Study suggests evolutionary change in protein function respects biophysical principles

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Some molecular biologists who study the proteins that regulate cell operations, including Elizabeth Vierling at the University of Massachusetts Amherst, do not confine their research to understanding the molecules' current roles. They also look deep into the proteins' evolutionary past to explore what structures have allowed proteins with new functions to develop in response to new needs.

An expert in how plants cope with heat, Vierling's interest for many years has been small heat shock proteins (HSPs), which accumulate in plants at high temperatures and appear to act as "molecular chaperones" to protect other proteins from damage.

For work reported in the current issue of *Science*, Vierling, Indu Santhanagoplan and Eman Basha at UMass Amherst and Vierling's longtime collaborator, Justin Benesch and his Oxford University group, experts in protein biophysics, looked at two types of small HSPs to address what they call a "basic evolutionary puzzle." That is, how two different types of small HSPs, Class I and Class II, evolved from a single type over 400 million years ago to form two distinct types with different functions.

"It's always important to consider evolution when you're looking at protein function, because it provides insight into potential functional differences, as well as features important for function," Vierling points

out.

She explains, "We know that mosses, some of the first plants to live on land, as well as all the other plants we see around us, can make both Class I and II small HSPs. We've also demonstrated that these two small HSPs have different functions, though exactly how they work remains unclear. However, the algae that came before land plants only have one type of these small HSPs. Therefore, sometime while plants were evolving functions needed to live on land, they basically duplicated their single small HSP to create two types of small HSPs, and this must have been advantageous."

For small HSPs to duplicate themselves and go on to evolve would be easy, she adds, if each acted as a single unit. "But most proteins work in complexes," she points out, "with partners of either more of the same protein units or different ones. This makes developing a new function harder, because a new function may require changing partners. New partners not only have to fit each other, but may also have to not be promiscuous. That is, they can't act in a complex with the original unit. This is the case for the small HSPs, which assemble into dodecamers with 12 of the same units."

"Millions of years ago when the small HSP duplication took place," the molecular biologist says, "the two would have been identical, like clones. At some point, they developed enough differences that they don't co-assemble anymore. They started to do different things."

For this work, Vierling says her lab contributed knowledge about the two small HSPs and understanding of their functional differences. They also created a mutant protein important for demonstrating structural similiarities and differences between the two. Benesch's lab contributed expertise in advanced biophysical characterizarion of proteins, the principles of protein architecture and assembly, and the biophysics

surrounding those.

Vierling says that usually when researchers look at how protein structures assemble, they look at where the structures touch, because that's where they are compatible. "One of the new understandings of this work is that we found there are places away from the interacting surfaces that affect whether or not they can assemble. So you can't just look at where they contact each other, you have to look at other factors."

She adds, "This paper does all the fancy biochemistry and biophysics to show why these two small HSPs cannot co-assemble. The reason has to do with the energetics of the final structure, and some of the data may be quite esoteric for evolutionary biologists. But because physical principles control protein structure and intereaction, these are important factors to consider in studies of protein evolution. This work also further solidifies the recognition that these two small HSPs have to have very distinct roles in the cell."

In addition to experiments, the team used computer simulations to look at how changes in the way the two proteins might look when bumping into each other could affect their ability to assemble as dodecamers, or 12-part units. One of the first co-authors, Georg Hochberg, also did extensive bioinformatics analysis of protein databases to put the work into a broad evolutionary context.

She says, "When the data are taken together, calculations of basic physical parameters could show that it was energetically favorable to make dodecamers of the same type of subunit. This was the result not only of very small changes in the parts of the proteins that stick together in the dodecamer, but also due to parts of the protein that flop around before they stick together. This information is of interest relative to designing protein complexes that can function in new ways."

In addition, the data predicted that complexes with many identical units like the Class I and II small HSPs are rare in nature, suggesting their importance to plants should not be underestimated and defining their precise mode of action in plant protection is an important goal. Vierling, who is a member of the Models to Medicine (M2M) protein homeostasis group at UMass Amherst's Institute of Applied Life Sciences, was supported by the U.S. National Institutes of Health and Massachusetts Life Sciences Center in this work.

More information: "Structural principles that enable oligomeric small heat-shock protein paralogs to evolve distinct functions" *Science* (2018). science.sciencemag.org/cgi/doi … 1126/science.aam7229

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