

Genetic clusters from Oyler-McCance et al. (2005).

Oyler-McCance, S.J., S.E. Taylor, and T.W. Quinn. 2005. A multilocus population genetic survey of the greater sage-grouse across their range. *Molecular ecology* 14(5):1293-1310.

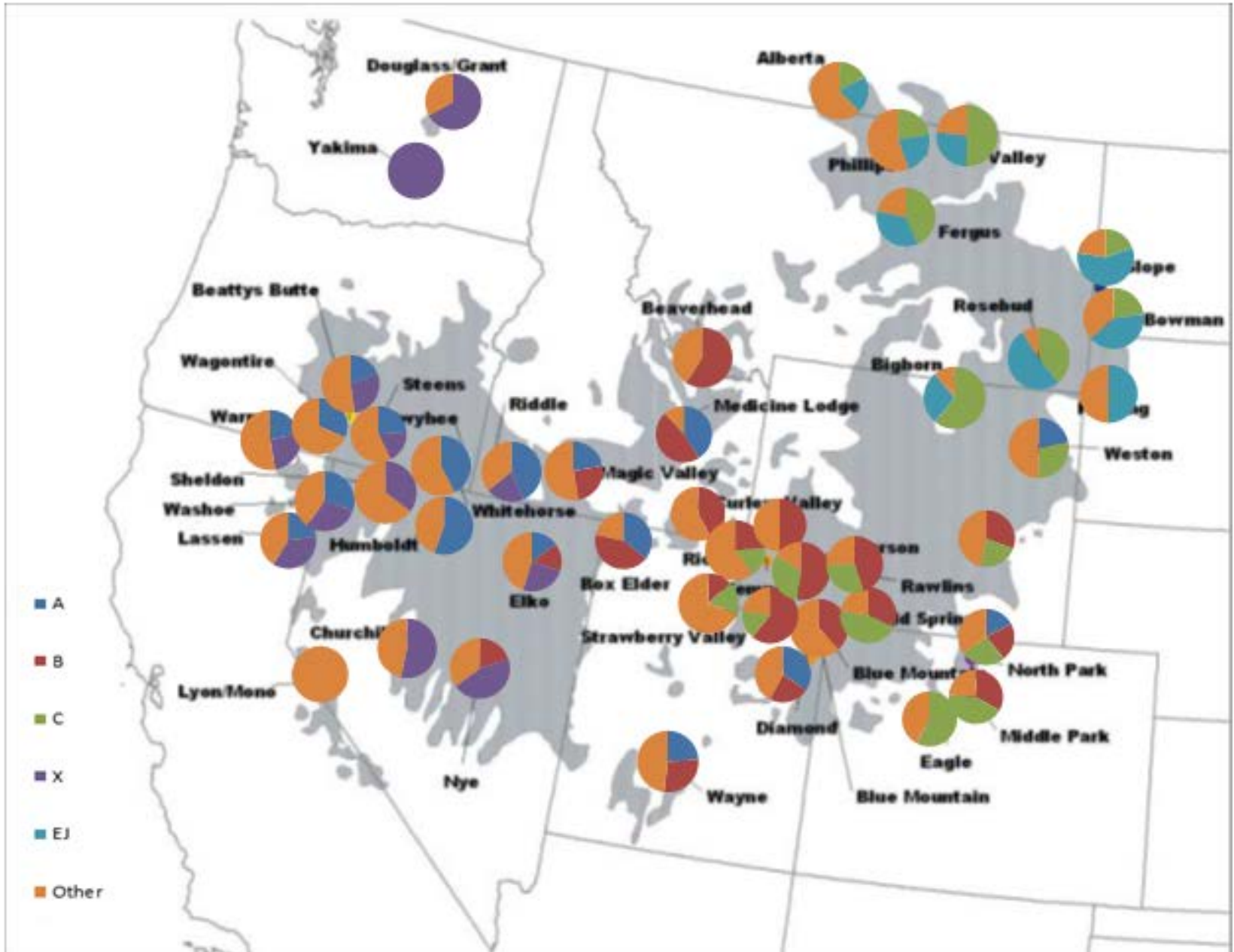
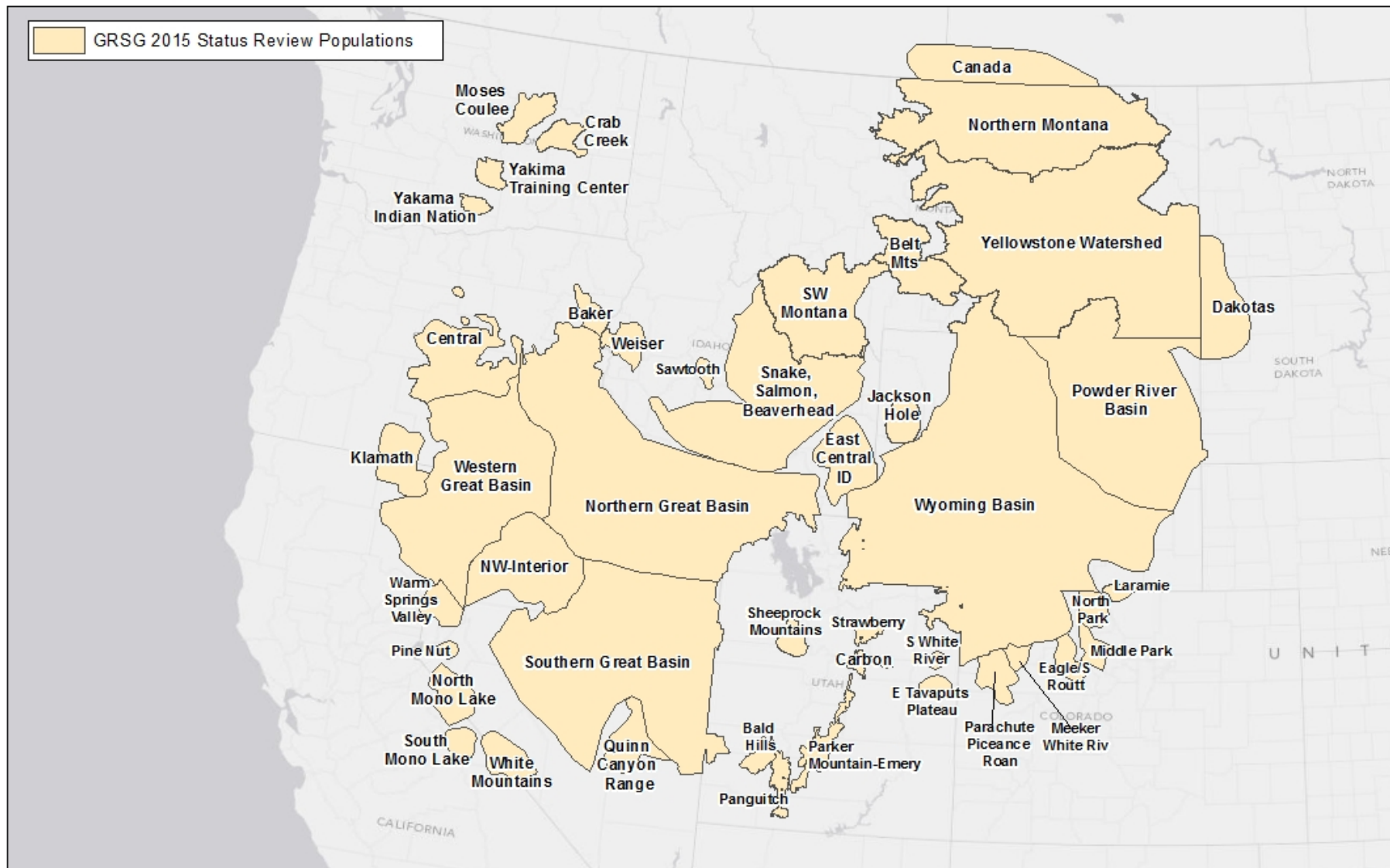


Fig. 3. Distribution of the most common mtDNA haplotypes, derived from Oyler-McCance et al. (2005). NOTE: Orange represents numerous other uncommon, and in some cases unique, haplotypes.

