

these sediments were also deposited in the Flood during an earlier phase. It also indicates that significant tectonic activity occurred during the first part of the Flood deforming the sediments after they were deposited.

Another feature that helps synchronize the geological section to the biblical Flood is the location of the existing land surface. As the floodwaters drained into the ocean they initially flowed in vast sheets which, as the water level reduced, eventually developed into huge channels.³ This period was primarily an erosional event on the continents, and it is expected that the present landscape was mostly formed at this time: “During the Recessive stage the waters moved off the continents into the present ocean basins. This was a highly erosive process.”¹² Holt called this period the “Erodozoic”.¹³

When we examine the horizontal land surface that runs across the section we can assume that it was mainly carved during the Recessive stage of the Flood. Of significance is the way the geological strata intersect this present land surface. On the cross section it can be seen that, as the strata rise upwards to the east, they have been *truncated* at the land surface. This means that the thick strata extended much further to the east and that they have been eroded away. The enormous area of land surface affected and the quantity of material removed is a feature consistent with the global Flood.

Conclusion

A preliminary examination of the geological cross-section for Goondiwindi (figure 3) illustrates how geological maps can reveal the sequence of events occurring during Noah’s Flood. The readily available maps provide an excellent overview. Of course these preliminary ideas need to be checked and tested for consistency with other geological details, such as the information available in field guides, map commentaries, research

papers and field reconnaissance. But this analysis shows that geological maps can be used to develop an authentic geological history of the area that fits within the biblical perspective. As these connections between geology and the Bible are made more widely available to the general community it will affect the way people view the world.

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Antifreeze protein evolution: turning wrenches into hammers

Shaun Doyle

Evolutionists have often claimed that gene duplication provides the raw material to produce new functions through subsequent mutation and natural selection. However, finding gene duplications that have produced new functions hasn’t been easy. Most gene duplications studied have been silenced and subjected to deleterious mutations, rendering them useless.¹ However, a class of proteins called antifreeze proteins (AFPs) appear to have gone against this trend. AFPs are found in a wide variety of organisms: fish, insects, plants and microbes. They also take as many different forms as there are organisms that have them, and many are believed to have evolved via gene duplication events. These proteins bind to the surface of ice crystals and prevent water molecules from binding to the ice crystals, preventing the ice crystals from growing. This enables organisms to survive in sub-zero temperatures without freezing.

However, postulating that gene duplication and subsequent mutation can result in new functional proteins is not enough. To build a plausible case for neo-Darwinism one needs to identify the source of the new gene and outline the major mutations that actually lead to the change. Researchers have recently posited a detailed evolutionary scenario for the evolution of an antifreeze protein from such a gene duplication event in a species of Antarctic eelpout (ray-finned fish), *Lycodichthys dearborni*.² So do these AFPs represent a neo-Darwinian mechanism producing a new protein? And if they are, what does this say for the plausibility of neo-Darwinism forming the mechanistic basis for microbes-to-man evolution?

The edge of eelpout evolution

Lycodichthys dearborni is one of several species of Antarctic eelpout of the family Zoarcidae. It is found in McMurdo Sound, south of the Ross Sea, off the coast of Antarctica. Zoarcids are one of only two families of fish to possess a particular class of AFPs, type III. The origin of type III AFPs has been particularly difficult for evolutionists to trace.³

The researchers proposed that the evolutionary model ‘Escape from Adaptive Conflict’ (EAC) fits the evolution of the AFP in the *L. dearborni*. EAC states that conflict between an old and an emerging new function within a single gene could preserve a gene duplication, which would allow each duplicate to freely optimize one of the functions. They proposed that a type III antifreeze protein gene evolved from a duplicated

copy of the sialic acid synthase (SAS) gene called *LdSAS-B* (*Ld* stands for *Lycodichthys dearborni*). They posit that in one duplicate, the N-terminal SAS domain was deleted and replaced with a new signal peptide (figure 1). This removed conflict between SAS and ice-binding functions in the duplicate and allowed rapid optimization of the remaining C-terminal domain to become a secreted AFP.

