1. Introduction
   1. Climate change = “hard” selection causing rapid selection for stress-tolerant genotypes (Reusch & Wood 2007)
   2. Rapid evolution = occurs simultaneously to but alters ecological dynamics (Hairston et al. 2005)
2. Background on selection and adaptation
   1. Need variability in traits for selection to work (Graur & Li 2000)
   2. Adaptation = shift in distribution of phenotypes/year caused by change in genotype (microevolution) or phenotypic plasticity (Visser 2008)
      1. Shifting phenotypes can mean adaptation or disruption
      2. Need stabilizing, not directional, selection for adaptation
      3. Directional change means that phenotype can occur without genotype change (Gienapp et al. 2008)
   3. If evolutionary or plastic response is impossible then physiology changes according to environmental variation and demographic response = local extinction (Chown et al. 2010)
   4. Response to climate change necessitates evidence of 1. Selection of trait, 2. Selection caused by/linked to climate change, 3. There is genetic change in trait (Gienapp et al. 2008)
   5. Adaptation to climate change depends on: 1. Magnitude and rate of climate change, 2. Ecological breadth of individual genotypes, 3. Distribution and genetic variation of relevant traits, 4. Extent of gene flow, 5. Demographic flux of populations, 6. Changing interspecific competition based on different responses to climate change (Davis et al. 1995)
   6. Heritable traits respond to selection following Falconer & Mackay 1996: R=h2\*s, R=phenotypic selection response, h2=heritability, s=selection differential (Gienapp et al. 2008)
   7. Constraints on adaptation: lack of variability, inbreeding due to shrinking populations (Gienapp et al. 2008)
   8. Genetic constraint arises from correlations among traits (Davis et al. 1995)
   9. Evolutionary stasis despite directional selection: lack of polymorphism in genes, negative trait correlations caused by pleiotropy or linkage, metabolic costs and associated trade-offs. (Reusch & Wood 2007)
3. Genetic changes in wild populations
   1. *Daphnia pulex*: 9 gene families have expanded independently in daphnia and other aquatic lineages = photoreceptive and photoresponsive. High rate of gene duplication, but 47% non-allelic so concerted evolution on protein coding sequence; some paralogs with low sequence divergence also show differential gene expression in different environmental conditions. Functionally divergent gene duplicates maintained via preservation by entrainment (Colbourne et al. 2011)
   2. Old world anchovies *Engraulis* spp.: historically large populations in N hemisphere and recent colonization in S. Long shorelines during ancient climate change (Pleistocene, ocean T and sea levels) allowed N to shift range, but S could not and was later re-colonized by N. (Grant & Bowen 2006)
   3. Killifish *Fundulus heteroclitus*: pollution exposure 50+ years, pollution tolerant and sensitive populations to F2 in lab. Sensitive had a greater transcriptional response to PCBs and dose-dependent (no dose dependence in tolerant) (Whitehead et al. 2010)
   4. Tomcod *Microgradus tomcod*: 1947-1976 GE facilities released 590,000 kg of PCBs into the Hudson River. Four out of 5 polymorphisms in aryl hydrocarbon receptor 2 are fixed in HR compared to references (2 synonymous, 1 nonsynonymous, 6 bp deletion). WT allele only in heterozygotes in HR. No evidence of genetic bottleneck in HR. HR allele has 5x lower binding affinity for toxicants. Rapid evolutionary change 50-100 years manifested in functional changes in coding region of gene (Wirgin et al. 2011)
   5. Darwin’s finches: El Nino changed relative abundances of spp *Geospiza scandens* and *G. fortis*. Fewer scandens because climate made food (cactus) less abundant. Smaller *G. fortis* did better (smaller beak size selected for by different food resources) and beak traits are highly heritable/mortality was size-selective. (Grant & Grant 1993)
      1. Evolution changes faster than ecology x2.2 for body and beak size, no effect of beak shape (Hairston et al. 2005)
   6. *Tamiasciurus hudsonicus* American red squirrels: plastic and microevolutionary response (advancement in breeding) to change in food abundance and increased spring temperature over 27 years. Partruition date has significant genetic variation and under selection (Réale et al. 2003)
   7. Urchin *Centrstephanus rodgersii*: historic and newly colonized ranges (warmer waters). Gene diversity in expansion zone ~source population. No founder or bottleneck effect – continuous expansion and gene flow (Banks et al. 2010)
   8. Weedy mustard *Sinapis arvenis*: 3 generations of selection to high boron, high light, low light, low water and low nutrients. Tested selection pressures on F5. No adaptation to stresses in terms of fecundity, although effects on phenotype and phenology (Stanton et al. 2000)
   9. New Zealand snapper *Pagrus auratus*: loss of genetic diversity in Tasman Bay (low mean Hz, decreased no. alleles, decreased gene diversity in 6/7 loci, Ne/N ~10^-5) comared to Haruaki Gulf and from 1950. (Hauser et al. 2002)
4. Rate of genetic change vs. rate of climate change
   1. Need specific selection pressure or gradient
   2. If genetic variability not there, change won’t happen
   3. Decreases in genetic variance increase the lag of population mean phenotype behind optimum. This increases selection, decreasing Ne, thus decreasing genetic variance through drift. Without mutation, population will go extinct (Burger & Lynch 1995)
   4. Counter-gradient variation: opposing temporal patterns of phenotypic and genetic divergence – phenotype can be misleading. In climate change there is a rapid response to removal of environmental constraints on phenotype (Gienapp et al. 2008)
   5. For a large rate of environmental change, any population will go rapidly extinct, no matter size. With low variability, a population can respond evolutionarily for a long time (Burger & Lynch 1995)
   6. When something is rapidly selected for, other genes may hitchhike along
5. Pros and Cons of studying genetic changes in wild populations
   1. Will have the potential to acclimate/adapt to future change
   2. Allows for the chance to work within the structure of the variability that occurs naturally
   3. Harder to study multiple generations
   4. Don’t know history
   5. Acclimation vs adaptation
   6. Killifish: 12.5C cline ME-GA with significant IBD population differentiation. High intrapopulation differences in gene expression (balancing selection), but some interpopulation (41 out of 329 genes). Residual variation after genetic distance is adaptive (Whitehead & Crawford 2006)
   7. In studies in field, access to multiple co-occurring stressors
   8. Complexity of organism-environment interaction: what is the mechanism of response?
   9. Complexity of genome: how do genes interact with each other?
6. Conclusion