Alberta's upcoming grizzly bear population inventories

Background



Hair based DNA sampling techniques are a non-invasive adaptation of capture-mark-recapture methods, and are ideally suited for monitoring rare or hard-to-detect species like grizzly bears. The Alberta Grizzly Bear Recovery Plan (2008-2013) recommended that each population unit be inventoried every



five years to assist managers in understanding demographic trends, and to aid in evaluating ongoing land management and recovery efforts.

What's been surveyed?



Previous hair snag DNA population census projects:

BMA 1-2017 BMA 2-2008 BMA 3-2004, 2014 BMA 4- 2005, 2018 BMA 5-2006, 2015 BMA 6- 2007, 2014 BMA 7- no prior survey, 2018









Anja Sorensen, Sarah Milligan, Gordon Stenhouse

BMA 4, Clearwater

BMA 4 was surveyed in 2005. Using spatially explicit capture recapture (SECR) models, the population estimate was 41.45 grizzly bears (CI = 27.77 - 50.04) within the 2005 grid.

Objectives of the upcoming 2018 inventory:

- Obtain population and density estimates that can be directly compared to the 2005 inventory estimates
- Evaluate existing resource selection function (RSF) models 2. with the 2018 DNA inventory results
- Assess changes in grizzly bear distribution relative to core 3 and secondary regions, and landscape change within BMA 4 (forest state, road density, and linear features)





Questions? Contact BMA 4 Project Lead Anja Sorensen: asorensen@friresearch.ca Or BMA 7 Project Lead Sarah Milligan: smilligan@friresearch.ca

BMA 7, Swan Hills

Swan Hills is the only provincial BMA that has not been surveyed using hair based DNA mark-recapture.

Objectives of the upcoming 2018 inventory:

- Obtain an estimate of population size of grizzly bears
- Assess the spatial distribution of grizzly bears relative to core and secondary areas defined by previous RSF
- modelling (Nielsen et al. 2009)
- Examine genetic connectivity between BMAs
- Evaluate bear distribution relative to forest management
- activities, current road networks and linear features

