

Figure S1. Maximum likelihood phylogram of the ptDNA of *Smilax weniæ* and 34 other *Smilax* species, representing an Old World Smilacaceae clade. Posterior probabilities (PP > 0.50) and bootstrap values (BS > 50%) based on Bayesian and maximum likelihood (ML) analyses are shown near the branches. Clade information adopted from Qi et al.[1].

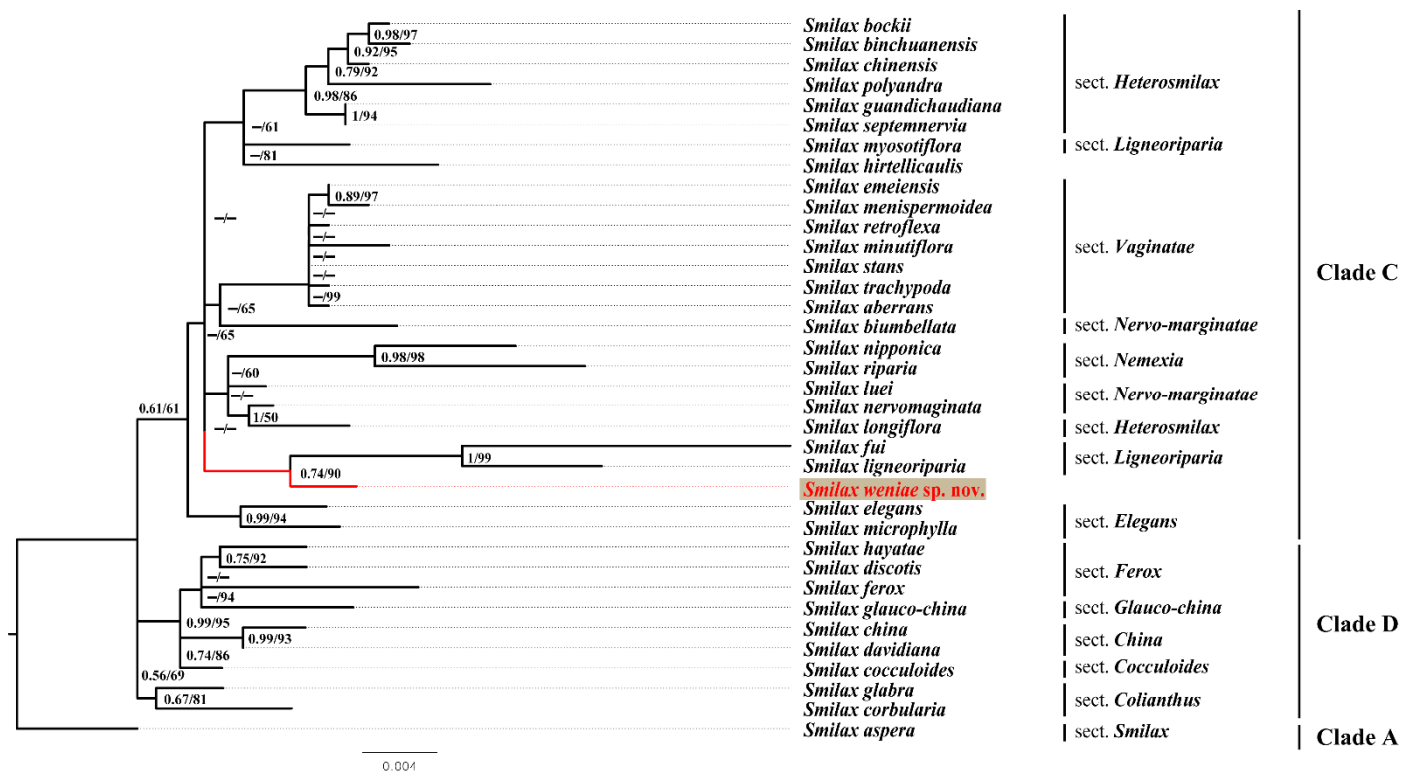


Figure S2. Maximum likelihood phylogram of the nrITS of *Smilax weniæ* and 34 other *Smilax* species, representing an Old World Smilacaceae clade. Posterior probabilities (PP > 0.50) and bootstrap values (BS > 50%) based on Bayesian and maximum likelihood (ML) analyses are shown near the branches. Clade information adopted from Qi et al.[1].

