redder over the duration of its emission. This reddening and the molecular absorption lines in its spectrum are both reminiscent of those of a red nova, thus implying that the source originated from a merging event. However, De and colleagues noted that the luminosity of ZTF SLRN-2020 was much lower than for other red novae, suggesting that an object smaller than a star was involved in the merger event.

The authors' high-spatial-resolution imaging revealed a faint progenitor source, consistent with a Sun-like star. From the source's brightness as a function of time and from observations before the outburst, they inferred that the mass of its merging companion was roughly that of Jupiter or Neptune. The story of the event, therefore, began to unfold: a giant planet had ventured too close to its parent star, interacting with it for a while before the outburst, which probably correlated with the engulfment of the planet by the star (Fig. 1). The authors' observation of dust and gas from before the outburst suggests that the interaction lasted 6–12 years.

Compared with during a merger of two stars, the outburst and amount of material ejected from ZTF SLRN-2020 were less impressive. Moreover, the star's radius did not change substantially while it was consuming its planet. This implies that the subsequent decay of the infrared emission represents the hydrodynamic and thermal readjustment of the star post-engulfment, which is consistent with the star having consumed a planet. The low luminosity of the event indicates that the amount of hydrogen released from the star was only a tiny proportion (about one-hundredth or one-thousandth) of its mass, resulting in a relatively constant brightness and a reddening of the source as the optical emission faded. And the mid-infrared emission during this decay is a plausible signature of a warm dust shell around the star as it slowly cooled down.

A combination of theoretical modelling and indirect observations has given rise to many predictions that planetary engulfment might be detectable[4–9]. But whether a planet will ultimately be consumed by its star depends on certain conditions. Modelling suggests that gravitational interactions between a planet and other objects in the system (such as other planets or a companion star) can slowly push a planet towards its host star. These companions have certain features that make them vulnerable to such extreme gravitational interactions, for example high inclination angles or proximity to other planets.

Tidal (gravitational) interactions between a star and a planet in close orbit around it can also slowly drive the planet to its demise. As a star exhausts its core hydrogen fuel, it expands and becomes a sub-giant. At this stage, it will start to engulf its nearby planets – in a few billion years, the Sun will undergo this process. Although exoplanets have been observed around various host stars that have a range of masses and are at different stages of evolution, there seems to be a deficit of old and sub-giant stars hosting planets in close orbits.

Other indirect signatures that indicate engulfment include stars that are spinning faster than usual and those that are enriched in various chemical elements. Future observations of ZTF SLRN-2020 can therefore test for these attributes and bolster De and colleagues' claim of the first direct detection of a star consuming its planet. Such tests will no doubt open up a vast body of investigations of similar events, as well as the mechanisms that drive them.

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Translation

An unexpected timer for cell division

Silke Hauf

A serendipitous observation has revealed that cells make several versions of a key protein needed for cell division. The ratio of these protein isoforms influences how long division can be delayed when errors arise. **See p.154**

Cells have a safety mechanism that delays cell division when chromosomes are not properly oriented for their correct distribution into daughter cells. When engaged, this safety mechanism inhibits the protein CDC20, whose activity is crucial for completing division, and this inhibition provides a window of opportunity for errors to be fixed. On page 154, Tsang and Cheeseman[1] report that cells produce several versions (isoforms) of CDC20 that differ in their susceptibility to inhibition. These isoforms arise when the messenger RNA encoding CDC20 undergoes translation — a process that typically produces only one version of a protein. Mutations found in cancer cells modify the isoform ratio to shorten the length of the delay, even if errors have not been fixed, which probably promotes malignancy.

"The authors could have discarded their observation as an oddity and moved on, but instead they dug deeper."

This finding has an interesting backstory that exemplifies the fact that scientific discoveries are not always intentional. Tsang and Cheeseman did not set out to uncover whether CDC20 isoforms exist. Rather, they intended to inactivate CDC20 by introducing a genetic mutation. They obtained the intended mutation, but the gene surprisingly remained functional. Tsang and Cheeseman could have discarded their observation as an oddity and moved on, but instead they dug deeper. This led them to discover that CDC20 protein production can start not just at one, but at several positions in the corresponding mRNA, which results in CDC20 isoforms that have distinct characteristics.

Normally, protein production during translation of an mRNA begins at the first AUG nucleotide sequence in the mRNA (termed the start codon). The macromolecular machine that synthesizes proteins, the ribosome, scans the mRNA from one end until it encounters this start codon. Occasionally, however, in a process called leaky scanning, a ribosome ignores this first start codon and instead continues to the next AUG sequence to initiate protein synthesis[2].

Tsang and Cheeseman found that CDC20

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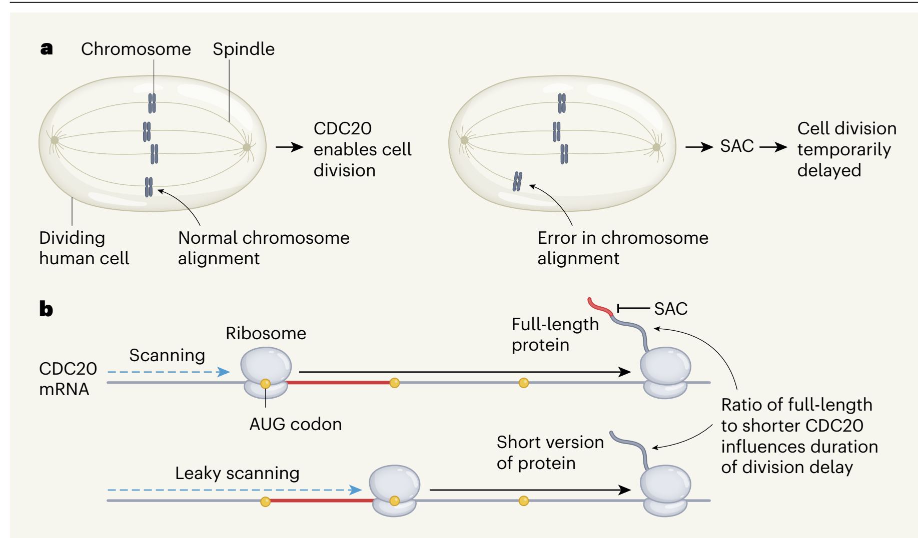

