ECOLOGY

Poole resources

M. LANE/ALAMY

The Manila clam has been on the move for decades. It is native to the western Pacific, but following introduction to other parts of the Pacific, and then to southern Europe, it was brought to Britain in the 1980s as a source of seafood. At one site in Britain, Poole Harbour in Dorset, the clam (*Tapes philippinarum*) has now become naturalized.

This could be worrying: when colonizing fresh regions, invasive species may devastate components of the existing flora and fauna. For the Eurasian oystercatcher, however, the advent of the clam at Poole is good news, as Richard Caldow and colleagues report (R. G. W. Caldow *et al. Proc. R. Soc. B* doi: 10.1098/rspb.2007.0072). This species of bird, *Haematopus ostralegus ostralegus* (pictured), overwinters in Poole Harbour. From their observations of its feeding habits, and from modelling studies, the authors conclude that the oystercatchers have benefited considerably from the extra source of food.

Their observations show that a large proportion of the overwintering oystercatcher population of around 1,200 feeds on the clams, a habit not previously recorded, and that clam meat constitutes a notable part of the birds' diet.

The simulations were carried out with an 'individuals-based' model of shorebird foraging, with the aim of providing a population-level estimate of the effect of the additional food source. The predicted result is a significant reduction in the mortality of the birds, which face the prospect of starvation in the period between September and March.

As yet, there is no evidence that the Manila clam has affected other species of bivalve at Poole, although it occurs at low densities there compared with populations of the species elsewhere. But the clams' occupation of this northern site was probably made possible by locally warm sea temperatures, and Caldow *et al.* raise the inevitable question of what consequences a continued warming might have. They envisage a further spread north. That process might exacerbate the retreat of the cold-water species that currently constitute food sources for shorebirds. But if, like the Eurasian oystercatcher, other birds develop a taste for the clam, the results might even be beneficial — at least from the avian point of view.

Tim Lincoln

of the other half of the fusion protein. However, the results provide clear evidence that two SecY complexes are necessary to form an active channel. Moreover, because the inactivating mutation was previously shown to affect the binding of SecA to the channel[9], such complementary action could be explained only if SecA binds to one SecY copy and the protein substrate crosses the membrane through the other. Osborne and Rapoport confirm such a structural asymmetry. In the tandem construct, one SecY copy is cross-linked with the translocating protein substrate, and the other copy is cross-linked near the ATPase motor domain of SecA.

On the basis of these findings, Osborne and Rapoport[1] provide a refined model of SecA-mediated protein translocation (Fig. 1). One SecY complex serves as the protein-conducting channel, whereas its non-translocating counterpart forms a static docking site for the ATPase motor domain of SecA. This model is consistent with results[10] showing that a single SecY complex is sufficient to bind to SecA. Taking into consideration the dimensions of the SecY dimer and SecA, the authors propose that the deep groove observed in the crystal structure of SecA (ref. 11), and postulated to be involved in binding to signal sequences and polypeptide chains, would be located just below the active copy of SecY in the channel. This would be an optimal position for pushing the protein substrate through.

How exactly SecA, which also forms a dimer in solution, binds to the Sec channel, and how it converts chemical energy into mechanical work, remains to be discovered. But the present study[1] is a milestone on the way to understanding the intricate organization of the translocon. It reveals once again the unique characteristics of this remarkable machine. ■

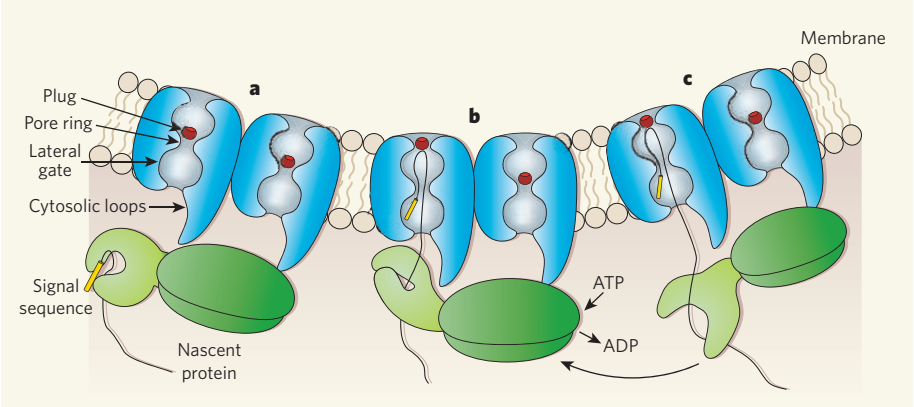

Figure 1 | The protein translocation process as proposed by Osborne and Rapoport[1]. This simplified representation shows some of the structural elements of the dimeric SecY channel (blue) and the SecA ATPase (green), from a cut-away view of the membrane. **a,** At the beginning of the reaction, the conduits of the SecY dimer are sealed by the constricted pore ring and the plug domain (red). The protein substrate and its signal sequence (yellow) are engaged with the protein-binding domain of SecA (light green), whereas its ATPase domain (dark green) is anchored to the cytosolic loops of one SecY copy. **b,** On binding and hydrolysis of ATP, SecA pushes the signal sequence as a hairpin loop into the neighbouring SecY copy. The insertion of the hairpin causes the plug to move away from the centre of the conduit and fixes the pore in the open state. **c,** The ATPase domain of SecA remains anchored to one copy of SecY, and its protein-binding domain grasps another, downstream, segment of the polypeptide chain. The ATP-dependent cycle is repeated until the polypeptide is entirely transferred across the membrane.

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