**Rationale: Many consider reciprocal transplant to be the gold standard for demonstrating local adaptation, but recently genomic data collected from different populations has been used to argue for local adaptation. This week we want the RCN to compare and contrast different approaches toward measuring local adaptation.**

**Papers – Sanford and Worth 2010 (Ecology); Kolaczkowski et al. 2011 (Genetics)**

**22 Groups: 107+ participants**

**1.) When does landscape genomic data present good evidence of local adaptation (without experiments)?**

**Rutgers:**

* If local adaptation is a measurable increase in fitness, then no. Genomics in this sense can’t present conclusive evidence of LA. No quantitative measure of fitness based only on genetic differences.
* The question was raised whether you could have these genomic signals favoring spatially divergent selection when no LA is happening. A few examples of alternative explanations included allele-surfing and other genetic drift, error, and non-random mating. Matting success is part of a phenotype, even if it depends on the organism’s social environment.
* We ended up back at K’s statement that phenotype has too many dimensions to quantify in the same way as genomics. Genomics and transplants together, when appropriate for the same organism, highlight the genetic as well as phenotypic mechanisms behind apparent local adaptation.

**Univ. Southern California:**

* In an ideal scenario, such a study system has well-defined drivers for local adaptation, such as thermal cline of Australian Drosophila. In cases with well annotated genomes and large effective populations sizes, markers that strongly deviate from expected genetic variability offer a suite of potential regions under selection.
* Careful consideration of the ecologically relevant factors that may drive local adaptation and how an organism would account for deviations in factors physiologically can be used as a guide when analyzing genomic data from spatial regions in which LA may have occurred. A strong understanding of the potential selective pressures and how they could be solved genetically would be the strongest evidence for local adaptation.
* In the absence of this knowledge, we should be wary about constructing “just so” statements from genomic regions that segregate with each population. By integrating previous experimental data, and/or in-depth knowledge of the study system landscape genomic data can be used to generate and test hypotheses. Unfortunately, most study systems do not allow for genetic manipulation of candidate genes to assess functionality or the impact on fitness.

**CSU Northridge:**

* Not too many cases where genomic data can present good evidence for local adaptation.
* Two instances they came up with were when landscape genomic data could contribute evidence to (but not necessarily result in proof) of local adaptation would be if 1. These data were paired with environmental parameters that you could attribute to changes in genomic data, or 2. Identifying the phenotypes of genes that were different.
* Found fly paper interesting but failed to see how the authors concluded that there were “fundamental biological differences between flies from these two geographic regions”

**Virtual Group:**

* Most genomic data alone do not provide much evidence of local adaptation, though if there are very strong signals of selection, perhaps this could be suggestive. However, gene by environment interactions are the exception to this and are fairly compelling in identifying loci that are likely under selection due to the environment (so parallel mechanisms of local adaptation).
* Conclusion that integration of ecological/experimental approaches is best. Doesn’t make sense to do a bunch of sequencing if there is no evidence of interesting biology. The fly paper falls into this category in that a ton of work has been done indicating there is adaptation to temperature, the genomic follow up is a logical next step to get at mechanism.

**Washington State U:**

* Never. We need an assay of fitness (ecological context) to provide proof that differences at the genetic level actually manifest at the phenotypic level, where selection is acting.
* Also depends on your audience how important this is, but generally we expect some tie to fitness to be able to say something about local adaptation if it can be mapped to specific coding sequences, but that’s making assumptions about how selection works.
* Sometimes fine that even the most in-depth sequencing doesn’t provide with nucleotide that matters, especially in complex traits and environments. There are multiple ways to arrive at certain phenotypes on the genotype level, so it can be difficult to discern local adaptation even for a relatively simple phenotype or trait. Using just genetic sequencing, especially when we don’t have adequate knowledge of function, it is very difficult to label local adaptation for complex traits.

**Northeastern MSC:**

* Agreed that landscape genomics approach can provide good insight into novel system that perhaps does not have much a priori information.
* However, in the full absence of manipulative experimental procedure it generally should be relied upon more to provide indicators of local adaptation, as opposed to providing more conclusive evidence of it.
* With regard to local adaptation it is not enough to know an allele’s effect on a trait, but also that trait’s effect on fitness.

