1. Molecular Genetics
   1. Genetic parentage
      1. Keller et al. 2001
   2. Genome scan
      1. Colbourne et al. 2011
      2. Namroud et al. 2008
      3. Bonin et al. 2006
   3. NGS
   4. Physiology
      1. Whitehead et al. 2010
      2. Wirgin et al. 2011
      3. Wheat et al. 2011
2. Quantitative Genetics
   1. Roff & Mousseau 1986
   2. Animal model
      1. Réale et al. 2003
      2. Nussey et al. 2005
      3. Kruuk 2004
      4. Gienapp et al. 2006
   3. Multiple generations under selection in the lab
      1. Hard et al. 1993
      2. Reznick et al. 1997
   4. Tagging of wild populations – multiple seasons and generations
      1. Grant & Grant 2006
      2. Bradshaw & Holzapfel 2001
      3. Grant & Grant 1995
   5. Estimate heritability
3. Roff & Mousseau 1986
   1. Heritabilities calculated from database of *Drosophila* data
   2. Most morphological (and physiological) traits have heritability >10% (10-60%); most behavioral and some life history are 0-10%
      1. Life history and behavioral traits could more directly affect fitness
   3. General trends, there are exceptions
4. Réale et al. 2003 – followed phenotypic change over multiple seasons and generations
   1. Plastic response = same females’ parturition dates over multiple breeding seasons
      1. Cone abundance accounted for most of advancement of breeding timing of 3.7 days/generation
   2. Microevolution = changes in estimated breeding values across generations
      1. EBVs advanced by 0.8 days/generation
   3. Parturition date has significant genetic variation, h^2 = 0.16, and under directional selection
   4. Breeding day advanced 18 days over 10 years
   5. Environmental change and plastic response caused greater than predicted directional response
5. Nussey et al. 2005 – selection for greater plasticity
   1. Great tits – 833 females that laid more than one season from 1973-2004
      1. Plastic response to spring temperature, but variation among females in terms of laying date and magnitude of response to T
      2. Earlier laying females have the most plastic response
   2. Predictors for each females reaction norm: laying date in an average environment and change in laying date in response to environment
      1. Used “animal model” to estimate genetic component
   3. Laying date plasticity h^2 = 0.3 and has significant genetic variation
   4. Earlier laying, more plastic females also had higher fitness (offspring become breeding adults)
      1. Breed in closer synchrony with resource availability for young
   5. Selection over time has increased
6. Kruuk 2004 – model for determining genetic contribution to traits
   1. Animal model = mixed model = linear regression in which explanatory terms are of both fixed and random effects
   2. Model defined at level of individual animal
   3. Provides estimates of parameters from which heritability can be estimated
   4. Breeding value for a trait = total additive effect of its genes on that trait (Falconer & Mackay 1996)
   5. Must construct pedigree with known parentage: observations or genetics
7. Gienapp et al. 2006 – animal model to find genetic and phenotypic components to change masked by environmental variability
   1. Animal model, restricted maximum-likelihood, to estimate genetic and nongenetic variance components, fixed effects, predict additive genetic and other random effects
   2. Data collected 1973-2003
   3. Heritability = VA/(VA + VPE + VR)
      1. P = phenotypic variance, A = additive genetic variance, PE = permanent environment effects
   4. Pedigree/parentage determined by mating pairs
   5. Relative fitness = individual fitness/annual mean fitness
      1. Fitness = number of recruits or survival
   6. Standardized selection gradients calculated from yearly regression models, including relative fitness, standardized trait value, trait value, standardized selection gradient, standardized nonlinear selection gradient
   7. With no environmental bias, selection differential for predicted breeding values = expected response to selection on phenotypes (R=s\*h2)
      1. Calculated predicted response to selection for phenotypes and predicted breeding values
   8. Annual mean egg-laying dates advanced 5.4 days (not quite sig.) and predicted breeding values did not change
   9. Strong selection for early breeding, measured by fitness – strong directional selection at phenotypic level
      1. Mean phenotypic standardized selection differential = -0.21
   10. No evidence that selection affected evolution of trait: egg-laying date and clutch size (fitness) are not genetically correlated
   11. Evolutionary response = 1.5 days/30 years – hard to detect given large environmental variation in breeding time
8. Hard et al. 1993 – heritable trait with higher genetic variance in one part of range
   1. Larvae collected Florida to Ontario, brought to F2 in lab then separated early and late diapause by exposing to progressively increasing photoperiods – calculated heritability in F3, h^2=0.3-0.7
   2. Genetic variance of critical photoperiod higher in northern populations
      1. Much environmental variation in onset of favorable conditions (end of frost) could help maintain genetic variation
9. Reznick et al. 1997 – heritability and evolution faster in males
   1. Introduced guppies from high to low predation site and left for 11 years. Descendants of transplanted matured at a later age and larger size than the source population and produced fewer, larger offspring per litter.
