pinned down⁸. It was realized that the initial chemical composition of the white dwarf that undergoes a nova was a crucial determinant of the amount of ⁷Li synthesized in the explosion; depending on the mass of its progenitor star, the white dwarf is made of either carbon and oxygen (CO novae) or oxygen and neon (ONe novae).

In CO novae, the carbon content makes the hydrogen fusion proceed faster than in ONe novae, owing to the operation of the CNO cycle of fusion reactions. Such faster evolution prevents the destruction of ³He and ⁷Be (Fig. 1), and so results in a larger production of ⁷Be and ⁷Li. The amount of ⁷Li produced by a CO nova corresponds to about 10⁻¹⁰ of the Sun's mass, but this value largely depends on the total ejected mass.

In their study, Tajitsu *et al.* report the detection of highly blue-shifted absorption lines of the singly ionized radioactive isotope of ⁷Be, ⁷Be II, in the near-ultraviolet spectra of the CO classical nova V339 Del, between 38 and 52 days after the explosion. The spectra were obtained using the Subaru Telescope of the

National Astronomical Observatory of Japan, which delivers high spectral resolution (about 0.0052 nanometres) and so allowed the authors to tease apart the lines of ⁷Be II from those of ⁹Be II, both of which occur at wavelengths around 312–313 nm.

The finding lends support to the hypothesis that the Cameron–Fowler ⁷Be transport mechanism is at work in novae, as predicted theoretically 40 years ago⁶. The observations indicate that nova V339 Del produced at least as much ⁷Be and ⁷Li as predicted by theory.

The implications of these results are manifold. First, they mean that novae may play a larger part in lithium production than previously thought. Second, they may increase the probability of detecting the 478-keV γ -ray photons emitted in the ⁷Be-to-⁷Li reaction⁹, which have remained elusive despite observational efforts made by γ -ray missions^{10,11}. Third, and perhaps most importantly, they suggest that measurements of ⁷Be lines in the near-ultraviolet range and within the lifetime of the element may well provide a way

of estimating the contribution of novae to the lithium abundance in the Milky Way and in the Universe in its entirety. ■

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1. Tajitsu, A., Sadakane, K., Naito, H., Arai, A. & Aoki, W. *Nature* **518**, 381–384 (2015).
2. Burbidge, E. M., Burbidge, G. R., Fowler, W. A. & Hoyle, F. *Rev. Mod. Phys.* **29**, 547–650 (1957).
3. Romano, D., Matteucci, F., Molaro, P. & Bonifacio, P. *Astron. Astrophys.* **352**, 117–128 (1999).
4. Cameron, A. G. W. *Astrophys. J.* **121**, 144–160 (1955).
5. Cameron, A. G. W. & Fowler, W. A. *Astrophys. J.* **164**, 111–114 (1971).
6. Arnould, M. & Nørgaard, H. *Astron. Astrophys.* **42**, 55–70 (1975).
7. Starrfield, S., Truran, J. W., Sparks, W. M. & Arnould, M. *Astrophys. J.* **222**, 600–603 (1978).
8. Hernanz, M., José, J., Coc, A. & Isern, J. *Astrophys. J.* **465**, L27–L30 (1996).
9. Clayton, D. D. *Astrophys. J.* **244**, L97–L98 (1981).
10. Harris, M. J., Leising, M. D. & Share, G. H. *Astrophys. J.* **375**, 216–220 (1991).
11. Harris, M. J. *et al. Astrophys. J.* **563**, 950–957 (2001).

EVOLUTION

Finches sequenced

Darwin's finches played a key part in the formulation of his theory of evolution by natural selection. They have since become an iconic model for adaptive radiation — 14 species evolved from a common ancestor to occupy different niches on the Galapagos Islands, with 1 species living on Cocos Island. On page 371 of this issue, Lamichhaney *et al.* present the genome sequences of 120 individuals from among all 15 species and 2 close relatives (S. Lamichhaney *et al. Nature* **518**, 371–375; 2015).

The work marks the first extensive genomic characterization of these birds. Unexpectedly, the analysis reveals that breeding between species has continued throughout their adaptation, contributing to their evolution.

The morphology of Darwin's finches has been extensively studied, with a particular focus on the diverse shapes of their beaks (pictured: *Geospiza magnirostris*). The authors use their rich data set to probe the genetic basis of beak shape, and identify six genomic regions that have a role in craniofacial morphology.

One region, which encodes the protein ALX1, is a major player in the rapid beak-shape evolution seen both across Darwin's finches and within one species, the medium ground finch (*Geospiza fortis*). The function of ALX1 is evolutionarily conserved — mutations in this gene also affect craniofacial development in humans and zebrafish. **Magdalena Skipper**

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