Evolution and Adaptation

1. Adaptation to environmental changes
   1. Phillips & Hickey 2010. Genotype-dependent recovery from acute exposure to heavy metal in freshwater clam
      1. New Zealand fw clam *Sphaerturn novaezelandiae* – no larval stage, live young
      2. Exposed to Zn for 96 h: fitness measured by reburial into sediment
      3. Allozyme electrophoresis on whole body tissue for genotyping
      4. Significant effect of treatment on mortality – no contribution from genotype
      5. Genotype influences recovery rate
   2. Aldenhoven et al. 2010. Phylogeography of 9 spine sticklebacks in N. America: glacial refugia and the origins of adaptive traits
      1. 23 sites in north am., 9 in Eurasia
      2. mtDNA and microsat markers
      3. N.Am. sticklebacks survived Wisconsin glaciation in at least 3 refugia
      4. Major lineages emerged during Pleistocene – major clades in place before WI glaciation
      5. Morphological adaptive traits not associated with specific refugia – emerged multiple times independently
   3. Visser 2008 (review). Keeping up with a warming world; assessing the rate of adaptation to climate change
      1. Best-recorded climate-induced shifts: phenology & range shifts
      2. Others: changes in body size and strength of interspecific competition
      3. Adaptation: shift in distribution of phenotypes/year
         1. Caused by change in genotype (microevolution)
         2. Or phenotypic plasticity
      4. Interpretation of shifting phenotypes: disruption or adaptation
      5. Need selection for adaptation (not directional selection)
      6. Reaction norms = relationship between trait and environmental variation
         1. Slope=sensitivity of trait to environment
         2. Elevation=trait value in average environment
   4. Chown et al. 2010. (review) Adapting to climate change: a perspective from evolutionary physiology.
      1. If evolutionary or plastic response is impossible then physiology changes according to environmental variation and demographic response is local extinction
      2. Importance of performance curves: limits, breadth, optima, maxima
   5. Gienapp et al. 2008. (review) Climate change and evolution: disentangling environmental and genetic responses.
      1. To conclude that a population has responded to climate change, need evidence: 1. Selection of trait, 2. Selection caused by/linked to climate change, 3. There is a genetic change in trait
      2. Constraints on adaptation: 1. Lack of variability, 2. Inbreeding due to shrinking populations
      3. Heritable traits should respond to selection following Falconer & Mackay 1996: R=h2 \* s
         1. R=phenotypic selection response, h2 = heritability, s = selection differential
         2. Assumptions: frequently violate assumption of constant environment over generations
      4. Directional change in a population means phenotype can occur without genotype change
      5. Counter-gradient variation: opposing temporal patterns of phenotypic and genetic divergence -> phenotype can be misleading
         1. Important in climate change because rapid response – removal of environmental constraints on phenotype
   6. Davis et al. 2005(review). Evolutionary responses to climate change.
      1. 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
      2. Trees produce many seeds, 1000s of seedlings establish, climate change selection acts on genetic variance available from juveniles onwards -> increase frequency of genotypes that tolerate novel climates
      3. Genetic constraint arises from correlations among traits
   7. Stanton et al. 2000. Evolution in stressful environments. I. Phenotypic variability, phenotypic selection, and response to selection in 5 distinct environmental stresses
      1. Interaction selection pressures of disturbance frequency and environmental stresses lead to 3 life history strategies: 1) ruderal, 2) competitive, 3) stress tolerant
      2. Consequences of stress on life history evolution – do different selection patterns lead to common suite of adaptations?
      3. Weedy mustard (*Sinapis arvenis*) – field collected, 3 generations under selection (high boron, high light, low light, low water, low nutrients); 4th generation under control conditions; 5th generation tested at all selection pressures
      4. All stresses reduced female fecundity – variable importance of current environment vs. history & current environment
      5. No evidence for genetically-based variation in fecundity
      6. No adaptation to 5 stresses (sample may be too small)
      7. Significant effect of selection history on phenotype
      8. Even under different treatments, family-specific phenotypes apparent (genetic variation)
      9. Stresses had varying effects on phenology
   8. Réale et al. 2003. Genetic and plastic responses of a northern mammal to climate change.
      1. American red squirrels – female reproductive activity and parturition dates for 4 generations
      2. Over 27 years: spring temperature has increased ~2C
      3. Over 10 years: parturition date earlier by 2 weeks
      4. Food abundance significant for breeding date – lots of plasticity
      5. Parturition date has significant genetic variation and is under strong directional selection
      6. Life history traits respond to large changes in environment
      7. Advancement in breeding = plastic response to increases in food and microevolutionary response to selection
   9. Al-Hiyaly et al. 1993. The effect of zinc contamination from electricity pylons. Genetic constraints on selection for Zn…
      1. Grass *A. capillaris* seems to have developed some tolerance (in small parts of population) of Zn beneath pylons
      2. Collected grass from 5 pylons and tested for Zn tolerance
         1. 2 generations of artificial selection for Zn tolerance
      3. Collected from uncontaminated soil and tested tolerance
      4. Significant differences in tolerances between and within pylon populations and - similar results for uncontaminated soil
      5. Interpopulation differences in response to selection and across Zn concentrations
      6. Pylon populations with less tolerance also had less variability in tolerance and decreased heritability of trait – may be because recently contaminated or absence of genes for Zn tolerance
      7. evidence for genetic constraints limiting evolution of Zn tolerance (genes are present only in some populations)
      8. stochasticity provides variability
   10. Whitehead et al. 2010. Comparative transcriptomics implicates mechanisms of evolved pollution tolerance in a killifish population.