**Bodega/UC Davis/UC Santa Cruz:**

* Can present good evidence if you have several replicates of the same environmental cline and populations showing the same direction of allele frequency changes. However it will always be a correlation and not fully sufficient to demonstrate local adaptation.
* Comparison of various genomic metrics between populations can also provide insight into past selection, drift, or other demographic phenomena (e.g., using patterns of allelic diversity to infer selective sweeps).
* Economic motivation for comparing only the two endpoints of the drosophila range are understandable, we thought the study would benefit from the inclusion of an intermediate population to verify the progressive nature of allele frequency changes with latitude as opposed to geographic breaks.

**Nicholls State:**

* Genomic data provide valuable insights, specifically when researchers can link the genetics to the phenotype. Stronger cases can be made when additional data like transcriptomics, epigenomics, and proteomics. Pairing a study using multiple data types with experiments makes an even stronger case.
* We don’t believe that the discussion should be “genomics or experiments”. The question of local adaptation is too big to only use one tool. We should employ all tools when appropriate, which may vary based on the question (basic vs. applied science), the system, the scale, the organism, etc.
* When working with non-model and long-lived species, genomics can provide a good starting point to design an integrative approach to local adaptation.

**UMass Amherst:**

* Reminded that this is model based evaluation of adaptation, in which theory is used to describe what adaptation would look like, then actual genomes are examined for that pattern.
* Advantage of genomic approach is that markers of selection can be examined without phenotypes of selection. Also the direction of functional gain rather than neutral loss can be evaluated.
* Downside is that this approach requires good quality genomes to align reads against, which are not available for all organisms. Furthermore, deep insights and direct demonstration into what exactly the functional genes differing between organisms may do with respect to local adaptation is for the most part limited to model organisms and relatives.

**UConn/UT Arlington:**

* Phenotype is needed when analyzing genetic data. Therefore, experimentation is necessary at some point, especially because we can’t support that variances are due to selection and not drift without experimentation.
* If experimentation isn’t going to be carried out in a specific study, there would need to be very strong a priori information about fitness dynamics surrounding local adaptation.
* Felt that papers provided good general methods pipelines as Snail paper establishes that local adaptation exists within a species while the Fly paper seeks to explore the genetic basis for that adaptation.

**Old Dominion:**

* Depends on study system, which usually requires a biotic or abiotic gradient between populations that can produce differences in fitness such as temperature or prey availability.
* Also depends on which genes are under selection and the genomic techniques used to analyze local adaptation. For example, structural changes in genomic data can indicate divergence under environmental selection.
* Genome-environmental association analyses (GEAA) have become important for studies of local adaptation which are sensitive to gene variants associated with various environmental parameters. It is important to incorporate analysis of neutral genetic structure in studies of local adaptation as well.

**Cornell:**

* Highly dependent on study system, if good evidence of local adaptation can be presented without experiments and is dependent on conclusively linking genomic changes to phenotypic changes
* Not always possible for non-model systems for which we don’t know much about the functions of genes.
* However, if one can link genetic variation to phenotypic variation, particularly in populations along an environmental cline or across parallel cases of adaptation, then genomic data can provide good suggestive evidence of local adaptation.
* Genetic data are therefore most meaningful in the context of phenotypic information.
* Also discuss whether this would be conclusive proof for local adaptation since one wouldn’t know if these genetic changes really lead to higher fitness or not.
* In order to show local adaptation, one has to perform experiments.
* Even without experiments, genomic data can provide useful insights into the potential phenotypes under selection and thus provide a very good basis for experimental test of local adaptation. Experiments cannot be performed for many species, and genomic analyses can be the best evidence of local adaptation in these species.

**UConn Marine Science:**

* Landscape genomic data are useful in forming hypotheses about local adaptation, but insufficient to test for it.
* Not enough to determine how selection may be influencing certain genets, especially in non-model organisms without robust annotation or mapping data.
* Should be cautious in interpreting genomic differentiation if we are unsure of how those signatures relate to the environment.

**UC Santa Barbara:**

* Genomic data can suggest that local adaptation is occurring (but is not indicative of the degree to which fitness is changing) when genetic drift is controlled for.
* Changes in allele frequencies that are evident after controlling for genetic drift may be a smoking gun for selection on fitness-related traits. That said, measuring gene flow and/or dispersion is necessary for understanding genetic drift and therefore we agree that sequence data is not useful in this context purely on its own.

