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Critical Population Density Triggers Rapid Formation of Vast Oceanic Fish Shoals

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Similarities in the behavior of diverse animal species that form large groups have motivated attempts to establish general principles governing animal group behavior. It has been difficult, however, to make quantitative measurements of the temporal and spatial behavior of extensive animal groups in the wild, such as bird flocks, fish shoals, and locust swarms. By quantifying the formation processes of vast oceanic fish shoals during spawning, we show that (i) a rapid transition from disordered to highly synchronized behavior occurs as population density reaches a critical value; (ii) organized group migration occurs after this transition; and (iii) small sets of leaders significantly influence the actions of much larger groups. Each of these findings confirms general theoretical predictions believed to apply in nature irrespective of animal species.

Many species of oceanic fish band together in large shoals (1, 2) that can span tens of kilometers and involve hundreds of millions of individuals. Grouping leads to survival advantages through enhanced spawning, predator avoidance, and feeding mechanisms (3–6). Little information has been available about the formation process and behavior of large oceanic fish shoals. Traditional methods rely on local measurements from slow-moving research vessels that enable sampling of only a small fraction of a shoal during an entire survey, typically by vertical profiling, and cannot distinguish between temporal and spatial changes (7–9). Here, we describe fundamental temporal and spatial processes by which vast oceanic shoals form by observation of entire shoals in space and time over their full horizontal extent and relate these processes to likely governing mechanisms. We do this using Ocean Acoustic Waveguide Remote Sensing (OAWRS) (10), which enables instantaneous imaging and continuous monitoring of oceanic fish populations over tens of thousands of square kilometers.

We studied *Clupea harengus* (Atlantic herring), because they are known to regularly mass in large shoals for spawning at specific times and locations like other clupeid fish. Clupeids are keystone species in many of the world's major marine ecosystems, from the coastal upwelling regions of South America and Africa to the temperate areas of the Nordic Sea, Baltic Sea, and Gulf of Maine (11). They provide trophic links between plankton, such as krill, and larger predators, such as humans, birds, whales, dolphins, seals, sharks, cod, pollock, and haddock (12). Georges Bank is one of the primary spawning grounds for herring in the Gulf of Maine, which was

once one of the world's most productive fisheries before its collapse in the 1970s (8, 13). Herring migrate to Georges Bank to spawn in early autumn, typically September and October, from offshore regions of the Gulf of Maine and beyond (8, 14).

We used OAWRS to monitor herring behavior continuously on Georges Bank during the autumn 2006 spawning season, in conjunction with traditional conventional fish-finding sonar (CFFS) (9) and trawl (8) line transects. The OAWRS system instantaneously imaged areas spanning 100 km in diameter every 75 s and so enabled continuous time-space monitoring of shoaling behavior over an ecosystem scale. We focused our experiment on regions where herring shoals were most likely to form. We determined these regions by analysis of a decade of National Marine Fisheries Services (NMFS) annual surveys made with conventional line-transect methods. These historic data showed that the herring traditionally first mass in dense layers near the seafloor along the northern flank of Georges Bank in deeper water (150 to 200 m) before spawning just to the south in shallow waters on the bank (<50 m).

We found shoal formation to depend on initial conditions and to ensue rapidly when these conditions were satisfied. First, we found that the preexisting population density of diffusely scattered individuals had to reach a critical threshold of 0.2 fish per square meter (fish/m²). Given this, we found shoal formation to consistently commence in a highly organized fashion near sunset, apparently triggered by reduction in light level. The process depended on orderly and coherent horizontal convergences of leading individuals to produce denser and thicker vertical layers at a few discrete horizontal locations. This process occurred within favored bathymetric contours (Fig. 1). From preexisting diffuse background levels consistent with scattered individuals displaying no coherent interaction (Fig. 1A), small catalyzing clusters of much higher areal population density emerge in OAWRS imagery within the favored bathymetric contours (160 to 190 m) just before sunset (Fig. 1B), introducing bursts of coherent horizontal structure. Simultaneous vertical profiles from CFFS line transects show that, before the lead-

ing clusters form, the fish are widely distributed in a diffuse low-density layer within 5 m of the seafloor (Fig. 2A). The leading clusters (100-m horizontal scale) form as thick (10 to 30 m in the vertical) and dense groups within 20 to 40 m of the seafloor (Fig. 2A), when the fish rise slightly and converge in the horizontal as seen in both OAWRS (Fig. 1, A and B) and CFFS data (Fig. 2A). Formation of these denser clusters requires horizontal convergence by conservation of mass from the original thin, low-density layers.