       1. Collected killifish from pollution tolerant and sensitive populations
          1. Experiment on 2 generations removed from collected
       2. Responsiveness of embryos to PCB congener in lab
          1. Tolerant phenotype determined
          2. 4 or 5 embryos per treatment - microarray
       3. 150-fold difference in chemical tolerance based on observations
       4. more extreme phenotypic abnormalities in sensitive
       5. transcriptional response: sensitive>tolerant
       6. sensitive: number of genes differentially expressed and magnitude of expression increased with dose, at highest exposures more downregulated
          1. GO terms downregulated only in sensitive: contractile fiber, response to wounding, angiogenesis (mutants in genes show cardiomyopathies), cell adhesion, oxidative phosphorylation, glycolysis, calcium ion binding, protease inhibitor
          2. GO terms upregulated: cytochrome P450, haeme binding
       7. tolerant: individual variation in gene expression dependent on phenotype, not dose (normal physiology upregulated genes, abnormal failed to upregulate)
          1. most likely aryl hydrocarbon receptor pathway is blocked (evidence that it is upregulated in sensitive)
   11. Whitehead & Crawford 2006. Neutral and adaptive variation in gene expression.
       1. Fish collected maine to Georgia (T change ~12.5C, proxy for overall environmental gradient); acclimated to common environment for 2 months – microarrays
       2. Significant IBD and population differentiation
       3. High intrapopulation variation in gene expression
       4. Among populations, 12% (41/329) genes were different
       5. Habitat temperature contributes to significant variation of 18% of the genes (though confounded with genetic distances)
       6. Variation among taxa explained by IBD is probably from neutral drift and only variation beyond that can be adaptive variation (natural selection)
       7. After account for genetic distance, residual variation must regress with ecological factor to reject H0 of neutral drift – result = 13 genes
       8. Genes with no correlation with environmental cline or IBD are conserved for important function (stabilizing selection)
       9. Gene expression within populations > between (balancing selection)
       10. Selection on 44 of 329 genes: directional (13), stabilizing (24), balancing (7)
   12. Oleksiak et al. 2008. Variation in gene expression within and among natural populations.
       1. *Fundulus* fish – northern and southern *heteroclitus*, sister sp *grandis* (n=5 for each)
       2. Expression level of 18% of genes (n=161) were different within populations (alpha=0.01) – importance in considering individual variation
       3. Fold-difference between individuals typically ~1.5, but also greater than 2
       4. 15 genes differentially expressed between populations supporting northern *heteroclitus* and distinct from south and *grandis*
       5. small differences in mRNA amounts could be because biologically important and under stabilizing selection (and would necessarily have low within population variation)
       6. Northern gene expression significantly different from south and *grandis* but north and south most genetically similar – evolution by natural selection
       7. Variation required for evolution by natural selection is in measures of gene expression
   13. Nunn et al. 2010. Is there evidence for a shift in fish growth and recruitment success linked to climate change?
       1. Regime shift in N Atlantic in 1990s: increase of Gulf stream index until mid-late ’90s then decline
       2. Increased all river discharge (NE England) since late 1990s
       3. Also late 1990s, changes in relationship between *Rutilus rutilus* and environment
       4. Increase in discharge may negatively affect fish growth, survival, and recruitment
       5. More warm-and-wet years may reduce number of strong year classes
   14. Strüssmann et al. 2010. (review) Implications of climate change for the reproductive capacity and survival of New World silversides (family *Atherinopsidae*)
       1. Gonadal maturation and spawning in fishes dependent on T
       2. in genus *Odontesthes*, female fecundity and length of reproductive season is environmentally dependent
       3. summer heat can cause germ cell degeneration and reduced fertility
       4. fish with T sex determination more susceptible to sex determination by other environmental factors, such as environmental estrogens
       5. shorter spawning season or different T regime could affect sex ratios
       6. adaptations in *Menidia menidia*: T-insensitive genotypes, local acclimation (cut off T changes with latitude), frequency cline of T-insensitive genotype