**UC Merced:**

* Landscape genomic data, such as differential population genetics and Fst values, is not sufficient for supporting local adaptation because of the difficulty in excluding other potential causes of differentiation.
* Genomic data may be more useful in assessing locally adapted alleles in high dispersing, well mixed populations (problem may be cryptic species).

**Northeastern**:

* Discussed that genomic data is more convincing when it is paired with experimental data, and evidence can be further improved by pairing it with clear morphological and environmental differences. For example, genetic loci putatively linked to selection along a gradient that also tracks changes in phenotypes along the same hypothesized selective gradient could be taken, in tandem, as good evidence of local adaptation.
* Acknowledge that this scenario would likely contribute to a bias towards genes of large effect.
* Also, genomic data linked to genes that implicate differences in fitness along this gradient could represent a compelling case for local adaptation, although identifying such links (functional pathways) requires that sufficient annotations be available for the species of interest.
* A particular shortcoming of the Fly study was its reliance on only the temperature cline endpoints, without any genomic data from the middle of the temperature range. Without a more complete characterization of genomic data along the temperature cline, it is difficult to make conclusions about local adaptation.

**Louisiana State:**

* Although genomic data may provide evidence for local adaptation, generally agreed that genomic data alone are insufficient for concluding that local adaptation has taken place. Differential genotypes do not necessarily indicate differential fitness and may not be result of adaptive processes.
* All available data should be included and used for comparison against a null model, which could be used to predict the selection necessary to establish the difference among genotypes. The fly study could’ve used a null model to predict the selection that would’ve been necessary to establish the cline and compared genomic data against the model.
* It is methodologically problematic to select the 1,2, and 5% outliers and consider them as a priori differentiated since there will always be outliers, yet they may not be significant for detecting local adaptation. If the outliers are always considered differentiated, and if differentiation is evidence for local adaptation, then by definition there will always be evidence for local adaptation.
* Instead, genes with known phenotypic correlates should be chosen for analyzing whether or not their differential distribution along a cline is adaptively significant.
* By limiting the Fst windows to 1-kb gradual adaptation driven by weak selection involving larger sections of the genome may be missed. A SNP analysis may provide additional insight, but in the absence of knowledge about the fitness differences of different genotypes, a genomic analysis alone is unable to conclusively demonstrate the presence of local adaptation.

**CSU Monterey Bay:**

* Landscape genomic approaches are most relevant for exploring genetic mechanisms that might underlie local adaptation. Evidence that landscape genomics is largely context dependent.
* What lead to these studies to have such compelling arguments for local adaptation was that in both cases there was a context where local adaptation made compelling sense. Possible adaptation had been established in the snail before transplant experiments and their dispersal capability is already somewhat limited as compared to other marine species and there had already been work on Drosophila in Australia to suggest genetic clines or patterns of local adaptation.
* It was pointed out that neither of these studies demonstrated local adaptation as described by Week 2’s papers, neither paper well demonstrated local adaptation. In snail study, you had one population outperforming the other in multiple environments and in neither did they test for actual fitness.

**Univ. Queensland:**

* Landscape genomics provides good evidence for local adaptation if the study is replicated across multiple landscapes of the same environmental gradient. If such replication recovers the same set of loci, then it might support the idea of the local adaptation.
* But recovering same loci across replicates will not reject local adaptation caused by similar factors. Because landscape genomics is correlative in nature, we think that inferring the particular causative factor is difficult even in well replicated study.
* Similarly, using the genomic information to identify cellular/physiological processes that are likely to be influenced by environmental factor of interest might post challenges as well due to the possible links of many cellular (metabolic/physiological) pathways.

**2.) How do the different research approaches (experimental vs. genomic) give different insights?**

**Rutgers:**

* Experimental approach allowed the identification and manipulation of selective pressures in a non-laboratory experiment. The group behind the whelk study has an incredibly detailed understanding of their study system, and between the foundations placed by their previous work and the differences in fitness of local and distant phenotypes in CA plots, they make a strong case for the existence and drivers of local adaptation in this species.
* This approach does not, however, reveal the genetic mechanisms behind the drilling adaptations of the California snails. If researchers used a genomics approach on this species without the same system knowledge, they may find plenty of positively selected genetic differences, but they may attribute them to the climatic gradient between CA and WA rather than to differences in prey recruitment.
* Genomics approach can be used to look for genetic differences relatively quickly and to avoid the confounding effects of plasticity and maternal effects. But you need the resources (annotated genomes) to know that the outliers they find are likely to result in phenotypic difference.
* In addition, this approach gives a deep time perspective that is impossible to achieve with transplant experiments. These genetic differences integrate over all past conditions and over whatever factors you didn’t’ measure in the field.
* You can look at a broader scale of genetic change without examining specific drivers or phenotypic mechanisms, but you still get very detailed information on the mechanisms of genetic change.

