Evolutionary genetics

Social shifts in spiders

Sociality has evolved numerous times across a range of animals, but study results differ on the extent to which the genetic changes underlying these convergent transitions occur consistently in the same or similar genes. Now, a study published in *Nature Communications* involving comparative genomic analyses of 22 species of spiders provides new insight into the types of changes involved.

Previous studies had largely focused on hymenopteran insects (bees in particular), in which sociality has independently evolved 7–8 times, 20–150 million years ago. By contrast, spiders are estimated to have undergone more frequent and more recent transitions to sociality (15–16 independent events only a few million years ago), which the authors postulated should make it easier to detect common genomic signatures associated with the switch to a social lifestyle. Moreover, just like bees, spiders display a full range of sociality across their phylogeny (categorized in spiders as solitary, subsocial, prolonged subsocial and social).

The team generated new, or used existing, transcriptome and genome assemblies for eight social and 14 non-social (one prolonged subsocial, five subsocial and eight solitary) species representing eight independent origins of sociality. Gene annotation identified 7,590 orthologous groups and 3,832 core single-copy orthologues found in all 22 species, and these data were used to compile a phylogeny. To identify genomic changes associated with the shift to sociality, genome-wide, gene-wide and amino acid-level molecular evolution rates and selection were compared between social species and non-social species.

Genome-wide, the rate of molecular evolution was higher for social branches than non-social branches and was associated with a relaxation in selection. Gene-wide analysis revealed that many genes experienced shifts in selection between social and non-social branches, including some that have been associated with social behaviours in humans or other animals. Indeed, gene ontology (GO) analysis highlighted a number of processes likely to be functionally relevant to a shift in sociality, such as neurogenesis, behaviour, immunity and metabolism. At the amino acid level, site-specific substitutions between social and non-social species were detected that involved genes enriched for GO terms consistent with those identified in gene-wide analysis. However, none of these changes occurred in all social branches, and some were found in non-social branches.

This study shows that genomic signatures of convergent evolution of sociality in spiders can be detected, but no specific changes in particular genes are required for the transition to occur. Instead, evolution of complex phenotypes such as sociality may involve changes to genes encoding similar functions.

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Technique

A deep learning method to map tissue architecture

Changes in patterns at the tissue and organ level can be a sign of disease development, but combining single-cell data with maps of tissue structure to reveal these patterns relies on time-consuming manual annotation. A new computational method named UTAG (unsupervised discovery of tissue architecture with graphs) promises to identify and quantify organ-specific micro-anatomical domains from biological images without previous knowledge.

The central concept of UTAG is that it leverages multiplexed images to extract and then combine single-cell phenotypical data (such as cell morphology and gene or protein expression) with information on the physical proximity of cells in their native tissue context. Images can be obtained by a range of highly multiplexed single-cell imaging methods, including CODEX (codetection by indexing), CyCIF (cyclic immunofluorescence), IMC (imaging mass cytometry), MIBI (multiplexed ion beam imaging) and multiplexed spatial platforms.

UTAG uses unsupervised deep learning to convert cellular phenotypes, such as expression intensities, into a numeric feature matrix, which comprises every marker for each cell. In addition, the model constructs a graph of physical cellular interactions based on the spatial location of cells in the image. This graph is then converted to a binary adjacency matrix (0 for no interaction, 1 for interaction between cells). The two matrices are combined to create a new matrix comprising spatially aggregated phenotypic information, which can be used by clustering methods to group phenotypically and spatially related cells into tissue domains.

The team first tested UTAG on 26 highly multiplexed IMC images of healthy lung tissues, comprising 28 markers. To serve as a reference, micro-anatomical domains, such as airways and vessels, were manually annotated, and UTAG was able to accurately identify corresponding micro-anatomical domains.

Applying their method to diseased lung tissues, using a dataset of 239 IMC images with 37 markers, identified 6 micro-anatomical domains across different disease states, representing airways, vessels and connective tissue, among others. The relative abundance of the domains was dependent on disease state, with, for example, a large proportion of connective tissue in samples of a patient with late-stage COVID-19, which is indicative of fibrosis. The authors were also able to quantify physical interactions between domains, revealing structural differences between healthy and diseased tissues.

The authors note that the successful application UTAG depends on "the interpretation of the discovered topological domains in terms of their identity and biological relevance", and thus recommend the involvement of field experts such as pathologists when applying their approach.

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