          1. plasticity of T sex determination
   15. Colbourne et al. 2011. The ecoresponsive genome of *Daphnia pulex*.
       1. Reduced intron size compared to insects, nematode and mouse but comparable protein length
       2. Estimated intron gain/loss >1 – 78% of gains unique to lineage, 22% in parallel with gains in other lineages
       3. Only 4.5% of genes (n=1383) are pancrustacean
       4. *D.pulex* genes duplicate at rate 3x fly and nematode, 30% > humans – historic high and steady rate of tandem duplication
       5. 9 gene families expanded independently in daphnia and other aquatic lineages
          1. photoreceptive and photoresponsive: adaptation to complex aquatic light regime
       6. 47% of paralogs non-allelic – concerted evolution on protein coding sequence, e.g. duplication and divergence of hemoglobins to make daphnia very responsive to changes in O2
       7. some paralogs (with low sequence divergence) show differential gene expression in environmentally relevant conditions
       8. paralogs evolve differently partially due to initial differential gene expression
          1. functionally divergent gene duplicates maintained via preservation by entrainment
             1. entrainment = increased probability of maintaining a gene through functional interaction with other genes
          2. high rate of duplication -> co-regulated interacting genes -> environmental response
   16. Francis et al. 2003. (concept model & review) Effects of interdecadal climate variability on the oceanic ecosystems of the NE Pacific.
       1. Major component of climate change is shifts in surface wind stress from redistribution of atmospheric pressure, leading to
          1. Changes in surface circulation
          2. Effects on vertical circulation/upwelling
          3. Air-sea heat exchange, mixed-layer temperature and depth
       2. Phytoplankton distribution and concentration changes with changes in vertical mixing and circulation patterns -> cascade up to zooplankton -> foraged on by multiple life stages of higher organisms
       3. Changes in habitat and food availability will differentially favor different species in upper trophic
       4. Lower trophic levels with fast turnover closely track regime shifts, but higher levels lag
       5. Review of NE Pacific
          1. Climate regime shift winter 1976/77
          2. Decadal shifts in climate have marked effects on plankton and fish abundances
          3. PDO has significant effect on ocean circulation and mixing
          4. CA and AK current regions respond differently to climate change
          5. Bottom-up and top-down effects
2. Pace of Evolution
   1. Burger & Lynch 1995. Evolution and extinction in a changing environment: a quantitative-genetic analysis.
      1. How expected time to extinction depends on demography (potential population growth rate), environment (carrying capacity, selection), and genetics (rate of polygenic mutation)
      2. Population: randomly mating, finite, environmental selection
      3. Individual fitness determined by single quantitative character
      4. Mode with deterministic extinction but time to extinction depends on parameters
      5. For large rate of environmental change (k) any population, no matter size, will rapidly go extinct
      6. With strong stabilizing selection, random changes in mean phenotype leads more easily to extinction
      7. Decrease genetic variance -> increase population lag (population mean lags behind optimum phenotype as it changes with environment) -> increase selection -> decrease Ne -> large decreases in genetic variance because of drift (without mutation to rescue trait, population will go extinct)
      8. If k is low populations can respond evolutionarily for a long time
      9. Random deviations of mean phenotype from expectation are important genetic determinants of extinction risk
      10. Large k – population becomes extinct before genetic variance responds to directional selection
      11. even when variance is there to respond, there is a lag of one generation
   2. Kirkpatrick & Barton 1997. Evolution of a species’ range.
      1. Why do populations at the edge of a species range not adapt and spread: 1) sp has reached evolutionary capacity; 2) gene flow from center of population causes peripheral to act as demographic sinks
      2. Hypothesis: range limits determined by balance between adaptation and gene flow
      3. Effects of gene flow are not important when population sizes are equal throughout range (introduced alleles are at same frequency as resident)
      4. Model
         1. 3 factors influence evolution of trait’s mean: 1) diffusion of genes from random dispersal; 2) asymmetrical gene flow because of changes in density over space; 3) force of directional selection favoring ecologically optimal trait (z)
         2. exists trait optimum that maximizes survival and reproduction and changes with the environmental gradient
      5. dispersal causes gene flow that inhibits local adaptation
      6. deleterious effects of gene flow are the most severe in the periphery of range – strong enough to prevent expansion into new habitat
      7. amelioration: phenotypic plasticity or increase in genetic variation caused by admixture of gene flow
      8. extinction because environmental gradient too steep – local populations decline over finite range (large geographical range does not necessarily mean low extinction risk)
      9. genetic variance does not mean population persistence if species can colonize environmental gradient where adapted
      10. steepness of environmental gradient influences rare population’s fate
      11. maladaptation from gene flow causes populations to not expand range
      12. model not robust when 1) hard environmental boundary causes infinite mortality (inhabitable) 2) hard boundaries in dispersal when organism avoids habitat 3) ignores drift