[From: Framework for Identifying Greater Sage-grouse Conservation Units to Assist with Evaluation of the Status of the Species and Potential DPS Analyses. Draft, predecisional, deliberative internal FWS working document, draft updated 17 July 2014]



## Draft Map - GRSG 2015 Status Review Populations

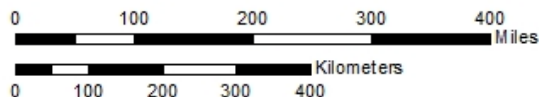


Created By: US FWS, Wyoming ES

Map Date: 8/14/2014

Source: FWS | BLM | WAFWA | Schroeder et al. (2004) |

Base Map: Canvas/World Light Gray Esri, HERE, DeLorme, MapmyIndia, ©  
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Datum: NAD 83

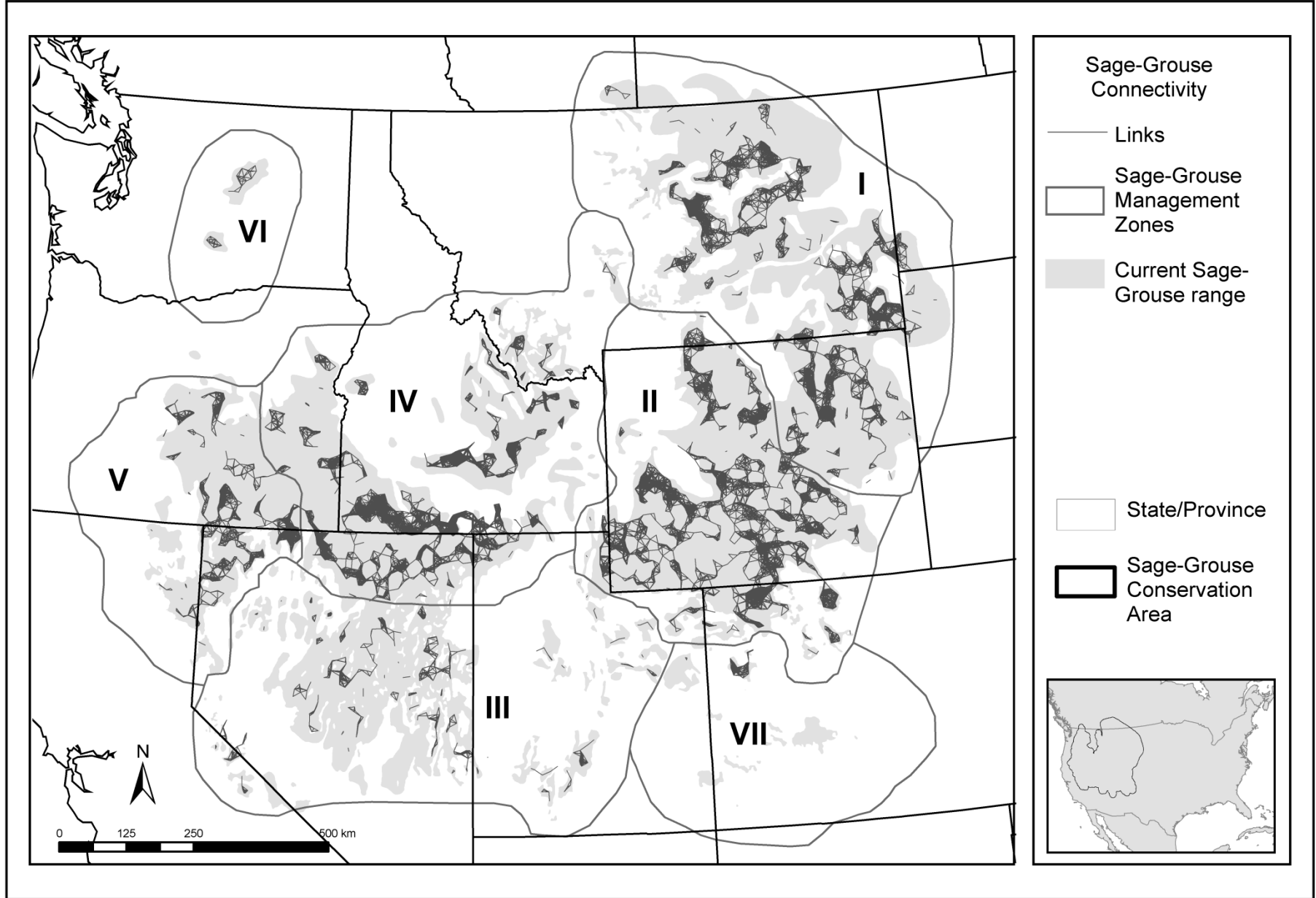


Figure 16.3 Distribution of current (2003-2007) Greater Sage-grouse leks. Populations at leks were connected if the straight-line distance to neighbors was <18 km. (From Knick and Hanser 2011)

Knick S.T. and S.E. Hanser. 2011. Connecting pattern and process in greater sage-grouse populations and sagebrush landscapes. Pages 383–405 in S.T. Knick, and J. Connelly, eds. Greater sage-grouse: ecology and conservation of a landscape species and its habitats. Studies in Avian Biology 38. University of California Press, Berkeley, California.



