There are several aspects of the biology of Savannah sparrows on Kent Island that make them especially well suited to exploring the dynamics of divorce. First, divorce is not confounded by a female's efforts to improve her nest site or location, unlike in species that must compete for a restricted number of artificial nest boxes or territories that vary in suitability (Garcia-Navas and Sanz 2011; Bai and Severinghaus 2012). Because Savannah sparrows construct their nests on the ground, nest sites are effectively unlimited, and there is no evidence that females attempt to upgrade territories as they gain in age, breeding experience, or social status (Otter and Ratcliffe 1996). Second, issues such as asynchrony in arrival times or incomplete or erroneous information about mates are not as relevant in Savannah sparrows as in some other species (Gonzalez-Solis et al. 1999; Jeschke and Kokko 2008). Savannah sparrows are opportunistically polygynous, with 10%–40% of males in a given year attracting more than one mate, and males actively court every female encountered near their territories. Time constraints for completing breeding are not as narrow as in many species (Bried et al. 1999), so males do not reject even late-arriving females. Females usually spend several weeks recovering from migration before laying their first clutch, which gives them ample opportunity to assess prospective mates. Third, divorce is not merely a mechanism

Power Analyses

Power analyses were run for four values of additive genetic variance (0, 1, 2, and 3) using simulated data based on data sets restricted to the individuals for which divorce had occurred (i.e., for which we had information in the actual data set). We used 30 replicates per additive genetic variance value. Simulated phenotypes were obtained using pedantics (Morrissey 2009; Morrissey and Wilson 2010). The R code is given online.

The results of these simulations were analyzed visually by overlapping the posterior distributions of the observed data with the simulated posterior distributions of the four additive genetic variance values. There was little or no power to detect additive genetic variance. However, for observed data, the posterior distribution of the additive genetic variance has a very high density close to zero (fig. S5). This was also apparent for simulated values of $_a = 0$ (simulations 2, 4, 9, 24) and $_a = 1$ (simulations 10, 15, 30) and more rarely for higher simulated values of $_a$ (but see simulation 24). Although we had little power to detect significant genetic variance, this suggests that additive genetic variance could indeed exist at very low levels.