The emergence of leading clusters of high population density set off chain reactions that caused rapid growth into vast shoals. We found the growth to propagate horizontally outward as convergence waves emanating from the cluster initiation points, which appeared to act as sources of the wave action. The waves propagated over tens of kilometers in tens of minutes, as can be seen for example in Fig. 1, A to F, and Fig. 3. The 3.0 to 6.0 m/s propagation speed of these waves (Fig. 3A) is an order of magnitude faster than the typical 0.2 m/s speed at which herring swim (15) and so is likely the apparent speed (10) of sequences of local synchronous convergence actions and reactions (16, 17) by members of the shoal. Such local actions define a propagating compressional wave in a medium of variable density (18). Our observations provide experimental evidence for the existence of compressional waves in vast fish shoals, which have been predicted in physical theories (19). We found these shoal-forming waves to be highly directional and to propagate most rapidly along the direction of favored bathymetric contours (Fig. 1, A to F). Before the waves appeared, areal population density slowly increased at a rate of 0.06 to 0.1 fish/m² per hour (Fig. 3, B and C). As soon as the critical density of 0.2 fish/m² was reached (Fig. 3, B and C), coherent shoal-forming waves appeared (Fig. 3A), and the population density rapidly increased at a rate of roughly 5 fish/m² per hour (Fig. 3, B and C).

After formation, we observed growth in shoal width and population as light levels remained low in the evening. Growth normal to the favored bathymetric contours appeared to be from movement of surrounding diffusely scattered fish populations to the shoal, which acted as an attractor (Fig. 1, G to L). These vast shoals, sometimes extending continuously for 40 km (Fig. 1I), would remain stable throughout the evening and dissipate as light levels increased with sunrise. When viewed vertically with CFFS transects, the shoals evolved from small, isolated, catalyzing clusters (Fig. 2A) to extensive, dense layers within 20 to 40 m of the sea floor, but typically disconnected from it by a few meters (Fig. 2B). The layer growth required horizontal convergence by conservation of fish mass.

Once vast shoals formed, they migrated at speeds consistent with the synchronous swimming of hundreds of millions of individual fish, in accord with the predictions of general behavioral models. The migrations, however, were not in a random direction, as in some theoretical models (19–21), but toward southern spawning grounds on Georges Bank, apparently for synchronized reproductive activities. Such a migration of the 3 October shoal's southern edge, from near the alpha-to-omega CFFS