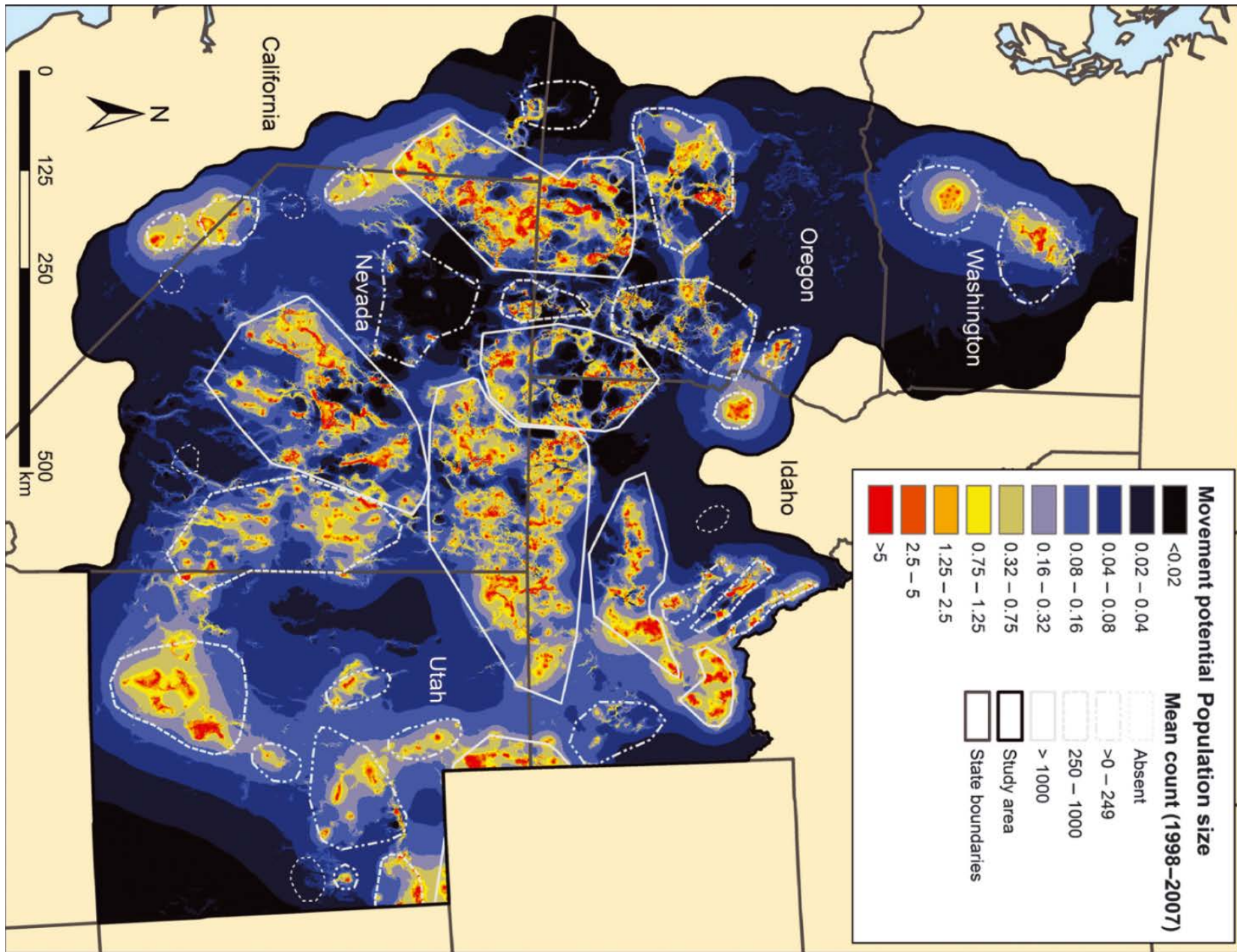


Figure 6. Estimated potential for sage-grouse movement among sage-grouse leks (Circuitscape; McRae 2006). Rescaled HSI values were used as a measure of landscape resistance. (From Knick et al. 2013)

Knick, S.T., S.E. Hanser, and K.L. Preston. 2013. Modeling ecological minimum requirements for distribution of greater sage-grouse leks: implications for population connectivity across their western range, USA. *Ecology and evolution* 3: 1539-1551.