   3. Blows & Hoffmann 2005 (review). A reassessment of genetic limits to evolutionary change.
      1. Effect of selection on a train in one generation: R=h2\*s
      2. Life history vs. morphological traits: heritability and variance
      3. Low genetic variance for traits may be from genetic drift, inhibition of gene flow into peripheral populations, inbreeding – signals in neutral and quantitative trait markers
      4. Mechanistic or physiological constraints decrease the probability that specific directional variation will be caused by mutation (i.e allometry) - Variance will decrease in trait but not other markers
      5. Factors that decrease genetic variance: low recombination rates, selection by decreasing expression of phenotypic variability, trait-trait and trait-environment interactions, and natural selection
      6. Extent of genetic covariance between trait and fitness limits response to selection in 2 ways: 1) environmental component of trait, not genetic, is under selection; 2) correlation between selected trait and fitness
      7. Selection unlikely to act on single trait – difference between variance of single vs. complex of traits
      8. Lack of genetic variation may be cause of limits to selection
   4. Wagner et al. 1997. A population genetic theory of canalization.
      1. Canalization based on: 1) mutations with major effect on phenotype can increase trait’s variance wrt wild type, supporting that wild type phenotypes are canalized (buffered against genetic variation); 2) environmental conditions reveal variation in phenotype; 3) canalization affects one gene/trait; 4) the greater a trait’s importance to fitness, the less sensitive it is to change; 5) environmental canalization can be caused by modifier (rescue) alleles
      2. Too strong stabilizing selection can prevent evolution of canalization
      3. Z=x+e, z= phenotype, x= genotype, e = environment
      4. Environmental canalization is the opposite of plasticity
      5. If genes have canalizing and direct effects, canalization limit does not depend on stabilizing selection
      6. Genetic canalization is distinct from genetic variance
      7. Rate of evolution of genetic canalization depends on genetic variation in populations
      8. Effects of stabilizing selection on genetic canalization: increased fitness benefit of canalization because strong selection for effect; decreasing fitness because decreasing genetic variation of trait
      9. Environmental canalization increases mean fitness
      10. Genetic canalization: no fitness benefit in mutation-selection equilibrium
      11. Genetic basis may be the same for both canalizations or both are evolutionary response to strong stabilizing selection
   5. Barrett et al. 2008. Natural selection on a major armor gene in threespine stickleback.
      1. *Eda* allele at much higher frequency in freshwater than ocean – does it confer a selective advantage?
      2. Introduced adult wild marine fish (n=45) into freshwater ponds and let breed
      3. Juvenile F1s with *Eda* were larger than those with marine allele (complete allele)
      4. Fitness of *Eda*: higher overwinter survival, reached sexual maturity sooner
      5. Higher frequency of *Eda* in F2, but more equal with complete by the end of the season
      6. Evidence of positive selection from reduced burden of producing armor plate in freshwater and decreased predation pressure
         1. But selection for *Eda* offset by selection for complete allele at earlier life stages
         2. Also possible selection on linked gene(s) or *Eda* has pleiotropic effects
   6. Tirosh & Barkai 2008. Evolution of gene sequence and gene expression are not correlated in yeast.
      1. 7 strains of yeast; compared levels of orthologous genes (expression divergence measured)
      2. evolutionary divergence estimated from associated coding sequence’s rates of nonsynonymous substitution
      3. no correlation between coding sequence divergence and gene expression divergence
      4. gene essentiality negatively correlated with gene expression divergence
      5. neutral drift with purifying selection are important for gene expression divergence
   7. Knutsen et al. 2011. Are low but statistically significant levels of genetic differentiation in marine fishes “biologically meaningful”? A case study of coastal Atlantic cod *Gadus morhua*
      1. 13 microsats and mark-recapture in Norway
      2. persistent substructure of cod over a few km
      3. low level of genetic differentiation Fst=0.0037, but highly significant and persistent over time
      4. juveniles cluster with adults from same area (MDS plot) – segregation into populations/units
      5. mark-recapture of tagged fish supports limited dispersal of adults
   8. Wirgin et al. 2011. Mechanistic basis of resistance to PCBs in Atlantic tomcod from the Hudson River
      1. 1947-76 two GE facilities released 590,000 kg PCBs into Hudson
      2. tomcod = *Microgradus tomcod*
      3. aryl hydrocarbon receptor: mediates toxicities of PCBs and xenobiotic metabolizing enzymes
      4. AHR2 more functionally active in fishes
      5. Compared full-length AHR2 from HR, one distant reference, one proximal reference
         1. 4/5 polymorphisms are fixed at HR compared to both references
            1. 2 synonymous, 1 nonsynonymous, 1 6-nt deletion (2 aa)
         2. allele with deletion only found in southern populations but at lower frequency than HR
         3. other allele monomorphic farther from HR and only seen in heterozygotes in HR
      6. evidence that del-allele present at low frequency in HR before pollution
      7. no evidence of genetic bottleneck in HR
      8. del-allele has 5x lower binding affinity for toxicants
      9. evidence of rapid evolutionary change in 50-100 years – functional changes in coding region of gene
3. Population ecology & demography behind adaptation to a changing environment
   1. Hewitt 1996. Some genetic consequences of ice ages and their role in divergence and speciation
      1. Height of glaciation: plants now covering land that was south of ice sheets (sometimes small enclaves)
         1. As ice receded, range expansion
      2. Southern and northern bands for species range where climate could increase or decrease optimal temperature range -> change in range or species shift
      3. Expansion from south -> long range dispersers arrive first and contribute most to the gene pools, others arrive later but contribute less
         1. Leading edge: series of bottlenecks for colonizing genome -> loss of alleles, homozygosity
      4. Different environmental conditions across range will select for different genomes
      5. Complex population histories necessitate studies with multiple types of markers
      6. Adaptive novelty and divergence could arise from the environment a population experiences in its refugium (molecular divergence between parapatric taxa)