There appears to be one random mutation that enabled the copy of *LdSAS-B* to translate a protein that ended up being an effective AFP: a 4.4 kb deletion coding for the SAS N-terminal domain from codon 7 of E1 (exon 1) to the end of E5 (exon 5).^{4,5} This achieved two fortuitous things that transformed the putative *SAS* gene into an *AFP* gene: it stripped it of any SAS function, and enabled a change in reading frame, which altered the signal

peptide, enabling the new protein to be secreted.

I suggest the large deletion mutation in the putative *LdSAS-B* copy produced *both* the increased ice-binding capabilities and enabled the putative AFP to be secreted out of the cell. The deletion was so large, it rendered the copy gene unrecognizable to the translation machinery as an *SAS* gene. It also destroyed the integrity of the first exon, which exposed coding for a signal peptide targeting the protein for secretion that was previously latent in the 5’ flanking region of *LdSAS-B*.

As Cheng *et al.* found:

“We discovered a precursor signal peptide coding sequence appropriately located in the extant *LdSAS-B*, starting from 54 nt upstream of the translation start site through the first six codons of *LdSAS-B* E1 (Fig. 2 and Fig. S2B). An intragenic deletion from the seventh codon of E1 through E5 of *LdSAS-B* and linkage of the new E1, the old I5 [intron 5], and E6 would complete the formation of the nascent two-exon *AFP* gene encoding the secretory antifreeze protein.”⁶

This latent coding was therefore mistakenly recognized by the translation machinery as the first exon (which had been truncated at the 3’ end due to the deletion mutation) rather than as part of the 5’ flanking region, and it became the signal peptide needed to signal the AFP (largely coded for on the second exon of *AFP*).

Strong selective pressure in the Antarctic waters would make tandem duplications of *AFP* a likely response to the conditions in order to increase the amount of AFP manufactured, and would kill off any eelpout that didn’t have the gene. Therefore, in short, the answer is *yes*, random mutation and natural selection is a likely mechanism for how this AFP and many others were produced.

From neo-Darwinism to evolution

However, the story doesn’t end there. The foundational question

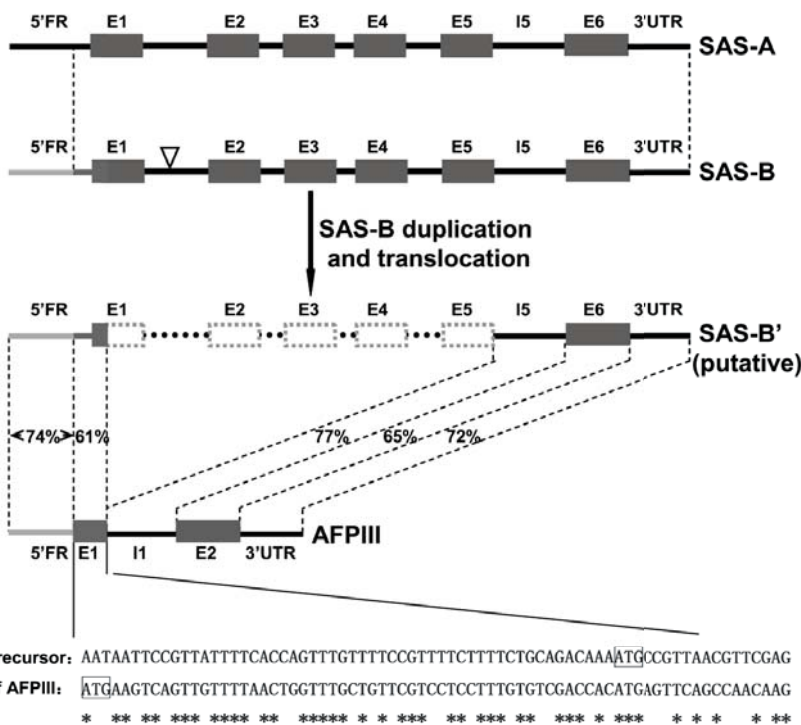


Figure 1. Molecular evolution of *AFP*III from *SAS-B*. One daughter *SAS-B* duplicate (*SAS-B'*) underwent N-terminal domain deletion (seventh codon of E1 through E5) and neofunctionalization into *AFP*III. Regions in *SAS-B'* corresponding to the regions in the two-exon *AFP*III gene are indicated with the same colours for the two genes, with nucleotide sequence identities given. The partly non-protein-coding signal peptide (SP) precursor sequence in *SAS-B'* that was modified to become a coding sequence for the *AFP*III signal peptide is shown at the bottom. *LdSAS-A* lacks the 5’ flanking sequence homology (grey bar) with *LdSAS-B* and *AFP*III; thus, it is not the evolutionary progenitor to *AFP*III. (From Deng *et al.*, ref. 2, p. 21595.)