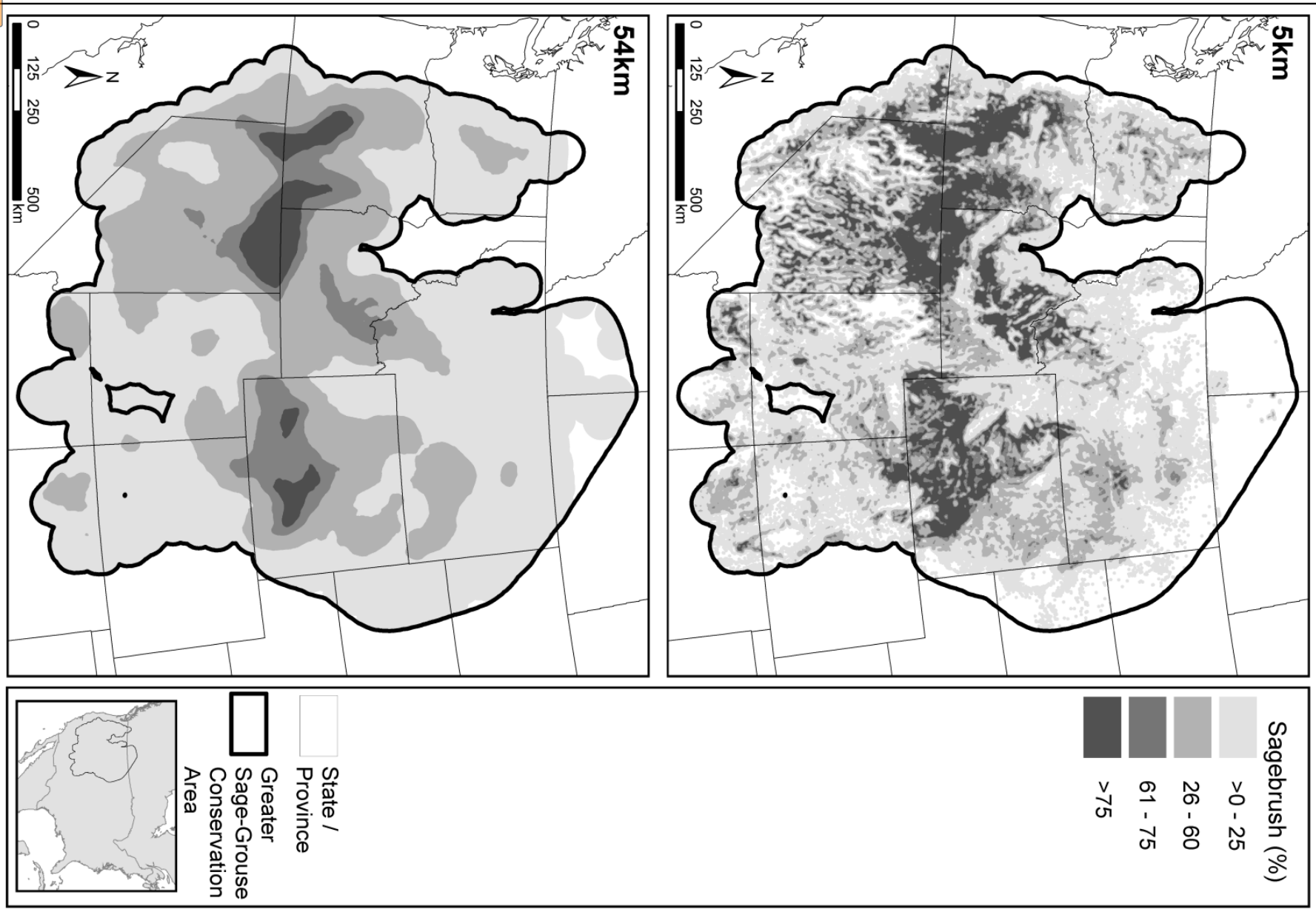


Figure 16.1. Percent of the landscape dominated by sagebrush within a 5-km (top) and 54-km (bottom) radius of each 0.5 km grid cell. (From Knick and Hanser 2011)

Knick S.T. and S.E. Hanser. 2011. Connecting pattern and process in greater sage-grouse populations and sagebrush landscapes. Pages 383–405 in S.T. Knick, and J. Connolly, eds. Greater sage-grouse: ecology and conservation of a landscape species and its habitats. Studies in Avian Biology 38. University of California Press, Berkeley, California.