   2. Banks et al. 2010. Genetic structure of a recent climate-driven range extension.
      1. Urchin *Centrostephanus rodgersii*: historic and newly colonized ranges; 8 microsats in both populations
      2. Gene diversity in expansion zone ~source population
      3. No founder or bottleneck effect – continuous expansion of population into newly warmed waters with continued full contact with pre-expansion population
   3. Allen et al. 2010. Does local adaptation to resources explain genetic differentiation among Daphnia populations?
      1. *D. pulex* from 4 ponds within 50 km of each other – grew pond-specific clonal daphniids in water from each pond in common garden, used 5 microsats
      2. No difference in inter-clone juvenile growth rates, although all clones responded similarly to resource richness – universal plasticity in response to resources
      3. Microsat alleles shared between populations – shared colonization history; significant inter-population differentiation
      4. No evidence of local adaptation: response to resources and evidence of significant gene flow between populations
   4. Bell et al. Preliminary Assessment of the effects of climate change on fisheries and aquaculture in the Pacific.
      1. Shift of equatorial divergence is root of Nino vs. Nina – divergence brings nutrient-rich waters to surface and stimulates phytoplankton and zooplankton production (stimulates fisheries)
      2. 1950-2007: global average land and sea T increase 0.12C per decade and tropical Pacific sea surface T 0.07 C/decade
      3. climate affects patterns of fish distribution: 1. Expanded distribution of warm water fisher towards poles, 2. Latitudinal shifts and contractions of cool water spp
      4. fish reproduction is sensitive to T fluctuations
      5. expect significant change in abundances of fish and inverts in the pacific
   5. Jeukens et al. 2010. The transcriptomics of sympatric dwarf and normal lake whitefish divergence revealed by NGS.
      1. Liver from both spp of whitefish -> RNAseq
      2. 948 contigs significantly differentially expressed
         1. normal increased expression: protein synthesis
         2. dwarf increased expression: energy metabolism, immunity, DNA replication and repair
      3. absence of correlation between sequence divergence at polymorphic sites and gene expression diversity
      4. dwarf had greater allelic imbalance
      5. gene expression patterns mirror life history trade-offs – dwarfs have high metabolic rate; normal put more energy to growth
      6. higher immune gene expression in dwarf = underlying mechanism of population divergence and speciation
      7. no correlation between gene expression divergence (expression regulation) and polymorphism rate (protein structure)
   6. Reusch & Wood 2007 (review). Molecular ecology of global change.
      1. Increasing climate extremes may impose intense (“hard”) selection on species and cause rapid selection for stress-tolerant genotypes
      2. Change in seasonality = “soft” selection, which increases intraspecific competition
      3. Selection within one generation is not equivalent to an evolutionary response
      4. Single stressors in lab may have results that are not applicable to complex multiple stressors
      5. Evolutionary stasis despite directional selection due to: lack of polymorphism in genes, negative trait correlations caused by pleiotropy or linkage, metabolic costs and associated trade-offs
   7. Grant & Bowen 2006. Living in a tilted world: climate change and geography limit speciation in Old World anchovies.
      1. Climate-induced fluctuations of OW anchovies using mtDNA (cytb)
      2. ~6 million years separated NW anchovies
      3. OW population genetic patterns: shallow separations among regions/putative spp; historically large populations in N hemisphere; recent colonization in S hemisphere
      4. Pleistocene climate change (strong change in ocean T and sea levels) influenced N and S hemisphere anchovies
         1. N and S Japan: similar diversity estimates, different demographies (mismatch and coalescence)
         2. N population growth predates S ~200,000 years
         3. S grew more rapidly and to larger size
      5. Small number of European anchovies colonized Africa (diversity indices)
      6. Long shorelines allow range shifts during climate change: Europe, japan, and NW
      7. Africa and Australia do not have same option and so have experienced episodic extinctions – evidence of historic colonizations from N