**Univ. Southern California:**

* Experimental approaches offer the ability to use a top-down method of hypothesis testing by manipulating specific ecological parameters of interest while still maintaining the complex environment available in situ that would be difficult to recapitulate in a lab setting.
* Genomic data employs a bottom up approach and allows for tracking of genetic information as the currency of evolution to ascertain if noted phenotypic differences appear in association with particular genotypes.
* Genomic information may also be acquired from a broad scale of organisms without direct manipulation in the field and such data is often relatively simple to generate and maintain, all the while knowing that it reflects the objective genetic character of natural populations (assuming adequate sampling).
* Coupling of the two approaches has the greatest potential to map ecologically applicable characteristics of the organism and their genotype to measurements of fitness to determine the validity of local adaptation in the system.

**William and Mary:**

* Question how much training across subdisciplines in biology matters here. If intro to adaptation is largely genomic/bioinformatic vs. natural historical, how does that drive the types of questions you’re asking?
* Both can be compelling but how do we bridge gap in training for students to appreciate and become adept at both if both are necessary?

**CSU Northridge:**

* After significant debate, concluded that experimental approaches provide ecologically-relevant insights into tangible implications such as management in response to changing environmental conditions, whereas genomic approaches give insights into detailed mechanistic aspects of adaptation.
* From experimental design standpoint, talked a lot about how to design experiments from both aspects that would target question of adaptation, and came to consensus that if the system was well studied, an experimental approach with targeted genomic data would be able to pinpoint both adaptation as well as mechanisms. However, if not much was known about a system, perhaps a “shotgun” approach of looking at a landscape genomic changes could be a good place to identify genes of interest then design ecological experiments around this.
* Also discussed – if we need genomic data to determine adaptation. If certain trait was being selected for and was identified, genetic data could provide a mechanistic cause, but perhaps would not be needed to prove adaptation.

**Hal-Dames Rule**:

* There are merits of incorporating both methods. Reciprocal transplant experiments can identify fitness differences which could show local adaptation, but genomic data is needed to show there is a genetic basis for the differences.
* For genomic studies, positive selection can be evaluated, but it does not necessarily mean the selected phenotypes are habitat specific; reciprocal transplant experiments are needed to evaluate habitat specificity.
* Alternatively, experiments are not always possible, and genomic studies can be insightful on their own if there are a-priori expectations of the region of the genome to target; candidate genes associated with traits expected to be under selection, complementary expression and trait data, and or clear phenotypic differences.
* For snails and flies, it is important to distinguish local adaptation from neutral processes like drift. Also, corridors connect subpopulations of both species. For flies, wind currents, human aided dispersal, and active flying and their range have the possibility of connecting the different populations. For the Snails, their movement across sites is primarily due to dispersal during the larval stage, so retention of larvae at a local site is needed to maintain adaptations.
* Comparing the two papers, the flies were also likely somewhat domesticated which can affect inference of what genes may be under selection.

**Virtual Group:**

* Think experimental work largely identifies patterns (local adaptation) while genomics gets us to the mechanism. Experimental work is fundamentally important to understand the drivers behind different performance of populations and which selective pressure may be driving adaptation. Genomics provides a nice way to identify the genes/mechanisms that may be responding to this selection.
* The issue with selection scans alone is linking the genotype to the phenotype that may be under selection, and how to avoid story telling with the results.
* Because environments are complex, it is unlikely that all selected regions are linked to temperature tolerance (or whatever trait), so parsing down the many regions identified as under selection to the set that drive temperature tolerance is important.
* One strategy is to use association mapping to link genotype to phenotype while simultaneously using selection scans. Then you can look for regions under selection that explain phenotypic variation in whatever trait.

