

Results from a meta-analysis investigating covariance between genetic and environmental (CovGE) effects in phenotypic results in published literature

Website: <https://www.bco-dmo.org/dataset/877425>

Data Type: model results

Version: 1

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Project

» [RCN: Evolution in Changing Seas](#) (RCN ECS)

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Abstract

Covariance can exist between the genetic and environmental influences on phenotype (CovGE) and can have an important role in ecological and evolutionary processes in nature and population responses to environmental change. CovGE is commonly called countergradient variation (CnGV; negative CovGE) or cogradients variation (CoGV; positive CovGE) and has been recognized in classic studies that have established several long-standing hypotheses about CnGV and CoGV. For instance, it is hypothesized that CnGV is more prevalent in nature than CoGV, that CnGV is more prevalent in fish, amphibian, and invertebrate taxa, across latitudinal or altitudinal environmental gradients, and more frequently occurs in metabolic compensation traits, including development, growth, feeding, metabolism, and activity, while CoGV is more commonly observed in morphological traits. The recent development of a standardized method to measure CovGE allows for the first rigorous quantitative exploration of these hypotheses. We use meta-analysis and apply the novel quantitative method to test whether the above hypotheses are supported in the literature. We found no differences in frequency of CnGV and CoGV, and no systematic patterns relative to taxa, environmental gradient, or trait type. However, our analyses suggest that CovGE may be as common as gene by environment (GxE) interactions. Given that CovGE is likely to have a strong impact on future outcomes for organisms experiencing environmental change, that significant CovGE occurred frequently, and the lack of systematic patterns in the occurrence of CovGE, we encourage a more widespread application of measuring CovGE.

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Methods & Sampling

We searched the Web of Science database for experimental studies that evaluated differences in phenotypic responses across different genotypes and environments. We conducted the initial search on June 24, 2019. We used the search terms, ("cogradients variation" OR "countergradient variation" OR "cogradients selection" OR "countergradient selection" OR "co-gradients variation" OR "counter-gradients variation" OR "co-gradients

selection" OR "counter-gradient selection") OR ("GxE" OR "genotype by environment" or "gene by environment") OR ("nonadaptive plast*" OR "non-adaptive plast*" OR "maladaptive plast*" OR "adaptive plast*") OR ("phenotypic plast*" AND "adapt*") AND ("common garden" OR "reciprocal transplant"). Initial searches returned approximately 5,900 hits. Results were further refined by including only those articles within Web of Science categories that related to ecology, evolution, or any ecological or evolutionary subdiscipline (e.g., papers categorized as engineering or biomedical were excluded). Refining reduced the search results to 4,458 studies. We also added studies that were included in previously published meta-analyses by Murren et al. (2015) and Hereford (2009) for screening.

Results were exported, compiled, and primed using package "metagear" (Lajeunesse 2016) in the R statistical environment (Team 2018). Studies were screened for inclusion by scanning titles and abstracts. We required that studies collect phenotypic data from at least two genotypes or populations across at least two different environments. We assumed that author-specified "populations" or "genotypes" are groups of interbreeding individuals experiencing different selection pressures and therefore are likely to be genetically divergent although we acknowledge that this is not always the case (Merilä and Hendry 2014). We excluded studies that only provided genomic data with no other phenotypic anchors, studies that did not provide information about the native environments of genotypes used in experiments, and studies that used genotypes produced by artificial selection. Additionally, a prerequisite for the estimation of CovGE is that phenotypic data from each genotype is required from the same environment in which the genotype evolved (i.e. its native environment). More simply, we cannot estimate CovGE if any genotype ('G') is missing its environment ('E'). Because we use linear models to generate estimated marginal mean phenotypes (see methods below), if the experimental treatments did not align to the home (native) environments of each genotype, interpolation would be required to predict the mean phenotype for each genotype and environment. In doing so, bias can be introduced. Therefore, we only included studies that match experimental treatments to each genotype's native environment (i.e., the environment from which genotypes were collected). Furthermore, a challenge in the meta-analysis was the presence of nonlinear reaction norms in experimental designs with continuous environmental treatments that are frequently observed in common garden experimental designs. Thus, we only included studies that used categorical experimental environments.

After compiling studies, we measured CovGE and GxE magnitude on phenotypic data. More methods can be found in the manuscript published in Ecology Letters in 2022.

See Related Dataset Albecker et al. (2022) for model code.

Data Processing Description

BCO-DMO Processing:

- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Missing data identifier 'NA' replaced with 'nd' (BCO-DMO's default missing data identifier)
- Added a conventional header with dataset name, PI names, version date
- Removed units of temperature from column "exp_env_cont"
- Replaced commas with semi-colons in the "trait_notes" column
- Removed apostrophes from the "trait_notes" column

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Data Files

File
covge_meta_analysis.csv (Comma Separated Values (.csv), 7.01 MB) MD5:fbcaf959b9d28440caf150eb1f4cfdb3
Primary data file for dataset ID 877425

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Related Publications

Albecker, M. A., Trussell, G. C., & Lotterhos, K. E. (2022). A novel analytical framework to quantify co-gradient and countergradient variation. *Ecology Letters*, 25(6), 1521–1533. Portico. <https://doi.org/10.1111/ele.14020>
Results

