Chapter 6

General Discussion, Conclusions and Future Perspectives

General Discussion

Fundamental aspects of animal biology are deeply rooted in evolutionary history, especially the formative stages characterised by the major transition from a unicellular ancestor to a state of obligate multicellularity. The changes in genetic make-up that our early animal ancestors must have undergone are inextricably tied to this profound shift in lifestyle. The subdivision of specific tasks amongst different cells resulted in the origin of different cell types. Contemporarily, the need for cells of a multicellular organism to communicate and coordinate with each other both for internal physiology and for responding collectively to external stimuli, presented a critical challenge (Ruiz-Trillo and Nedelcu 2015). Such evolutionary pressures drove the expansion of gene families involved in cell signalling (Paps and Holland 2018). The advent of vision, for instance, required a specialised cell type, the photoreceptor cell, capable both of detecting light, and of relaying this signal to other cells, that in turn can integrate this signal to elaborate a collective response. This was possible by coupling photosensitive molecules, the opsin bound to a cis-retinal molecule, with a phototransduction machinery capable of transducing the signal within the cell and culminating in ion channel modulation. The resulting flow of ions is responsible for the electrical signalling that starts the communication with other cells (REF). Similarly, cells of the immune system are responsible for maintaining the physiology of an organism both under normal conditions and when faced with external threats. Chemokine signalling, for example, plays an essential role in numerous processes in vertebrates by coordinating cell migrations throughout the body during development, homeostasis, and host defence. This system signals through small chemotactic proteins secreted by certain cells that are recognised by GPCR receptors on the target cells, which are induced to move along the gradient of these molecules (REF).

Acknowledging this evolutionary history and recognising the centrality of cell signalling for the maintenance of multicellularity is essential for a deeper understanding of animal biology and evolution. This principle was an inspiration for the research presented in this thesis, where I explored the evolution of vision and the chemokine system as examples of processes relying on cell signalling. To explore the evolutionary history of vision two primary aims were identified: first, investigating the evolution of photoreceptor cells by tracing the history of the phototransduction pathway components and the regulatory genes involved in the cell type specification; and second, reconstructing the evolution of the retinol metabolism pathway, which is responsible for the constant production of the photosensitive retinal that, when bound to opsin, enables the phototransduction process. To investigate the evolution of chemokine signalling, three main aims were pursued: first, clarifying the relationships between the “canonical” chemokines and chemokine receptors and “non-canonical” proteins that are also involved in the system; second, reconstructing the evolution of the ligand components; lastly, reconstructing the evolution of the receptor components. To address these aims, a combination of large-scale phylogenetic and bioinformatic methods were employed. Instead of limiting the focus to only a subset of molecular components, the analyses were conducted on a comprehensive set of components from the pathways and systems under investigation. This approach allowed to collect multiple pieces of evidence that combined created a broader picture of the trajectories of the systems under study, offering new insights into their evolution.

Summary of results for aim one: phototr and PRC:

-Most phototransduction broad gene families are distributed broadly throughout eukaryotes, suggesting ancient origin of the broad gene families. Broad gene families are often involved in multiple different pathways and processes, which may explain why they are present also outside of animals where they will not be involved in vision. However, within these big gene families, subfamilies can be identified. This allows to trace more in detail the evolution of the subfamilies that contain phototransduction genes known in model organisms phototransduction pathways. In this way we can see more details for example x,y,z.

-While these considerations are generally true for gene families composing both the major phototransduction pathways, ciliary and rhabdomeric, there are some differences. For example ciliary genes tend to be more vertebrate specific.

-using phototransduction genes as markers it was possible to identify single cell profiles for PRCs in animals, including candidates in non-bilaterians. However, in non-bilaterians not all components of the pathway were present, suggesting some species-specific differences. This is a very important avenue of research as indeed our knowledge of phototransduction currently stems on a super limited set of organisms, so it only makes sense that this might not be a good representation of the diversity of phototransduction systems in the animal kingdom. Interest is growing in trying to uncover potential differences in non-bilateria due to the hot topic of the field in vision evolution (REFS). However I argue not to forget also other bilaterian organisms that may help bridge the gaps between what may be found in non-bilaterians that are very distantly related, and the current limited model organisms. It is only when we will have a broad representation of animal phototransductions that an even clearer interpretation of its evolution can be done. In this sense, broad scale studies such as my phylogenetic one are very important, as I have identified these genes in the genomes, so in the future, as new single cell data from a broad range of animals come out, my set of marker genes can be readily used to look for photoreceptor cells. This combined with experimental approaches will help to add ever more pieces to the puzzle of the evolution of vision that has been the interest of researchers for many decades.

-Also my analysis of shared regulatory genes will be enhanced in the future as more and more animals can be added to the dataset. However, already now some interesting patterns were found. For example x.y.z.

Hints of future perspectives: what we still don’t know / new open questions.

Summary of results for aim two: retinol

Hints of future perspectives: what we still don’t know / new open questions.

Summary of results for aim three: chemokine

Hints of future perspectives: what we still don’t know / new open questions.

Conclusions and Future Perspectives

Comparison of methodologies and respective results.

General conclusions about the usefulness of these exploratory bioinformatic research.

Avenues that are opened for future research.

References

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