**Washington State U:**

* The inference/result per dollar in these types of datasets are very different. Also, there are some systems where one or the other approach is not feasible (long generation times).
* Best and cheapest way to make inferences about local adaptation, if animal is tractable, is experimental approaches. But most can’t be investigated this way.
* If experiments aren’t feasible, you may need to make genetic correlations with environment. We do like that the genomic approach gives historical context but can’t say for sure whether this is specifically due to local adaptation.
* Lots of discussion around how value of insight between two approaches is organism-specific.

**Northeastern MSC:**

* Experimental approaches seemed to us to be the basis of all studies aiming for insights into fitness, which we agreed should be a focal point in any discussion of local adaptation. But additionally, experimental studies have the advantage of allowing for questions ranging from the limits of endurance to extreme values of environmental factors or identifying instances of phenotypic plasticity.
* Genomic approaches allow for broader evolutionary considerations, and in some ways can be necessary to perform prior to other experimental work in order to establish proper population structure or establishing genotype-phenotype-ecotype relationships and considering multivariate interactions between environmental variables in GxE studies.

**Bodega/UC Davis/UC Santa Cruz:**

* Experimental studies: common garden and reciprocal transplant experiments like Snail study provide strong evidence of fitness differences between demes, and are useful in making informed conclusions about the ecological effects of these fitness differences. In other words, they make possible the empirical leap from evolutionary to ecological processes. However, they provide very little insight into the direct mechanisms of selection.
* Genomic studies: Assist in building hypotheses for candidate genes and the physiological mechanisms through which adaptation may occur, and also provide a genetic context for understanding the present and historical constraints on local adaptation like gene flow, linkage, and genetic architecture, but are correlative and can’t directly measure differential fitness.
* Component missing from both is the physiological link from genetics and expression to ecology (what is happening in different tissues and how is it happening? They attack question from both sides but did not converge in the middle.

**Nicholls State:**

* Experimental approach was more elegant and the researchers were able to tie the information directly into the ecology of the system. However the experimental approaches do not provide insight into mechanism. Conversely, genomic studies provide info on a mechanism, but sometimes we struggle to connect that to the ecology.
* Fruit fly paper provided a wealth of data on the pathways potentially affected by genomic differences, which is valuable information and definitely shows more work should be done along this cline.
* Work with model organisms can lay groundwork to do more with non-model organisms, but this kind of study would not be possible with many other organisms.
* With right study design, molecular work can be used to understand how plastic an organism is, which may be more difficult with experimental approaches.
* Epigenomics/proteomics/transcriptomics combined with modeling can provide estimates of how well a population may acclimate/adapt in a changing environment. May also be less invasive especially if working with endangered animal.
* Using both together is most powerful way than either by itself.

**UMass Amherst:**

* Wondered about F2 generations. How do we avoid biasing the response of different populations when we transplant them out into the field by selecting a common lab environment?
* Why f2 and not f8? Just because everyone does it?
* How do we balance adaptation in the lab with too many generations vs. not enough to remove maternal effects? What if maternal effects are the adaptation?
* Genomics offers evolutionary directionality, hypothesis generation, and looking at mechanisms. The transplant approach offers testing of specific hypotheses, results of adaptation/phenotypes, and use of non-model organisms in complex environments they evolved in.

**Old Dominion:**

* The best approach depends on study system and study species. Fly paper was able to measure a swath of genomic indices that could indicate adaptation or divergence in part because the whole genome of D. melanogaster has been sequenced, making it a great candidate species.
* Experimental studies can observe how or if genetic differences show up in the study system, but it is important to understand the functional properties of the genes under selection. Measuring regulatory elements can provide information about the pathways that are under selection and gene knockouts can determine the functionality of genes supposedly responsible for local adaptation.
* Important for collaboration between different but complementary disciplines to emphasize effects of genetic changes on local adaptation.

**Cornell:**

* Experimental and genomic approaches give insights into different aspects of local adaptation and therefore the integration of both is very powerful.
* While experimental approaches, common garden, or reciprocal transplant experiments can teach us a lot about differences in fitness, the role of divergent phenotypes and the drivers of selective agents, they don’t provide insight into the genetic mechanisms of local adaptation and are often not feasible.
* The experimental snail study does a neat job of showing that fitness differs between populations but falls short of its potential as they did not further explore potential phenotypic differences between populations.
* Linking such an experimental study with landscape genomic analyses, particularly along the entire cline, could however provide more insights into the processes and mechanisms of local adaptation, such as the migration-selection balance and identifying genes underlying adaptive phenotypes.
* We think one approach should be followed up by the other, order unimportant, if one wants to provide evidence of local adaptation. Genomic approaches could first provide insights into mechanisms and potential phenotypes under selection, which are then tested through experiments, or experimental approaches can reveal the presence of local adaptation and identify adaptive phenotypes, and genomic approaches could be then used to investigate the underlying proximate and ultimate mechanisms of adaptation.