      1. Lab-reared fish to F2 and F3
   2. Age and size at maturity are highly heritable, but more so in males than females.
      1. Allows males to evolve more quickly
10. Grant & Grant 2006 – Change in a trait over multiple generations
    1. Competition for limited resources causes directional selection and more small *G. fortis* survive because they exploit a unique food source (as opposed to large that are in competition with *G. magnirostris*)
    2. Mean beak size in generation after selection was significantly smaller than generation pre-selection
11. Grant & Grant 1995
    1. Multivariate change in traits in finches, 2 selection events (1976 and 1984)
    2. Strong directional selection manifested via microevolution in 1978 cohort and 1987
    3. Overall, observed matched predictions, but more so for first episode
    4. Evolution of bill length can occur counter to or in absence of selection because of trait correlation
    5. Unexpected results could be do to missing traits or unanticipated trait correlations
12. Bradshaw & Holzapfel 2001 – northern mosquitos respond more efficiently to selection
    1. Critical photoperiod = daylength where mosquito switches from active development to diapause
    2. Shift more pronounced in the north than south
    3. Why faster evolutionary response of northern population? Stronger selection and greater capacity to evolve (diversity)
13. Keller et al. 2001-high heritability of beak traits in finches
    1. Parents and offspring were measured for morphological traits and genotyped at microsatellite loci
    2. H^2 of bill size and shape is 0.85 and 0.88 – more than 85% of phenotypic variation is attributable to additive genetic variation (other traits have smaller h^2)
       1. Not confounded by low phenotypic variance
14. Whitehead et al. 2010
    1. Field collected killifish at contaminated and reference sites – bred to F2 in lab, exposed to PCBs, phenotype ranked
    2. Differences between populations in sensitivity to PCB congener in appearance of toxicity and survivorship
    3. Sensitive population had generally more changes in gene expression under exposure and magnitude of expression increased with dose
    4. Phenotype~expression correlation = genotype~phenotype link
15. Wirgin et al. 2011
    1. Fixed differences in AHR2 in Hudson river tomcod: on non-syn. and 2 synonymous, 6 bp deletion
       1. This allele is more prevalent in southern populations, but is at low frequency in non-impacted proximal populations
       2. Neutral markers showed differentiation between locales, gene flow between connected water bodies
    2. Deletion seems to be responsible for resistant phenotype – lowers binding affinity for toxins
16. Namroud et al. 2008
    1. Genome-wide SNP scan in white spruce
    2. Among population Fst = 0.006
    3. Used ESTs to find SNPs so all markers are located in expressed gene regions – SNPs for adaptation
    4. 49 SNPs showed trend of local adaptation
    5. large proportion of candidate SNPs for local adaptation were in introns and 5`- and 3`UTRs. Also many synonymous SNPs which could indicate natural selection leading to codon bias
    6. Adaptive SNPs unevenly distributed across populations. Seem to correspond to genes that maintain development & growth in stressful environments
17. Bonin et al. 2006
    1. Sampled frogs at 3 different altitudes
    2. Global Fst = 0.11 and altitude is responsible for 35.5% of molecular variance
    3. 4 loci linked to adaptive differences between altitudes; 3 are monomorphic in at least one population
    4. picked outlier loci based on confidence envelope for 20 demographic scenarios
18. Wheat et al. 2011
    1. Old populations (at least 5 years) and new – not genetically distinct - of the Glanville fritillary butterfly compared in common garden environment to F2 generation
    2. Microarray
    3. New populations
       1. Higher abdomen expression of larval serum protein genes & lipid transporters – transfer of nutrients to eggs
       2. Higher vitellogenin expression – egg provisioning protein
       3. Higher angiotensin converting enzyme – regulated oviposition
       4. Higher peak metabolic rate during flight
       5. Higher thorax (flight musculature) expression of proteasomes and chaperones – protein turnover in muscle
    4. Specific Pgi and Sdhd alleles associated with gene expression profiles of adaptation – life history and metabolism phenotypes
19. Beldade et al. 2011
    1. Cell differentiation during development = developmental plasticity and determines developmental trajectory

Rudimentary quantitative genetics follow the equation R=h^2\*s for one trait

Natural selection in wild populations will affect >1 trait and so needs a different approach. Could be provided by genome-wide scans, NGS, etc.