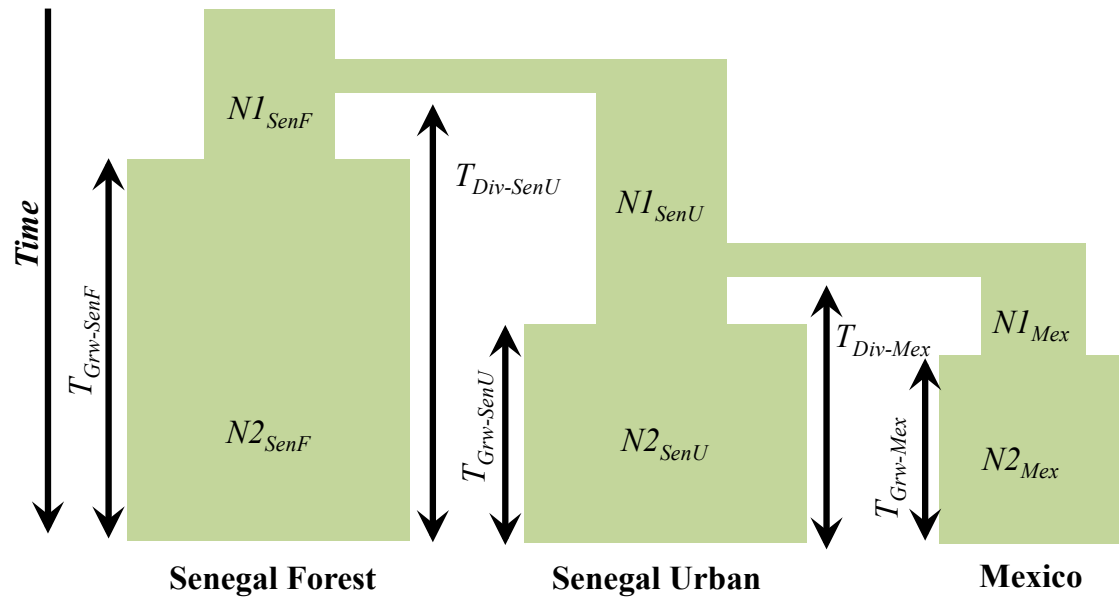
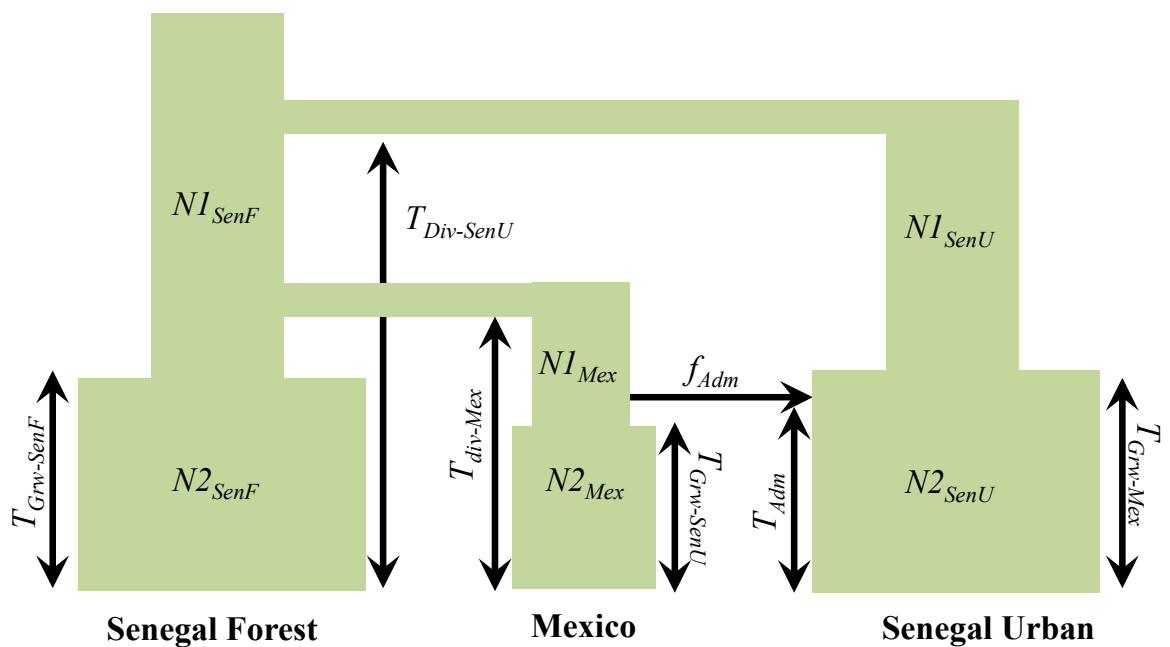