**UConn Marine Science:**

* Experiments test for local adaptation, genomics informs on mechanisms of adaptation. Both techniques must be executed in tandem and used to corroborate each other when assessing for mechanisms of adaptation.
* Must use experimental approaches to assess what traits are affected under certain environments, and must use genomics to understand how these traits are changing.
* Can also be subject to organism/habitat in question, which may help decide what analysis will produce the most impactful result.

**UC Santa Barbara:**

* Many of the major differences have already been brought up (transplantation studies provide quantitative insights into fitness differences, genomic approaches generate hypotheses about mechanisms of adaptation and they agree that integration of both approaches is ideal.
* Proposed following experimental design and wondered what info you could pull from this that you can’t determine using either on its own: Rear F2 hybrids of different demes under common garden conditions, outplant the F2 hybrids to home and away habitats where you measure fitness related traits in a large sample size of identifiable individuals and measure qtl associated with variation in fitness between both demes.
* If you could pull this off, you could understand what proportion of genetic divergence between demes is due to hybrid breakdown (which could be important in evaluating a high quality deme’s ability to rescue demes that are at risk.
* Limitations in this are fairly serious and we wondered to what extent this experiment would be possible in model marine systems.

**UC Merced:**

* Genomic and experimental research approaches can both show inherent population difference, but genomic approaches produce more mechanistic results, whereas ecological experimental approaches can give more general/holistic patterns.
* Linked to the aspect of scale incorporated in genomic and experimental approaches. For example, genomics provides smaller scaled insight for specific genes, while field experimentation can branch out showing organismal interactions and patterns in ecosystems. This suggests that both approaches are valid but become more useful when combined.

**Northeastern**:

* Genomic approaches can give insight into genetic differences, but not necessarily (directly) get at the agents of selection that are driving them. With experimental approaches, you can test hypothesized agents of selection.
* In general, genomic approaches may be more useful when an annotated genome is available for the organism of interest, as a way to make indirect inferences about function, which may limit the applicability of these approaches to non-model organisms.
* Spatial scope of inference is potentially much broader when using genomic techniques than that which is feasible through experiments. However, if the aim is to make associations between genetic and environmental differences across space, genome scan approaches would also require fine-scale characterization of the environment.
* Experimental approaches, alternatively, provide direct framework with which to test agents of selection, but require that the experimenter make a choice about the selective agent to test and the appropriate response variables to measure.
* A strength of experimental approaches like reciprocal transplant is that they often allow direct measurement of fitness (or traits that affect fitness) whereas a link to the relevant traits and organismal fitness is often missing from a purely genomic approach, even for those with well annotated genomes.

**Louisiana State:**

* Genomic approaches provide insight into allele frequency changes, whereas experimental approaches provide evidence for the adaptive significance of the allele frequency changes.

**CSU Monterey Bay:**

* Had debate on the nature and worth of deductive vs. inductive (abductive) reasoning. Experimental evidence is very convincing, but a strict deductive perspective is really one applicable to the scale of your experiment and the null hypothesis you are rejecting.
* The abductive/inductive approaches can be compelling in the context of the data presented and the authors seem to make good verbal argument for the expectation.
* One thing pointed out about landscape genomic approach is that the evidence identified based on the population allele frequencies would indicate a population-level response and possibly a metapopulation-level response, which is different than the experimental approach and its limited scale.
* People seemed to favor an approach that included both types of information is probably closest to an abductive reasoning model.

**Univ. Queensland:**

* The snail study allows us to infer particular phenotypes (or traits) that are likely underpinning fitness in some ways (phenotypes under selection).
* Experimental approach allows us to explicitly test for factors underlying local adaptation.
* Genomic approaches can possibly give us insights into the genetic underpinnings of local adaptation. Genomic studies may, however, give clues about genomic architecture underlying selection such as the number of loci involved, their sizes, etc.
* However, in the fly paper, the genomic approach is geared more toward generating hypotheses than inferring processes causing local adaptation.

