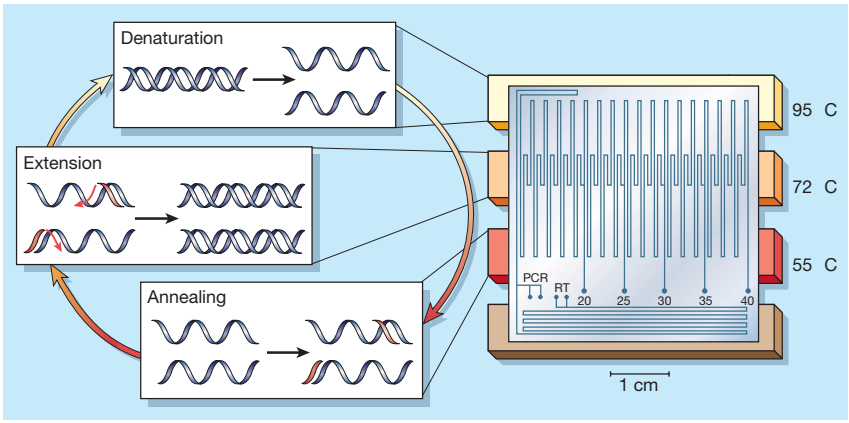

Figure 1 **DNA and chips. Obeid *et al.*[5] have built a microscale device in which DNA can be amplified quickly using the polymerase chain reaction (PCR). When a sample is added at either of the PCR inputs it flows over heating blocks whose temperatures are set to induce the three steps of PCR consecutively: denaturation, or unwinding of the DNA strands; annealing, in which primers are attached to the separated strands; and finally extension of the primers into complete DNA strands, to produce two copies of the original DNA strand. Samples can be extracted from the chip after between 20 and 40 PCR cycles, at the points indicated. A further advantage of this design is the channel for reverse transcription (RT), in which RNA samples can be transcribed into DNA before entering the PCR region of the chip for amplification.**

network defining four zones, one for reverse transcription and three for PCR (Fig. 1). Zone temperatures are controlled by simply placing the entire chip over four temperature-controlled heating blocks. Five outlets for product collection are located along the channel, so the product can be analysed after 20, 25, 30, 35 and 40 PCR cycles. Using their device, the authors demonstrate efficient amplification of DNA after 20 cycles in times as short as 5 minutes. Furthermore, by periodically injecting small samples (2 μl) into the system, separated by water and air plugs, simultaneous amplification of multiple samples can be performed in continuous flow without cross-contamination.

The benefit of continuous-flow amplification is further demonstrated by this device's ability to perform reverse transcription of RNA into DNA before PCR amplification — a process widely used for the quantification of messenger RNA levels. Reverse transcription is performed within a serpentine microchannel that, downstream, intersects the PCR channel, and subsequently proceeds through the heating zones. Integration of the two processes within a monolithic device is often problematic as reverse-transcription components at high concentration can interfere with the PCR. The authors tackle this problem by reducing the flow rate at which reverse transcription is performed, so that, at the intersection of the reverse-transcription and PCR channels, the reverse-transcription mixture constitutes about 10% of the PCR volume. With this approach, high-throughput reverse-transcription–PCR (of 0.7-μl volumes) is achieved in short times and without nonspecific amplification.

The work described by Obeid and colleagues demonstrates the true integration of biologically relevant processes within a monolithic device. Importantly, continuous-flow operation offers a direct route to automated sample introduction, mixing and reaction, and thus the possibility of high-throughput sequence analysis in many practical applications. ■

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Climate change

The earlier bird

Since 1909, researchers have been catching and marking migrating birds that stop over on the island of Helgoland in the southeastern North Sea. These birds breed in Scandinavia and spend the winter in either continental Europe (short-distance migrants) or Africa (long-distance migrants). The methods of trapping — one type of apparatus is shown in the photograph opposite — have not changed since 1960. Moreover, the data cover around two dozen species, and describe the mean time of migration for all trapped individuals, not just extremes in the form of first arrivals. All of this makes the Helgoland data sets some of the best available with which to study the timing of bird migration.

Ommo and Kathrin Hüppop have now analysed these data sets, with remarkable results (*Proc. R. Soc. Lond. B* **270,** 233–240; 2003). They find that all 23 migratory bird species for which sufficient data are available pass by Helgoland on their way to Scandinavia earlier now — by two to twelve days — than 40 years ago. There is a clear division between short-distance migrants, whose mean time of passing correlates well with local temperatures, and long-distance migrants, for which increases in the NAO index (a measure of the air pressure over the North Atlantic Ocean) give a much better explanation for the earlier time of passage.

Whether a migrating bird actually lands on a small island while passing over it depends on many factors. Sudden changes in weather play a large part. So it is important to analyse large data sets to disentangle general patterns from such isolated examples. The changes in the timing of migration are apparently strong enough to become evident.

These changes, in particular the earlier passage of the long-distance migrants, raise questions about the control of spring migration. There are three main hypotheses that might explain their earlier passage. First, the moment of leaving Africa has not changed, but refuelling in continental Europe proceeds more quickly, because more food — in the form of insects — is available earlier. (Increases in the NAO index generally indicate favourable spring conditions in Europe.) Second, if the weather in Africa is also correlated with the NAO index, then the birds might leave earlier because the seasons there also change earlier. Third, the weather in

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Africa has not changed, but natural selection has altered the 'trigger values' for starting migration. Each hypothesis, if true, would mark an exciting break with existing knowledge, and I eagerly await further results on changes in spring migration. **Arie J. van Noordwijk**

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