      8. Anchovy populations have 2 choices: shift range or extinction
   8. Derome & Bernatchez 2006. The transcriptomics of ecological convergence between 2 limnetic coregonine fishes.
      1. 2 whitefish ecotypes: cisco and normal
      2. 22 ESTs different between types
      3. upregulated in both but different genes: muscle contraction, energy metabolism
      4. dwarf vs. cisco: 13 genes are differentially regulated for energetic metabolism and muscle contraction
      5. dwarf vs. normal: more transcriptional changes than cisco vs. dwarf
      6. cisco = dwarf with regard to energy metabolism and swimming activity
         1. genes with parallel upregulation in dwarf and cisco were for muscle contraction and energetic metabolism
         2. all 6 EST clones upregulated in dwarf vs. normal also upregulated in cisco
      7. specific genes indicate that cisco favors speed over strength
      8. cisco is better adapted physiologically to pelagic niche than dwarf
      9. evidence of directional selection during recent rapid evolution of dwarf ecotype
   9. Parmesan 2006 (review). Ecological and evolutionary responses to recent climate change.
      1. 41% of species from compiled studies are impacted by climate change – documented changes in phenology, increasing asynchrony between spp, range shifts
      2. Antarctica: global climate change causes decreases in sea-ice, translating to trophic cascade effects on biological systems
      3. Arctic: species’ turnovers, terrestrial community shifts, migratory and range shifts
      4. Northern hemisphere temperate: mostly northward shifts as T increases
      5. Tropics: northward shifts
      6. Elevation: upward shifts
      7. Marine: shifts in plankton communities (poleward, changes in peak biomass); decreases in cold-adapted fish and increases in warm-adapted
      8. Pests and disease: moving up and north, decreases in generation time
      9. Extinctions/pre-extinctions: amphibians, tropical coral reefs
      10. Evolution: increase in frequency of more tolerant genotypes in middle of range, warming increases stress at equatorial range boundaries and decreases at poleward boundaries
      11. Species have always dispersed but climate change allows establishment and potential future dispersers is trait is heritable
   10. Schluter 1996 (review). Ecological causes of adaptive radiation.
       1. Adaptive radiation: proliferation of spp within single clade with significant interspecific divergence in resource exploitation and morphological and physiological traits used in resource exploitation (citation)
       2. Divergent natural selection causes adaptive radiation – 3 processes
          1. Differences in population and species phenotypes following resource environments
          2. Phenotypic difference caused by resource competition (divergent character displacement)
          3. Ecological speciation = evolution of reproductive isolation from divergent natural selection and resource competition
       3. Mechanisms of speciation: divergent selection, drift, founder effects, bottlenecks, fixation of alternative advantageous genes
       4. Example of 3 spined stickleback (*Gasterosteus aculeatus*)
          1. Sympatric species distinct morphologically based on habitat preferences and diet – limnetic and benthic
          2. Relatively little genetic divergence – young speciation (<13,000 years)
          3. Hypothesis: should be present a clear trade-off in optimizing fitness to one environment
             1. Transplant experiment: significant growth trade-off and efficiency at prey capture
          4. Hypothesis: speciation (in sticklebacks) during adaptive radiation is driven by same ecological forces as morphological differentiation
             1. ~yes, speciation associated with ecological differentiation, not time; selection against hybrids (ecologically based); assortative mating based on traits related to divergence; parallel evolution evidence of natural selection
   11. Hairston et al. 2005. (review) Rapid evolution and the convergence of ecological and evolutionary time.
       1. Evolution is rapid when it occurs simultaneously, but alters, ecological dynamics
       2. Heritable phenotypic trait occurs quickly to change trajectory of an ecological process while in progress
       3. Need resources/opportunity for evolution
       4. Framework (equation) for determining ecological and evolutionary roles in rate of evolution
       5. Darwin’s finches
          1. Response variable = rate of population growth, evolving traits = individual size and beak shape, ecological variable = total seed density and fraction of large seeds and rainfall
          2. Ecological change = evolutionary response
          3. Evolution changes faster than ecology (x2.2) for body and beak size
          4. No effect of beak shape
       6. Diapause in copepod
          1. Response = per capita diapausing eggs (mean realized fitness), trait = diapause switch date, ecological variable = predation
          2. Ecological > evolutionary but evolutionary still important (1/4 eco.)
       7. Ideal experiment: selected lines with different values for trait, response across range of ecological change
       8. Rate of evolution depends on ecological change
   12. Grant & Grant 1993. Evolution of Darwin’s finches caused by rare climatic event.
       1. Strong El Nino 1982-3 – heavy rain to Galapagos for 8 months, islands typically arid
       2. On Daphne Major large hard transition to small soft seeds
       3. Ecological effects of El Nino: prolong favorable breeding conditions, alteration in relative abundances of 2 endemic spp probably due to decline in main food (cactus) of *G. scandens*
       4. *G. fortis* bred less after Nino and small birds fared best, concurrent shift in beak size ->natural selection of environment (food resources), beak traits are highly heritable
       5. post-Nino conditions advantageous for hybrids
   13. Kinnison and Hairston 2007 (review). Eco-evolutionary conservation biology: contemporary evolution and the dynamics of persistence.