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Related Datasets

IsRelatedTo

Albecker, M., Trussell, G., Lotterhos, K. (2022) **Metadata for studies from meta-analysis investigating covariance between genetic and environmental (CovGE) effects in phenotypic results.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-08-09 doi:10.26008/1912/bco-dmo.877414.1 [[view at BCO-DMO](#)]

Albecker, M., Trussell, G., Lotterhos, K. (2022) **Results using simulated data used to conduct power analyses.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-10-14 doi:10.26008/1912/bco-dmo.877456.1 [[view at BCO-DMO](#)]

Software

Albecker, M. A., Casalott, & Lotterhos, K. (2022). *RCN-ECS/CnGV: Archived CGV data and code - April 2022* (Version 1.0) [Computer software]. Zenodo. <https://doi.org/10.5281/ZENODO.6470547>
<https://doi.org/10.5281/zenodo.6470547>

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Parameters

Parameter	Description	Units
Study_ID_phenotype	the combination of study ID and the unique phenotype for indexing	unitless
First_Author	identifier	unitless
gen_factor	name of genotype	unitless
Native_env_cont	continuous native environment	unitless
Native_env_cat	native environment if categorical	unitless
Native_env_cat_2	if multiple environments tested	unitless
nat_env_mean	native environment if data are presented as means only	unitless
nat_env_sd	standard deviation of continuous environment	unitless
nat_env_factor	name of native environment for categorical	unitless
exp_env_cont	description of experimental treatment for categorical	unitless
exp_env_cat	description of experimental treatment for continuous	unitless
exp_env_factor	name of environment in factor format	unitless
phen_n	sample size for each treatment	unitless
phen_data	the numeric value of the phenotypic measurement reported in the study	unitless
phen_SD	standard deviation for phenotypic data	unitless
phen_mean_SE	standard error if presented for means data	unitless
phen_mean_lowCI_095	confidence interval lower bound if presented for mean data	unitless
phen_mean_highCI_095	confidence interval upper bound if presented for mean data	unitless
Comments	notes if necessary	unitless
Design	either reciprocal transplant or common garden	unitless
trait_class	category of phenotype	unitless
trait_notes	notes if necessary	unitless

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Project Information

RCN: Evolution in Changing Seas (RCN ECS)

Website: <https://rcn-ecs.github.io/>

Coverage: United States

NSF abstract:

How marine species will react to changing environment and climate is not well understood. While the interaction between oceanographic and ecological processes has yielded considerable insight into the ecology of marine species, the evolutionary responses of marine species are not well integrated into this framework. This project research coordinated network on "Evolution in Changing Seas" (ECSRCN), will bring marine scientists together with evolutionary biologists having expertise in population genetics, eco-evolutionary dynamics, and phylogenetics to better understand and predict the evolutionary responses of marine species to climate stressors. ECS-RCN will increase the impact of evolutionary studies in marine systems through increased collaboration among scientists from diverse fields. Furthermore, the empirical robustness of these studies will also be improved through the development of standards for experimental design and statistical analysis, especially for genomics data analysis. ECS-RCN will build a diverse network through a dedicated workshop for early-career participants, by advertising with diversity groups, and by dedicating funds to increase diversity. This project will support one postdoctoral researcher who will play a key role in coordinating scientific activities of the network as well as receive interdisciplinary training through network activities,

strongly positioning them to become a leader in the field. ECS-RCN will also build the foundation for a lasting network through establishment of a listserv, open access to publications, development of a website, and development of teaching modules for undergraduate and graduate curriculum.

Specifically, ECS-RCN will consider how coupling between oceanographic and evolutionary processes shape adaptive and plastic responses to climate change, from the fundamental level of genomes scaled up to entire populations. Under this theme, the objectives of ECS-RCN are to synthesize the current state of knowledge, to prioritize lines of inquiry that will advance knowledge in marine and evolutionary biology, to determine the appropriate experimental designs and statistical approaches for robustly testing these lines of inquiry (including genomics approaches), and to build a foundation for a diverse and lasting network. These goals will be realized over the course of 3 years, starting with a Synthesis Workshop in Year 1 where working groups will be established, followed by working group meetings and formation of a Genomics Subcommittee in Year 2, and ending with an Integration and Training Workshop aimed at early career scientists in Year 3. To promote synthesis and self-organization at workshops, the workshops will employ the Open Space format. ECS-RCN will promote evolutionary thinking in biological oceanography and integrate unique aspects of marine life-histories into evolutionary principles. ECS-RCN will also advance knowledge in both marine and evolutionary biology through synthesis and the development of frameworks for merging genomics and ecology. The activities will provide novel insights into pressing questions in both marine and evolutionary ecology, such as: what drives geographic patterns of local (mal)adaptation and plasticity?; what are the mechanisms that generate adaptive vs. nonadaptive plasticity?; what is the role of genotype dependent dispersal in adaptation?; what are the genetic constraints on adaptation of function-valued traits to climate change?; and how do epigenetic modifications act as a mediator between adaptation and plasticity? Ultimately, the RCN aims to develop a quantitative understanding of the relative importance of ecological versus evolutionary responses to climate change.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1764316

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