## **GRIZZLY BEAR POPULATION TREND ESTIMATED USING GENETIC DETECTION**

Katherine C. Kendall\*, USGS Glacier Field Station, West Glacier, MT Amy C. Macleod, Wildlife Ecology and Management, University of Alberta, Edmonton, AB J. Andrew Royle, USGS Patuxant Wildlife Research Center, Laurel, MD John Boulanger, Integrated Ecological Research, Nelson, BC Tabitha Graves, USGS, Northern Rocky Mountain Science Center, West Glacier, MT Kevin S. McKelvey, USFS Rocky Mountain Research Station, Missoula, MT

We use genetic detection data from natural bear rub sites to estimate annual rate of change for a threatened grizzly bear (Ursus arctos) population in the 33,300 km2 Northern Continental Divide Ecosystem (NCDE) in northwestern Montana, USA). Bear rubs were surveyed twice annually in 2004, 2009-2012 (3,580 - 4,805 rubs). We detected approximately 1/3 of the grizzly bear population annually. Using spatially explicit capturerecapture (SCR) models in a maximum likelihood framework, we estimate growth rate from the slope of a linear regression fit to the log of density estimates. To evaluate the usefulness of our estimates, we compare them to estimates of  $\lambda$  made using independent data from known-fate telemetry monitoring for our population. Total annual population rate of change was 1.056 (95% CI = 1.033 - 1.079). The large sample sizes generated by genetic detection provided information on variation in density and trend within the NCDE useful for designing monitoring and management strategies tailored to area-specific needs and priorities. Local rates of change within the NCDE were higher in areas of lower density and population expansion than in Glacier NP, the area with highest density. As density increased, the amount of space used by bears estimated by the SCR models,  $\sigma$ , decreased. Hair collection from natural bear rub sites was an efficient sampling approach able to generate precise estimates of annual growth rate from 2 years of data.