       1. How to reconcile rapid evolution and extinction
       2. Natural selection can lead to extinction
       3. Genetic load plays a role in selection-fitness equilibrium
       4. Heritabilities can slow approach to new evolutionary optimum
       5. Persistence: adaptive evolution gives rise to positive fitness and large population size; decreases in drift, inbreeding and extinction risk
       6. Ecological-evolutionary dynamics determine population success or failure
       7. Conservation (anthropogenic changes) is an eco-evo problem
   14. Olsen et al. 2004. Maturation trends indicative of rapid evolution preceded the collapse of northern cod.
       1. *Gadus morhua*
       2. Early maturation in fished populations – induced change or plasticity?
       3. 1980 to 1987: females mature earlier (at smaller size)
       4. late 80s, early 90s: northern cod body condition declining (environmental influences could also be factor)
       5. early-maturing genotype favored over late during collapse
       6. intense fishing prompted evolution of life history traits, closure of fishery halted the evolutionary trend
   15. Joseph et al. 2009. A tangled tale of two teal: population history of the grey *Anas gracilis* and chestnut teal *A. castanea* of Australia
       1. *Ag* is widespread, *Ac* is restricted to Australia
       2. Most likely diverged ~103,000 years BP (IMa), late Pleistocene
       3. Low or 0 gene flow between species – incomplete lineage sorting probable cause of shared haplotypes (not hybridization)
       4. Australia not glaciated during Pleistocene so populations did not experience severe bottlenecks
       5. Geographically unstructured low diversity consequence of range expansion post-LGM
   16. Faurby et al. 2010. Population dynamics of American horseshoe crabs – historic climatic events and recent anthropogenic pressures
       1. Most northern (ME) and most southern (Mexico) diverged from central sites that are more similar
       2. Strong bottlenecks in all regions except MX (expansion)
       3. Very low Ne in all: 3-200
       4. Evidence of decline in all populations – most intense in northern ME
          1. 832-6200 years ago
          2. more recent in ME and 2 other sites
       5. ice age and recolonization impacted all populations – may not have reached equilibrium before new impacts
       6. different factors responsible for additional decline in populations
       7. patterns in ME probably from founder effect, other populations show signature of anthropogenic effects
       8. very low Ne/N (~10-5) probably due to variation in reproductive success – and founder effects after ice age and fluctuations in population size
       9. such low Ne could mean loss of genetic variability and adaptation potential to climate change
   17. Hauser et al. 2002. Loss of microsatellite diversity and low effective population size in an overexploited population of New Zealand snapper (*Pagrus auratus*)
       1. Dried scales 1950-1986, contemporary 1998
       2. Tasman Bay: decreased mean Hz, decreased number of alleles, decreased genetic diversity in 6 out of 7 loci, Ne small and Ne/N ~ 10-5
       3. Hauraki Gulf: random fluctuations in mean Hz and alleles, one locus decreased Hz and number of alleles, Ne not significantly different from infinity
       4. Loss of genetic diversity event though N estimated at 3 million
       5. 1950 genetic diversity TB > HG, but reversed in 1998
       6. low Ne/N characteristic of highly fecund spp with high juvenile mortality
       7. Ne of TB population, as characterized by microsatellites, small enough to lose alleles at neutral and weakly selected genes – implications for adaptation? These genes could be adaptive in some environments
   18. Brander 2010. (review) Cod *Gadus morhua* and climate change: processes, productivity, and prediction
       1. International landings have declined since 1981
       2. Stock growth-overfished for >40 years, also recruitment-overfished with spawning stock biomass <10% of 1982
       3. Upper thermal boundary = Irish and Celctic seas
       4. Growth rate changes with T and light regimes
       5. Response to climate change: greater at low T and more effect on smaller life stages
       6. Changes in salinity affects buoyancy of eggs
       7. 2 forms of management: precautionary and predictive
       8. Change of cod biomass in Baltic Sea due to 4 factors: seal predation, eutrophication, climate driven salinity change, fishing
   19. Sharma & Liermann 2010. Using hierarchical models to estimate effects of ocean anomalies on north-west Pacific Chinook *Oncorynchus tshawytscha* recruitment
       1. Model includes SST, ENSO, PDO
       2. 3 environmental variables explained only small proportion of unexplained recruitment results