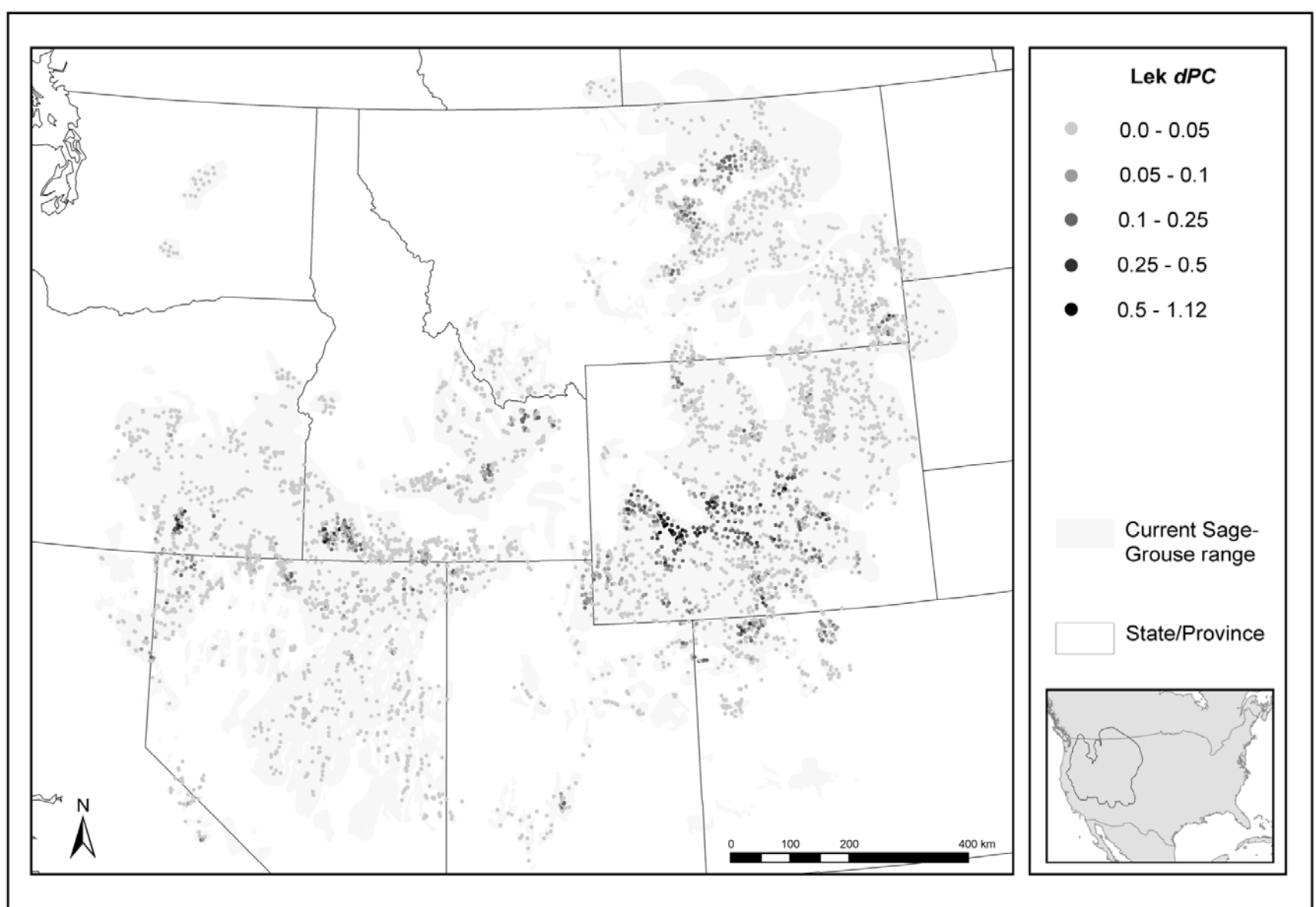


Figure 16.4. Importance of individual leks in maintaining connectivity in the range-wide distribution of Greater Sage-Grouse. Lek *dPC* measures change in landscape connectivity that results when a lek is removed from the network. Higher *dPC* values reflect larger numbers of sage-grouse at a lek and greater connectivity with the network.

Knick S.T. and S.E. Hanser. 2011. Connecting pattern and process in greater sage-grouse populations and sagebrush landscapes. Pages 383–405 *in* S.T. Knick, and J. Connelly, eds. Greater sage-grouse: ecology and conservation of a landscape species and its habitats. Studies in Avian Biology 38. University of California Press, Berkeley, California.