**3.) How are the processes that drive local adaptation in the snail differ from the fly? How are they similar?**

**Rutgers:**

* Do we really know whats driving adaptation in the fly? In the snail paper, abiotic environmental factors drove changes in biotic distribution, which lead to local adaptation through predator-prey interactions. This could be happening in the flies too, but we can only hypothesize based on changes in protein structure and regulation that are impacted by the genetic differences that were found.
* In theory, doing genomics on the snails and experiments on the flies would allow researchers to make important connections between physical properties of chromosomes, likely mutations, and the effects of these mutations on phenotype.

**Univ. Southern California:**

* The snail system makes a cogent case for both biotic and abiotic determinants driving potential for local adaptation. In drosophila the cline was largely noted as being driven by climate and temperature without specific reference to biotic aspects.
* It is possible that populations of Drosophila across the cline experience drastically different biotic environments such as the predominant food item available especially in the case of agricultural products which may have different amounts of insecticide.
* In both systems there is a latitudinal gradient to the adaptation albeit that the determination of a cline in the snail population is difficult given data from four populations.

**CSU Northridge:**

* Discussed how differences in life history between the two species could drive local adaptation. With snails, processes of localized recruitment, shorter spatial dispersal, availability of prey could increase selective pressure for certain traits in microhabitats. In the fly system, we were unsure how the organismal interaction with the environment would affect its ability to adapt.
* Authors in the fly study identify differences in the genome across latitudinal clines, however there are many factors that may drive changes in the genome (temp, prey resources, habitat availability).
* Annotation of genes would be necessary to determine the processes that may drive local adaptation, and that a further ecological context is needed to interpret if this is in fact local adaptation.

**Virtual Group:**

* Lots of similarities between the systems, mainly nice clinal systems and large population sizes.
* Differences in life history may make the snails more likely to have local adaptation at small scales – short dispersal with very local recruitment. The main difference is that the snail system took the abiotic variation along the cline and identified the biotic consequences as compared to the rather straightforward abiotic focus in the flies. That extension is really nice and highlights how we need to focus on how abiotic parameters affect more than just physiological processes.
* Patterns of adaptation in snails very interesting. Because southern snails lack preferred prey, they have evolved to be able to consume a more broad array of prey than northern snails; their niche is expanded. This leads to an interesting reaction norm where southern snails have no change in fitness but northern snails have an adaptive pattern.
* We discussed for a while which population has actually adapted to their environment. On the surface it appears that the northern population has evolved, but probably the southern population has adapted to be able to consume larger prey? If this is true, then the population that has adapted shows no patterns of local adaptation.

**Washington State U:**

* Papers were too different to give a fair comparison. Question is not answerable based on these two papers alone, but thinking about general knowledge about these animals, we can say that the reproductive, environmental, dispersal, and many other processes are still so different they cannot be compared.

**Northeastern MSC:**

* The Nucella study was focused on prey availability and feeding behaviors of the Oregon and California populations. While some abiotic factors like temperature, were accounted for, other factors, like the long term shaping of population behavior by winter temperature differences couldn’t be explicitly considered. Experimental approach does require focusing on very explicit factors driving local adaptation.
* Drosophila study highlighted a range of factors potentially driving local adaptation, including thermal stress, insecticide resistance, circadian cycle differences, and mating behavior.
* Agreed that genomic approaches are very useful for hypothesis generation and can in fact generate multiple potential hypotheses per study while experimental approaches serve better to test explicit hypotheses and are by necessity only focused on a few factors.
* Wish that authors of snail paper had clarified terms instead of saying “show local adaptation” to “show signatures of local adaptation” since without knowing which population is ancestral, can’t say which is showing the adaptation.

**Bodega/UC Davis/UC Santa Cruz:**

* In both examples, local adaptation is driven by differences in environmental variables, but directly so in the case of drosophila, while there was no evidence that temperature differences were driving divergent selection in Nucella.
* However, regional differences in upwelling lead to changes in the strength of species interactions of Nucella with various prey species, driving differences in foraging pressures. Drosophila case, latitude factors. Snail, prey availability driven by differential recruitment.
* Nucella’s life history traits limit gene glow, but drosophila seem to have fewer physical boundaries to gene flow. Effective population size of drosophila also much greater, leading to a minimal impact of drift.

