Buckley, B.A. and G.N. Somero. 2009. cDNA microarray analysis reveals the capacity of the cold-adapted Antarctic fish *Trematomus bernacchii* to alter gene expression in response to heat stress. *Polar Biology* 32:403-415.

After years of living in the extreme and stable cold conditions of McMurdo Sound, Antarctica, a species of fish, *Trematomus bernacchii*, has lost the ability to up-regulate heat shock proteins (HPS) in response to elevated temperatures. As global climate change is predicted to further increase sea temperatures, it is important to find the extent at which other patterns of gene expression related to the adaptation of increased temperatures have been lost in these species over time. In order to do so, specimens of *T. bernacchii* were collected and placed into three groups of three. The first group of fish were heat shocked at 4°C for four hours in a 400-L aquarium, then killed and their gills were removed and frozen. The second group of fish, the control group, were placed in an identical aquarium where temperatures were held at -1.8°C for four hours, then killed and their gills removed and frozen. The third group of fish were heat shocked at 4°C for four hours in an identical aquarium then transferred to another aquarium where temperature was returned to -1.8°C. The fish were allowed to recover at intervals of two and four hours where upon their gills were removed and frozen. All frozen gills were thawed and total RNA extracted for use in a comparative analysis using cDNA microarray hybridization. The results showed gene expressions responsible for overall enhancement in functions involving cytoskeleton organization, metabolic pathways, protein synthesis, and cell progression and growth in response to warmer temperatures. It is apparent based on these results that although up-regulation of HRP is absent in *T. bernacchii*, modifications in expressions involving hundreds of other genes has been retained.

Cooper, S.M., H.M. Scott, G.R. de la Garza, A.L. Deck, and J.C. Cathey. 2010. Distribution and interspecies contact of feral swine and cattle on rangeland in south Texas: implications for disease transmission. *Journal of Wildlife Diseases* 46:152-164.

Foot-and-mouth disease (FMD) is the most costly livestock disease in the world, and infects feral swine (*Sus scrofa*). The FMD virus (FMDV) can be transmitted by direct contact of infected animals, indirect contact with the environment of an infected host, and by aerosols. In this study researchers examined the seasonal habitat selection of feral swine and cattle on rangeland regarding water sources, riparian areas, and roads, to identify locations of spatial and temporal overlap between species. Rates of direct and indirect contact between feral swine and cattle were also determined. The study was conducted on a 35,000 hectare ranch in Zavala County, Texas. Main vegetation is semiarid shrub community with native and introduced grasses and taller woody species in riparian areas. GPS were placed on four cattle and eight hogs for each of the eight trials, but data was only obtained 3-1 cattle and 5-3 feral swine. Scientists defined direct contact as < 20 m and within 15 minutes, and indirect contact as < 20 m and within 360 minutes. GPS data showed direct contact between feral swine and cattle only occurred 12 times during the study, but indirect contact occurred 284 times. Direct contact happened mainly near water sources and indirect contact being highest in cultivated fields and near water sources. The least amount of contact occurred in the riparian habitat. This study demonstrated that animals were not randomly distributed throughout the landscape. According to GPS data, water sources and cultivated fields are the primary targets for disease transmission between livestock and feral swine. Reduction of contact rates is important for limiting FMD transmission. Incorporation of this information into geographic-automata models will increase prediction capabilities, and therefore improving response and control methods to limit potential disease incursions.