

Yellowstone Bison Genetics: Let Us Move Forward

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White and Wallen (2012) disagree with the conclusions and suggestions made in our recent assessment of population structure among Yellowstone National Park (YNP) bison based on 46 autosomal microsatellite loci in 661 animals (Halbert et al. 2012).

First, they suggest that “the existing genetic substructure (that we observed) was artificially created.” Specifically, they suggest that the substructure observed between the northern and central populations is the result of human activities, both historical and recent. In fact, the genetic composition of all known existing bison herds was created by, or has been influenced by, anthropogenic activities, although this obviously does not reduce the value of these herds for genetic conservation (Dratch and Gogan 2010). As perspective, many, if not most, species of conservation concern have been influenced by human actions and as a result currently exist as isolated populations. However, it is quite difficult to distinguish between genetic differences caused by human actions and important ancestral variation contained in separate populations without data from early time periods. Therefore, to not lose genetic variation that may be significant or indicative of important genetic variation, the generally acceptable management approach is to attempt to retain this variation based on the observed population genetic subdivision (Hedrick et al. 1986).

Potential support for the opinion of White and Wallen (2012) about the large contribution of human actions to the observed genetic differentiation in YNP bison could come from genetic evaluation of bison samples from just before the relocation efforts of 1935–1936 (Cahalane 1944) or from the end of the period of intensive livestock-like management in the 1950s (Meagher 1973). However, if the observed differences were created by human-influenced events before the 1950s, then one would predict that in the last half century since then, natural exchange between the subpopulations would have greatly reduced or eliminated this genetic signal of differentiation. Regardless of the level of human influence on the observed levels of population differentiation, we must collectively move forward as good stewards of this natural resource with the best available scientific information. As

such, it is paramount that we consider the long-term effects of current human interventions (bison “management”) on patterns of genetic diversity.

Second, White and Wallen (2012) state that the low level of gene flow (based on F_{ST}) we reported is no longer present because of recent higher population numbers. They suggest that radiocollared bison movement data from 2002 to 2011 and a genetics study (nuclear microsatellites) of fecal samples from 99 different animals for 17 of our loci from 2006 and 2008 support a recent higher rate of gene flow between the two subpopulations. However, the details of the movement study and the genetic study are unpublished. We encourage White and Wallen to submit these for peer-review publication so the research can be more fully evaluated and used to inform additional research.

Estimates of population structure based on maternally inherited mitochondrial DNA from Gardipee (2007) showed very high differentiation between groups. Further, we examined sex-biased gene flow using her data and found gene flow values that were consistent with estimates from our nuclear data. The unpublished radiocollared bison movement data White and Wallen (2012) report found no movement between the groups for female bison until the years 2006 to 2007. In other words, the lower F_{ST} that they report for 2006 surprisingly measures lower differentiation before this documentation of movement between groups. To evaluate the potential effect of recent higher gene flow, let us assume that F_{ST} declined from 0.032 (our estimated value) to 0.017 (the average of their two values) in one generation from around 2000 to 2007. Using expression (1) in Halbert et al. (2012), then the rate of gene flow would have had to be 27.1% each way between the two groups. This seems unrealistically high.

Furthermore, the substantial evidence of cryptic population structure reported by Halbert et al. (2012) should give pause to observational studies linking YNP bison to particular breeding ranges or subpopulations. That is, while radiocollared bison movement data are immensely useful in understanding patterns of movement (e.g., Olexa and Gogan 2007), empirical genetic data are needed to establish the subpopulation origin of individuals: movement of

individuals is not equal to gene flow. Furthermore, even if higher gene flow is occurring today, unidentified loci, differentiated due to selection, may be still present among the YNP subpopulations.

Finally, White and Wallen (2012) suggest that conservation of ecological processes is more important than genomic conservation. Here, it is critical to keep in mind that ecological processes alone do not define populations. Ecological processes can, however, shape the genetic architecture of a population. That is, a bison population is not defined by whether it migrates or has predators, but rather is determined by the genetic composition of the population and exchange of gene flow with other populations, even if cryptic in nature. Increasingly, ecological processes themselves are highly influenced by anthropogenic activities. For instance, the movement patterns of YNP bison have been continually influenced by humans (hunters, private land owners, government employees) since before YNP even became a park (Meagher 1973). To conclude that ecological processes are somehow more important to population conservation than genomic content is ill conceived, as both warrant consideration in the management of YNP bison.

We submit that a cautious approach be used for conservation of the YNP bison in light of our evidence that significant genetic differences exist between subpopulations. To be clear, we are not proposing that the management goals for YNP bison should include the preservation of the F_{ST} value or specific alleles reported by Halbert et al. (2012). We suggest that there be continuing annual documentation of genetic variation in YNP using as large samples as possible and the most current and comprehensive genetic approaches to document both female and male gene flow and recommend that future management of YNP bison strive to minimally interfere with the distribution of genetic diversity among YNP subpopulations. While culling of bison around YNP without regard for the potential impact on genetic substructure has occurred since the mid-1980s (Plumb et al. 2009; White et al. 2011), a “minimally interfering” strategy acknowledges that genetic diversity is nonrandomly distributed in this population and aspires to develop culling strategies that are sensitive

to the size of each subpopulation. The appropriate use of the best-available scientific information is the best foundation for development of management policies moving forward for this irreplaceable natural resource.

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