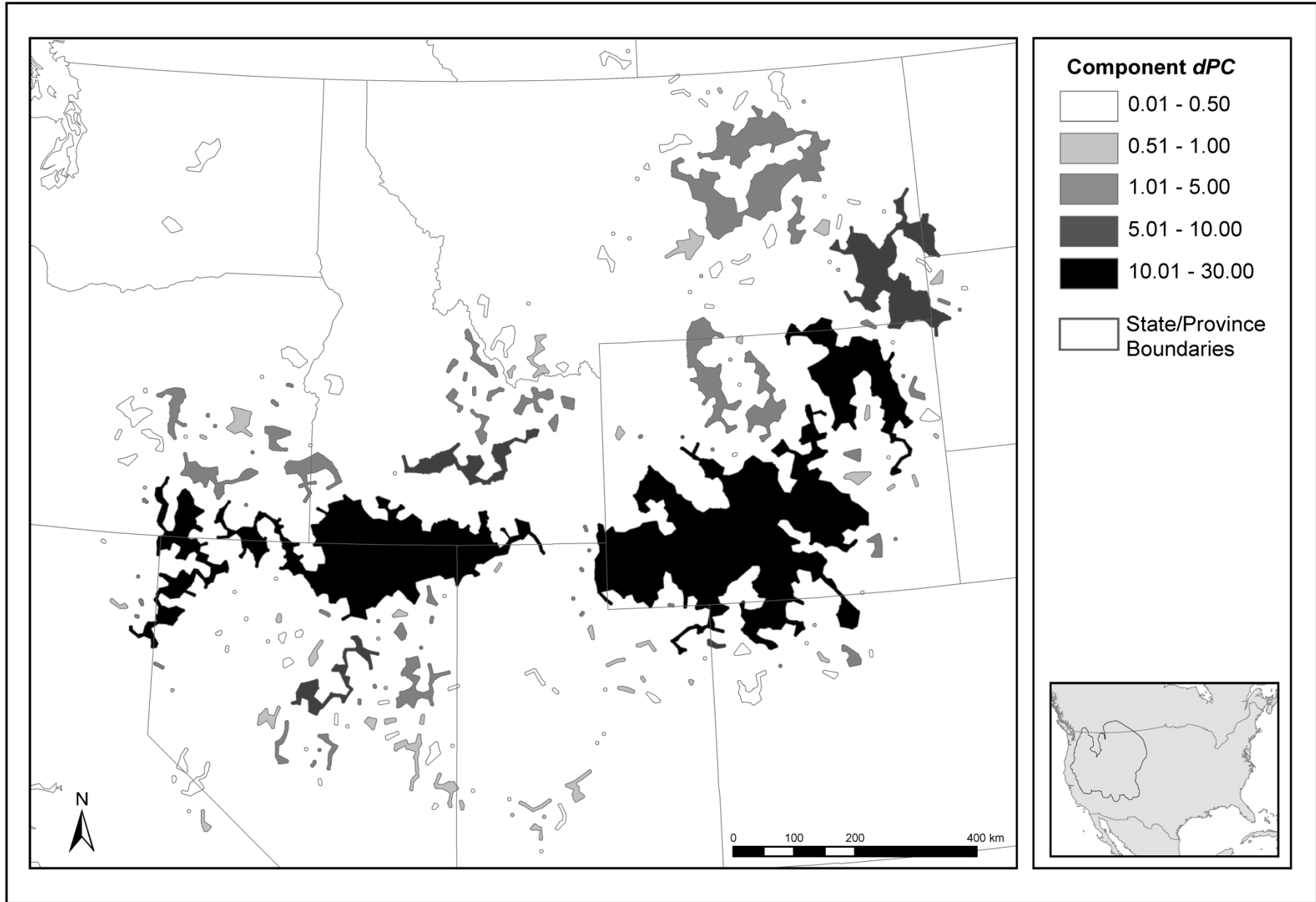


Figure 16.6. Location of 209 components and their importance (*dPC*) in maintaining connectivity across the range-wide distribution of Greater Sage-Grouse. Number and spatial arrangement of components was evaluated for a dispersal distance of 18 km. (From Knick and Hanser 2011)

Knick S.T. and S.E. Hanser. 2011. Connecting pattern and process in greater sage-grouse populations and sagebrush landscapes. Pages 383–405 in S.T. Knick, and J. Connelly, eds. Greater sage-grouse: ecology and conservation of a landscape species and its habitats. Studies in Avian Biology 38. University of California Press, Berkeley, California.