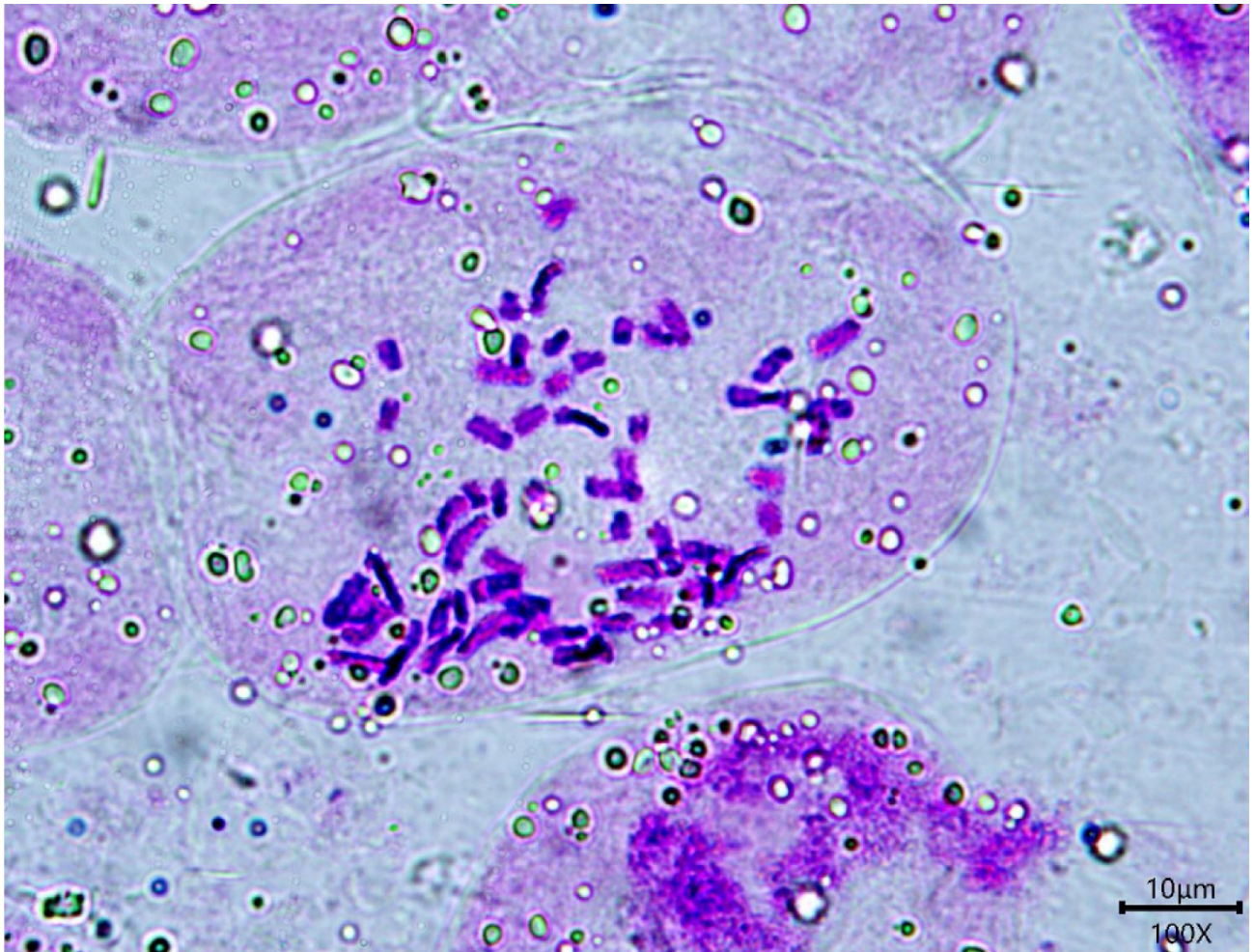


Figure S3. Mitotic chromosomes of *Smilax weniæ*. The most probable basic chromosome number seems to be $2n = 60$.