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# Book of Abstracts

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and/or genetic control. However, because of T3's higher affinity to bind to the nuclear receptors, selection should act on T3 rather than T4. This begs the question whether T3 still has ample capacity to respond to selection, or if it is constrained by T4. We approach this question by examining variation in T3 and T4, and covariation between them, at the individual, population, and species levels. Our results will generate specific and testable hypotheses for further experimental work to understand the selective potential of hormone-mediated transgenerational plasticity.

**Abstract ID: 1837**

**Poster board number:**

P347

### **Does the definition of a novel environment affect the ability to detect cryptic genetic variation?**

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Anthropogenic change is exposing populations to novel environments which are hypothesised to release cryptic genetic variation, a hidden store of variance that can fuel evolution. However, support for this hypothesis is mixed. One reason could be a lack of clarity in what we mean by 'novel environment', an umbrella term encompassing environments that were previously infrequent or entirely absent from a population's evolutionary history. These different types of novelty could have contrasting implications for whether phenotypic plasticity hides, or exposes, cryptic genetic variation. Here we use a meta-analytic approach to investigate changes in the total genetic variance of multivariate traits in ancestral versus novel environments. We compared absolute novel environments, those not represented in a population's evolutionary past, to extreme novel environments, involving frequency or magnitude changes to conditions present in a population's ancestry. Overall, we identified no broadscale pattern of increased genetic variance in novel environments and found the type of novel environment did not explain any significant variation in effect sizes. When effect sizes were partitioned by experimental design, we found increased genetic variation in studies based on broad-sense measures of variance, and decreased variation in narrow-sense studies. Therefore, study design, not the definition of novelty, is important in understanding environment-dependant variation, revealing non-additive sources as a key component of cryptic variation.

**Abstract ID: 1914**

**Poster board number:**

P348

### **Phenotypic plasticity of *Iris pumila* leaf functional traits in response to experimental warming**

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Plant physiology, fitness and distribution largely depend on temperature, hence it is expected that global warming will extensively alter their biodiversity as well as the ecosystem functioning. Variations in plant functional traits are widely used to predict the

impact of global warming on vegetation, as they usually reflect the plant's adaptive strategies to essential environmental resources, including temperature. To assess how plants respond to climate warming, we investigated the phenotypic expression of two major leaf functional traits, specific leaf area (SLA) and stomatal density (SD), to a temperature rise of 1°C. A total of 40 *Iris pumila* genotypes, which were consistently cultivated in a growth room at baseline temperature (23/19°C day/night), were exposed to elevated temperature (24/20°C day/night). Within each temperature treatment, the last fully developed leaf was harvested from every genotype and analyzed for the SLA and SD. The mean value of both investigated traits increased significantly with temperature. Leaves developed under elevated temperature exhibited 7% greater SLA and 22% higher SD compared to those developed under ambient temperature. These results suggest that *I. pumila* plants are able to counteract rising temperatures by the plastic response of SLA and SD. Such a capacity to acclimate its major leaf functional traits to altered temperature conditions may provide *I. pumila* a resilience to climate warming that will be occurring within its natural habitats.

**Abstract ID: 1929**

**Poster board number:**

P349

### **The role of juvenile hormone in developmental polyphenism of an ant with obligately sterile workers**

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Ants express extreme forms of polyphenism in which the same genome generates discrete castes that fulfill distinct functions in colonies. The degree of polyphenism varies among species, from colonies composed of morphologically undifferentiated individuals to colonies with queens specialized for reproduction and obligately sterile workers responsible for all other colony tasks. This makes ants excellent models to study proximate mechanisms underlying caste polyphenism, which ultimately allowed the major evolutionary transition to superorganismality. Juvenile hormone (JH) is known to play a key role in caste development in honeybees, and can mediate differential growth of ant worker castes. However, understanding the role of JH in ant caste polyphenism has remained challenging because of the diversity of factors associated with caste determination in ants, and the lack of adequate model species for such studies. The latter problem has been partly resolved by the recent discovery that caste is determined and can be identified visually in the egg stage of the tramp ant *Cardiocondyla obscurior*. This model system gives us the opportunity to manipulate the JH content of eggs and larvae of known caste trajectory. In my project, I characterize the growth of queens and workers over the course of development. I then use experimental manipulation of JH levels in eggs and larvae to quantify how the hormone affects caste-specific growth and development. Finally, I assess caste-specific expression of JH-responsive genes. This project will provide insight into the general mechanisms underlying polyphenism in ants, improving our understanding of this fundamental aspect of superorganismality.

**Abstract ID: 1938**

**Poster board number:**

P350

### **Trait-dependent mechanisms influence lifespan and behavioural plasticity in *Drosophila melanogaster***