**A Schematics of the demographic models tested and respective parameters.**  
 Note that in the Admixture-back-to-Africa model it is possible for  $T_{div-Mex}$  to be greater than  $T_{div-SenU}$ , which alters the topology so the two Senegal populations are most closely related.

**Serial Founder**



**Admixture-back-to-Africa**



**B** Maximum Likelihood Estimate parameter values from Admixture and Serial-Founder demographic models.

Parameter	Admixture	Admixture with Growth	Serial Founder	Serial Founder with Growth (95% CI)
<i>Log Likelihood</i>	-4,619,583.39	-4,530,874.12	-4,629,091.78	-4,505,380.34
<i>AIC</i> <sup>A</sup>	9,239,179	9,061,772	9,258,192	9,010,781
<i>NI</i> <sub>SenF</sub>		1,268,992		1,122,292 (1,055,832-1,162,543)
<i>NI</i> <sub>SenU</sub>		1,019,454		2,553,390 (2,236,267-3,045,154)
<i>NI</i> <sub>Mex</sub>		543		1,043,544 (333,873-955,603)
<i>N2</i> <sub>SenU</sub>	1,215,256	4,938	1,634,990	24,561 (10,457-32,722)
<i>N2</i> <sub>Mex</sub> <sup>B</sup>	4,310	6,085	9,495	4,968 (3,648-5,815)
<i>T</i> <sub>Div-Mex</sub> <sup>C</sup>	8,907	4,595	5,341	4,366 (3384-5617)
<i>T</i> <sub>Div-SenU</sub>	215,878	98,576	173,350	163,825 (149,044-169,951)
<i>T</i> <sub>Grw-SenF</sub>		587		163,606 (138,53-163,844)
<i>T</i> <sub>Grw-SenU</sub>		81,362		4,150 (1,556-5,192)
<i>T</i> <sub>Grw-Mex</sub>		1,365		2,938 (2275-3637)
<i>T</i> <sub>Adm</sub>	2,141	1,434		
<i>f</i> <sub>Adm</sub> <sup>D</sup>	0.6507	0.5276		

A - Akaike Information Criterion ( $AIC$ ) =  $2d - 2(\text{Log Likelihood})$ , where  $d$  is the number of free variables in the model. We note that our  $AIC$  values are based on composite likelihood values and should therefore be interpreted with caution.

B - Effective sizes given in the number of diploid individuals. The current effective size of Senegal Forest was fixed as  $10^6$  in each model to reduce free parameters.

C - All time parameters ( $T$ ) given in generations before present and are dependent on our assumption of a mutation rate of  $3.5 \times 10^{-9}$ .

D - The fraction of Mexico lineages included in a single pulse admixture event within the Admixture models.

**C Comparison of observed and expected 2D Site Frequency Spectra under four Maximum Likelihood Estimated demographic models.** Each model was fit using Fastsimcoal2 (see Methods) and MLE models were plotted using *dadi*. Colors indicate the number of mutations in each bin as indicated by corresponding scales.