**Nicholls State:**

* Only discussed that snail is in an intertidal zone and the scale of the experiment was much smaller than the temperate versus tropical scale of the fruit fly.
* How can this be communicated to a broader audience? Is one type easier to communicate to the public when trying to explain importance of local adaptation to climate change?

**UConn/UT Arlington:**

* If local adaptation means increased fitness within an environment, got nitpicky that fitness wasn’t defined in the Fly paper. Drosophila altered development in response to abiotic forces, while Snails altered biology to deal with biotic forces (prey availability).
* Discussion that patterns in biology tend to be in response to abiotic forces (longitude and upwelling).

**Old Dominion:**

* Both papers investigate heterogenous environments with populations separated by geographic barriers resulting in restrictions of realized gene flow. Local adaptation in both examples are driven by abiotic processes, but biotic processes are also drivers of local adaptation in the snail.
* Biological processes under local adaptation at the genomic level were not as thoroughly analyzed in the fly paper.

**Cornell:**

* Ultimately, the processes driving local adaptation in both systems are directly or indirectly linked to differences in abiotic factors – either climate or upwelling.
* In the snail, differences in prey abundance, which are associated with abiotic differences are drivers of local adaptation, whereas in the fly paper, abiotic differences seem to directly be the driver of local adaptation.

**UConn Marine Science:**

* Obvious differences in the scope of both studies. Snail study uses system with similar climatic environments but different oceanographic contexts and prey availability. The fly paper uses a system that spans a larger geographic range with more distinct environmental differences.
* Comparing the two, one might interpret the lack of prey and difference in climates to drive adaptation for each respective study (how they are different), while both papers suggest that trait differentiation within the metapopulation seems to be the result of local adaptation (similarities).
* We are not convinced that either represents the local adaptation they seem to suggest. Both papers suggest evidence for some traits that are the result of adaptation, but without measuring fitness for each trait difference with respect to the environment, we cannot conclude that either the snails or the flies are locally adapted. This does not suggest that the information presented is invaluable, just suggests that that the way the data is presented leads the way for future studies.

**UC Santa Barbara:**

* Found snail paper unique in that both the selective pressures and the fitness-related traits being studied were directly linked to community level processes rather than purely organismal ones.
* Much of local adaptation literature is rooted in organismal processes, community- and ecosystem-level variation is crucial when considering how marine systems will be impacted by changing environmental conditions. In the case of flies, there are likely a myriad of selective pressures that differ between the two habitats that were studied, which were likely rooted in community and ecosystem processes and not just the physical environment.

**UC Merced:**

* Specific to these studies, it is difficult to define processes and compare the lines of evidence provided, because they are so different.
* Aside, transplants on ecosystems in the wild are approached with caution much more now than in the past.

**Northeastern**:

* Processes that drive LA in the snail are mediated by both biotic and abiotic processes, via spatially consistent differences in upwelling that lead to differences in prey recruitment. In contrast, the processes that drive LA in the flies are primarily abiotic.
* Both selective regimes were persistent in space.

**Louisiana State:**

* Do not agree the fly paper demonstrated presence of local adaptation in the fruit fly. Analysis of differential genotypes led to the detection of interesting patterns, which may be a good starting point for formulating hypotheses that should be methodically pursued, but patterns do not necessarily correspond with local adaptation.
* Paper on snails challenged to rethink definition of local adaptation, which they originally defined as reciprocity in fitness as a result of home/away comparison, because, on the one hand, we view the fitness differences (local vs foreign) between the CA and OR populations in the California sites as evidence for local adaptation, but on the other hand, we view the fitness differences between the populations in OR as fitness differences but not necessarily evidence of local adaptation.
* In the case of the snails, since there are many unknowns and variables to be considered such as the effect of drilling efficiency/likelihood of mussels on snail fecundity, concluded that Snail paper provided evidence for local adaptation in California sites, there was not enough to definitively determine that local adaptation was occurring. Not every population has to be locally adapted in their own locality.

**CSU Monterey Bay:**

* Didn’t spend much time, ultimately it was the same evolutionary forces at work here that we would see in any study, although of course, things like the nature of selection could definitely vary.

**Univ. Queensland:**

* In the snail experiment, biotic factors impose selection on the snails. In contrast, the fly study seems to examine the effect of physical factor, particularly temperature, in inducing local adaptation.
* Note that inferring spatial factors underlying local adaptation will be difficult with few populations