^{4N_ev-1} (1-x)^{4N_eu-1} dx$$

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

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



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



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



Fyodor Kondrashov



Mateusz Konczal

Luis Zapata, Francisco Camara, Anna Vlasova, Carla Bello,  
Christelle Fraïsse, Marta Gut, Romain Derelle,  
Maria N. Tutukina, Maria Plyuscheva, Claudia Fontsero,  
Pavel Tomkovich, Nikolay Yakushev, Ivan Shepelev,  
Vladimir Arkhipov, Christoph Zöckler, Roland Digby,  
Egor Loktionov, Elena Lappo, Stephan Ossowski,  
Tomas Marques, Roderic Guigo, Evgeny Syroechkovskiy