A NKASWAN**QLIPINT**ALTLIMM
 KAEV**TP**MGIPAEDIPRIIG**MQ**
 VNRAPLGTTLMPDMVKNYEK



Figure 2. The structure of a mature type III AFP of *Lycodichthys dearborni*. **A.** The primary structure peptides in bold are thought to form the flat ice-binding surface typical of type III AFPs (from Deng *et al.*, ref. 2, supporting information, Figure S6; and Protein Data Base www.rcsb.org/pdb, entry 1UCS.pdb). **B.** Tertiary structure, positioned to show the ice-binding surface, with the peptides with an active ice-binding function highlighted in black (from Protein Data Base www.rcsb.org/pdb, entry 1UCS.pdb, displayed in Protein Workshop).

remains: is this an example of neo-Darwinism evidence for molecules-to-man evolution? There is no doubt that this is a new, functional protein; many readers might be convinced that it answers the creationist's demand for evidence for naturalistic evolution. But it's not that simple: to possibly stand as evidence for molecules-to-man evolution, evidence for new proteins has to have at least four characteristics:

1. they need to be formed by a *plausible* naturalistic mechanism,
2. they need to be *complex*,
3. they need to be *specified*, and
4. they need to be *functionally integrated* into the organism's biochemical processes.

AFPs generally fill criterion 1: there is good evidence that many, if not most, are formed through random mutation and natural selection. Moreover, this particular naturalistic

scenario for the Antarctic eelpout AFP is plausible. One may wonder whether designed mechanisms for variation had some role to play, especially given the large number of tandem repeats and the retrotransposon attached to the 5' end of the gene cluster. The origin of such designed adaptability is hard for evolution to explain, but it is speculative at best for this particular scenario.

Not all AFPs fulfil criterion two: many are very simple, yet very ordered.⁷ The Antarctic eelpout's AFP is only 65 peptides long, but is not arranged in a repetitious sequence.⁸ Moreover, many short sentences that carry a lot of information are less than 65 characters long. Consider how the original Greek text of John 1:1 would've been written:

ENAPXHIHNOLOGOSKAIOLO
 GOSHNIPROSTONΘEONKAIΘEOS
 HNOLOGOS

That sentence is only 52 characters long (51 if the subscript iota is left out), and there is much more repetition of characters there than in the AFP. Complexity is therefore not merely a measure of sequence length, but also largely of the lack of repetition in the sequence. So while short, it is of sufficient complexity to satisfy criterion 2.

Criterion three, specificity, is where AFPs in general run into major problems. As stated previously, AFPs are notorious for having as many forms as the creatures that possess them. Consider a hammer and a wrench. Each is designed for a different function: a hammer can't do all that a wrench can, but many things can be used to do the job of a hammer when a hammer isn't available, including a wrench. However, everyone knows that a wrench was not designed to be a hammer, and if you try to use it as a hammer too often, it may no longer work as a wrench.

The SAS protein is like the wrench, and AFPs are like hammers. All that AFPs are required to do is bind to ice, and for that they basically need only a hydrophobic end and a hydrophilic end—i.e. they must be amphiphilic. The hydrophilic end binds to the ice

crystals, while the hydrophobic end repels water molecules, stopping them from binding to the ice. Such a situation is found in many proteins with completely different structures because of the 20 universal amino acids that comprise proteins, half of which are hydrophilic and half are hydrophobic.⁹ Being an AFP is a very non-specific job that many different random proteins could perform.

