



Population and landscape genetics of a reintroduction ·

the Asiatic wild ass *Equus hemionus* in Israel

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Reintroductions are a powerful conservation tool for the recovery of threatened species; however, success rates are often low. The most important determinants for long-term success are i) the genetic makeup of the reintroduced population ii) and the availability of large areas of suitable habitat. Genetic makeup is important since small population size during the early stages of the reintroduction can cause the loss of genetic diversity and evolutionary potential of the established population. Low structural connectivity of the habitat can lead to spatial fragmentation, resulting genetic isolation of subpopulations and increasing the risk of extinction. For my PhD I studied the reintroduced Asiatic wild ass *Equus hemionus* population in Israel. The population was established from eleven founder individuals in 1968 and today counts approximately 300 individuals ranging across a highly heterogenous landscape. The population offers a special case study as founders were sourced from two different subspecies. Successful admixture between these may have enhanced genetic diversity while barriers to admixture could have resulted in cryptic population structure. Furthermore, habitat effects have been suspected to restrict gene flow across the landscape. I applied reduced representation sequencing methods to investigate the population and landscape genetic aspects of this reintroduction. Genetic analysis revealed high levels of subspecies admixture consistent with a significant heterozygote excess. Additionally, I detected a weak genetic structure of the



population. I then combined genetic analysis with individual movement data and electronic circuit theory to investigate landscape effects on gene flow. The analysis revealed no effect of habitat resistance on genetic relatedness. These results suggest that sourcing individuals from two different subspecies may have benefitted the reintroduction. Furthermore, the heterogenous landscape does not appear to impact gene flow in the reintroduced population, however, we cannot exclude the possibility that a potential effect may become apparent in the future.

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