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, Ramsey, Andrew D. ORCID: <https://orcid.org/0000-0002-5550-9977> and
Sinclair, Billy (2009) Connectivity in brown bear populations: an assessment of
gene flow in coastal British Columbia. In: 2nd European Congress of
Conservation Biology (ECCB), 1-5 September 2009, Czech University of Life
Sciences, Prague, Czech Republic.

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Clapham M, Nevin OT, Ramsey AD & Sinclair B (2009) Connectivity in brown bear populations: an assessment of gene flow in coastal British Columbia.
2nd European Congress of Conservation Biology

Brown bear (*Ursus arctos*) populations have experienced declines in both number and range due to changes in land use and persecution. Identifying and protecting areas with adequate gene flow between populations is now of fundamental importance to the survival of some populations. This study assessed genetic variance and relatedness between individuals from two coastal regions of British Columbia. Samples were analysed at 8 microsatellite loci to determine individual genotypes for statistical analysis. The mean expected heterozygosity (H_e) of all individuals was 0.69. A difference in H_e was highlighted between genders, with females displaying homozygosity for 2 out of 8 loci. Genetic differentiation was low ($F_{ST} = 0.06$) between coastal individuals. Dispersal distances of bears in the area would suggest the possibility of gene flow between the two regions. Genetic distance estimates, through kinship coefficients and the proportion of shared alleles, further reiterated a link between the two densely populated areas. Data from this study indicates dispersal via gene flow between the brown bears of southwest coastal British Columbia. Comparisons can now be made with European populations, regarding relatedness and assessment of the connectivity of landscapes. Implications for the conservation of this species in Europe's fragmented landscape will be discussed.