AFPs also fail to satisfy the fourth criterion: functional integration into the cell's biochemical processes. They are not known to interact in any other cellular process other than secretion from the cell and binding to ice crystals.¹⁰ 'Proteins' such as AFPs effectively slow the efficiency of other functions in the cell by cluttering it with degenerate debris.¹¹ Under normal circumstances, any mutation that enables the translation of either degenerate DNA or non-coding DNA will merely 'gum up the works' of the cell and 'distract' the transcription and translation machinery from other tasks, slowing cellular processes down.¹² But again, fortuitous combinations *that were already latent in the LdSAS-B gene* meant that the translation of this particular debris was beneficial for survival *in a particular environment*.

This example may cause some excitement for evolutionists, but it doesn't contradict what we may expect within a biblical scenario. It is a far cry from demonstrating that mutation and natural selection are necessary and sufficient to explain the history of life. Evolutionists have failed to grasp the evidential burden they have to actually substantiate their just-so stories on how high-information-content biological structures could form naturalistically. AFPs in general, and this example in particular, fail as evidence for molecules-to-man evolution.

Conclusion

AFPs are demonstrably simplistic proteins in their function, more akin to beneficial debris than a new complex and specified protein. Creating an antifreeze protein naturalistically is qualitatively different from creating, for example, the blood-clotting cascade,

cellular differentiation programs, the photosynthetic pathway, or a bacterial flagellum. The difference is between incidental (and accidental) function and essential biological structure.

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Is the faint young sun paradox solved?

Michael J. Oard

Scientists who believe in evolution find themselves confronted with many paradoxes. One of those paradoxes is the existence of males and females within each kind. Logically, reproduction in evolution should be asexual; it is a very difficult problem to figure out why there should be a male and female in evolution. This conundrum was one of the top 18 science mysteries showcased in the Aug 18–25, 1997, issue of *U.S. News & World Report*, under the title of ‘Why should males exist?’¹ This is really a problem of their own making because they’ve chosen to believe in evolution. This is where Bible believing Christians have the evidence hands down in this area, since it says in Genesis 1:27 that God created man in His own image and “male and female He created them”. Another paradox of their own making is the faint young sun paradox.²

What is the faint young sun paradox?

It was discovered about 40 years ago that in the evolutionary origin of the solar system the sun would have been significantly less luminous with the earth receiving about 20 to 30% less sunlight than today.³ This difference is believed to have been caused by a higher ratio of hydrogen to helium in the sun’s core at that time. Even in the late Precambrian, solar luminosity is estimated to still be about 6% less than today.⁴ On this basis, the earth should have been totally glaciated from near its beginning, after it cooled down from its initially hot state within evolutionary scenarios. This is because a slight decrease in solar luminosity is enough to cause an ice age:

“Simple energy-balance climate models of the Budyko/Sellers type predict that a small (2–5%) decrease in solar output could result in a runaway glaciation on

the Earth. But solar fluxes 25–30% lower early in the Earth’s history apparently did not lead to this result.”⁵

So the early earth should have been easily glaciated from the poles to the equator.

This glaciation should have continued indefinitely to this day with no possible biological evolution, unless something drastic occurred to warm the earth:

“Without any change in atmospheric $p\text{CO}_2$ [CO_2 partial pressure], an increase in solar flux by ~27% above the present value would be needed to melt the equatorial ice (emphasis mine).”⁶

A 27% increase over the present solar luminosity seems like an impossible task.

So, the evolutionary scientists have a major paradox since most of the Precambrian, except for several global and near global ‘ice ages’,⁷ shows evidence of relatively warm temperatures:

“One of the major puzzles of the Earth’s history is that the global-average surface temperature has been fairly constant over geological time scales (within about 10 deg of the current value) even though solar luminosity was as much as 20–30% lower 4×10^9 years ago, according to established knowledge about stellar evolution.”⁸

A further problem is that evolutionary scientists need the earth relatively warm for the evolution of life, which would be impossible within their paradigm if the earth is totally frozen over. The issue is even more of a puzzle since some evolutionary scientists believe that the ocean water, which would heat the atmosphere, was extremely hot back then, around 55–85°C!⁹

Attempted resolution of the paradox

The faint young sun paradox has generated a lot of hypotheses that attempt to explain it. To counter the much lower solar luminosity and keep Earth temperatures relatively warm, researchers have suggested