Figure 1 | Delay in cell division in response to errors is tuned by different versions of the CDC20 protein. **a**, During normal cell division, chromosomes align on a structure called the spindle and CDC20 promotes cell division. If misalignment occurs, this triggers a spindle assembly checkpoint (SAC), which pauses division. **b**, Tsang and Cheeseman[1] reveal that distinct versions of CDC20 are made, and that these differ in their responsiveness to the SAC. Production of CDC20 can start at one of several AUG codons (a sequence of A, U and G nucleotide bases) in the CDC20 messenger RNA. If the protein-production machinery of the ribosome scans along this mRNA and starts to generate a protein from the first AUG codon, then full-length CDC20 is made. This version of CDC20 is inhibited by the SAC. If the ribosome skips the first AUG codon because of what is called leaky scanning, this generates a short version of CDC20 that is not inhibited by the SAC. The ratio of isoforms acts as a timer to affect the delay in division when errors arise.

mRNA is susceptible to leaky scanning. Protein synthesis started at the first AUG sequence as well as at two subsequent sites. This produced proteins that were shortened at their front ends, but otherwise identical to the full-length CDC20 (Fig. 1). Thus, CDC20 joins a small number of proteins for which leaky scanning produces functionally distinct isoforms[2]. Although such a scenario is currently thought to be rare, more cases might remain to be uncovered[3].

Leaky scanning, far from being a faulty kind of translation, seems to be integral to the function of CDC20. The alternative start codons are found across multicellular animals (metazoans), and Tsang and Cheeseman provide evidence that these codons are used to initiate protein synthesis in both human and mouse cells. Leaky scanning is promoted because the nucleotide sequence surrounding the first start codon is not optimal for initiating protein synthesis. Making the sequence even less optimal leads to enhanced leaky scanning. By contrast, making it more optimal improves usage of the first start codon and suppresses leaky scanning. The authors examined databases of sequences found in cancer cells. These revealed mutations that favour the alternative start codons, indicating that the shorter isoforms might be beneficial for the proliferation of cancer cells.

CDC20 is essential for cell division and is the target of a safety mechanism, called the spindle assembly checkpoint (SAC), that delays division if necessary. The protein MAD2, which functions in the SAC pathway, binds to CDC20 to inhibit its activity. This binding requires a region of CDC20 that is present only in the full-length isoform[4,5]. The more of the full-length isoform that is present, the longer the possible length of the delay. During a prolonged delay, however, the longer isoform is less stable than the shorter ones, leading to a shift towards the shorter forms and, ultimately, completion of cell division even if errors persist.

Thus, the ratio of CDC20 isoforms acts as a timer. The isoform ratio at the beginning of cell division sets the timer, and division ensues when supplies of the long isoform run out.

By favouring shorter isoforms of CDC20, cancer cells presumably set the timer to their advantage, opting for shorter delay times, faster proliferation and a higher error rate – a hallmark of cancer cells that promotes continuous evolution of the genome[6]. Insidiously, this isoform misbalance can also make cancer cells resistant to drugs designed to delay cell division, as Tsang and Cheeseman report. Knowledge of the isoforms' existence is crucial for correctly working out the effects of CDC20 mutations in cancers, and possibly for adjusting therapy accordingly. Before Tsang and Cheeseman's work, many mutations that shorten the delay would have been falsely thought to inactivate CDC20 and block cell division.

Cancer cells can hijack the isoform timer, but the role of the isoforms in healthy cells remains unclear. The evolutionary conservation of the later start codons across metazoans suggests that they are important. The strength of the SAC is known to vary between cell types[7,8]. This latest study suggests that SAC strength might be modified by changes in the CDC20 isoform ratio. If so, how might healthy cells tweak the ratio?

Tsang and Cheeseman describe two cancer cell lines that differ in their isoform ratio despite having identical CDC20 sequences. This hints at the existence of regulatory mechanisms – yet to be identified – that alter the ratio, possibly through translation factors that accompany the ribosome[9]. If the isoform ratio is indeed altered in healthy cells, is this regulation specific to CDC20, or could other proteins with translationally produced isoforms be co-regulated with CDC20?

To understand the influence of the CDC20 isoforms, it will also be necessary to understand their interactions. The SAC inhibits CDC20 by capturing not just one, but two CDC20 molecules in a large complex[10,11]. Only one of the CDC20 molecules is bound by MAD2 directly, which requires the sequences that are unique to the full-length isoform. Hence, SAC strength might not scale linearly with the isoform ratio. Moreover, delay time is tuned by pathways other than the isoform timer[12,13]. To fully understand what sets delay time, the interplay of all of these influences will need to be understood.

These latest findings are surprising because CDC20 has been studied intensely for decades, yet the isoforms of CDC20 have been overlooked. They might have been observed but mistaken for degradation products from experimental manipulation, rather than recognized as biologically relevant versions. Credit must go to Tsang and Cheeseman for digging deeper.

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