4. Population Genetics of *C. gigas*
   1. Launey & Hedgecock 2001. Genetic load in *C. gigas*.
      1. Large load of highly deleterious recessive mutations
      2. Even larger number of sublethal, subvital, or mildly deleterious that affect survival and growth
   2. Taris et al. 2009. Mitochondrial and nuclear DNA analysis of genetic heterogeneity among recruitment cohorts of European flat oyster *O. edulis*
      1. 3 cohorts *O. edulis* over 1 summer (June-Aug); 4th cohort (seasonal) collected over entire season
      2. 4 msats, 12s rRNA
      3. msats: genetic variation within cohorts not significantly different from adults, pairwise Fst between cohorts not significant
      4. mt: significant Fst between cohort 1 and seasonal, 1 and adults
      5. evidence for higher variation in female vs. male reproductive success (discrepancy in mt vs msats)
      6. degree of chance in how strong effect of sweepstakes is, depends on reproductive biology and environmental conditions
   3. Sauvage et al. 2007. Single nucleotide polymorphisms and their relationship to codon usage bias in *C. gigas*
      1. Codon bias is indicative of level of constraint upon genes in oyster genome
      2. 84 ESTs, 15 are related to summer mortality
      3. sequenced 10.5 kb with 290 SNPs (69% non-coding)
      4. SNPs in coding ~1/60 bp, 1/40 in non-coding – many more than in other animals
      5. Consequences of GC-poor genome: amino acid version without G/C over-represented in lowly expressed genes (G/C increased with more highly expressed genes) – GC content at 3rd coding position is proportional to expression level
   4. Powell et al. 2011. Generation time and the stability of sex-determining alleles in oyster populations as deduced using a gene-based population dynamics model.
      1. Sex alleles M & F: M=dominant, FF=protandrous, M=always male
         1. M at ~25% in populations
      2. Highly skewed sex ratio to male provided by protandry – why maintain M?
      3. Model of oyster population
      4. Generation time: shorter generation time characteristic of modern heavily exploited and diseased populations, resulted in loss of M
         1. Because of generation time, not smaller populations and drift
         2. Cause of loss of M
      5. Increasing age of protandrous switch decreases loss of M
      6. Mortality (Dermo, MSX) also causes loss of M
      7. Factors contributing to loss of MF individuals: decreased generation time (MF have less fecundity)
      8. Why retain M?
         1. Selective advantage – not supported
         2. Happenstance – stabilized by multiple spawns per year as seen in southern range
      9. Without M, greatly increase female:male decreases chance of fertilization
   5. Wu et al. 2010. Comparison of 7 Crassostrea mitogenomes and phylogenetic analysis.
      1. Crassostrea spp: ariakensis, iredalei, angulate, sikaemea, hongkongensis, virginica, gigas
      2. Similarities between mitogenomes: skewed away from C and favoring G (also favors T over A); AT content 61.1%-65.3% (similar to other bivalves)
      3. Six Asian oysters have:
         1. 12 protein coding genes, 2 rRNA genes and varying number of tRNA genes
         2. duplicated rrnS gene
      4. Most use conventional ATG start, but others as well (flexible but not random)
      5. All have splitting of rrnL gene – possibly a characteristic of the genus
      6. Similar phylogeny to COI but more robust support
   6. Jackson et al. 2010. Parallel evolution of nacre building gene sets in molluscs
      1. ESTs from part of mantle responsible for secreting nacre – *Pinctada maxima, Haliotis asinine* (n=1)
      2. Transcriptomes of nacre-producing cells significantly different – nacre building is convergent
      3. Differences in gene content and expression levels
   7. Milbury et al. 2010. Fragmentation of the large subunit ribosomal RNA gene in oyster mitochondrial genomes.
      1. 3 species: *Crassostrea* *virginica, gigas, hongkongensis*
      2. LSU rRNA split into 2 fragments by large number of nucleotides in all 3
      3. 3’ half of sequence more conserved than 5’ – high nucleotide identity
      4. 5’ has more A + T content (66-69%), similar to complete LSU genes – same selective pressures
      5. so far not seen in other molluscs
5. Fundamentals of Molecular Evolution. Graur & Li 2000
   1. New mutation to become evolutionarily significant must become fixed in population – need
      1. Natural selection (driving force of evolution)
      2. And genetic drift (evolution at molecular level)
   2. Deterministic vs. stochastic models of evolution
   3. Need variability in traits for natural selection to work
   4. Because of environment’s carrying capacity, evolutionary success of an individual is due to its relative fitness, not absolute fitness
   5. Drift is cumulative from one generation to the next – allele frequency will deviate more and more from original
   6. Gene substitution – mutant allele replaces wild type
      1. Fixation probability dependent on frequency, selection coefficient, Ne: P = (1-e^-4Nesq)/(1-e^-4Nes) where q = initial frequency
      2. Fixation time depends on frequency, selection coefficient, and population size
         1. for a neutral mutation t = 4N generations
         2. for a selective advantage t = (2/s)ln(2N)
   7. Rate of substitution determined by rate of mutation and probability of fixation
   8. Functional constraints slow substitution rate
   9. Differences between synonymous and nonsynonymous substitution rates within a gene indicate intensity of purifying selection
   10. Most important factor in determining nonsynonymous mutation rate is purifying selection intensity (determined by functional constraints)
   11. Relaxation of selection can occur when gene function lost – acceleration of nonsynonymous substitution rate
   12. Mammalian vertebrate male germ line mutation rate > female
   13. Positive selection: rate of nonsynonymous substitution > synonymous