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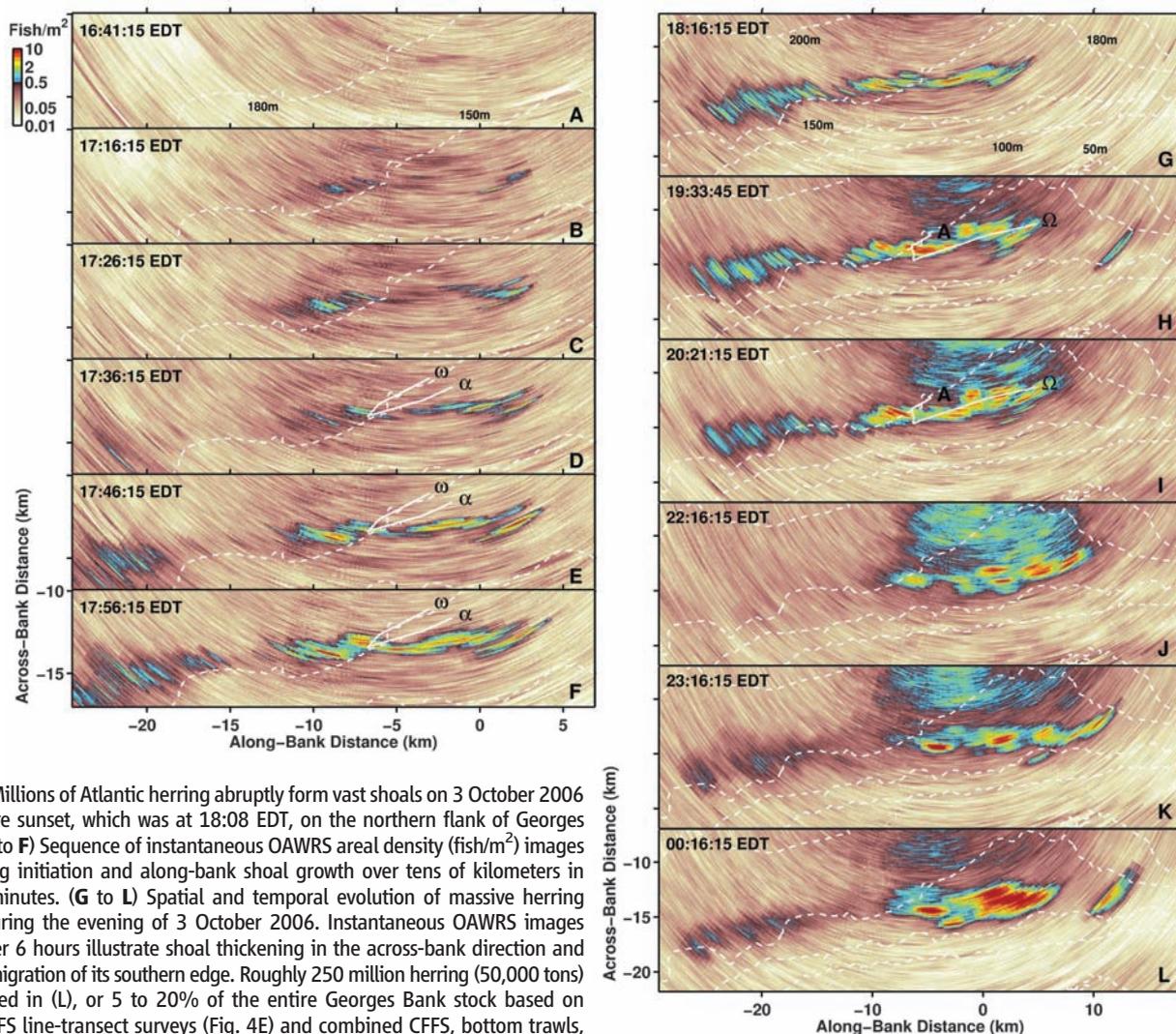
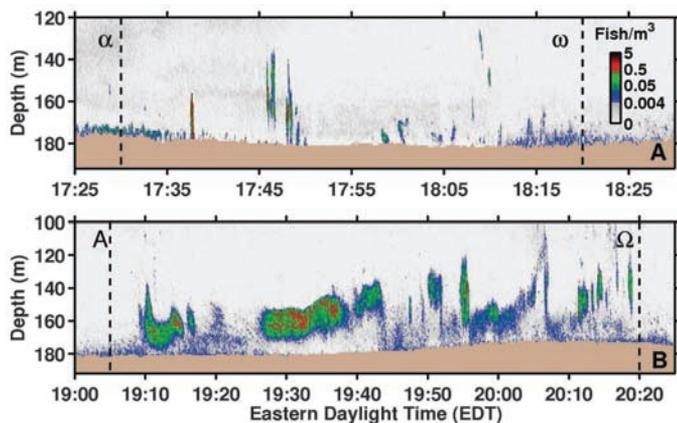


Fig. 1. Millions of Atlantic herring abruptly form vast shoals on 3 October 2006 just before sunset, which was at 18:08 EDT, on the northern flank of Georges Bank. (A to F) Sequence of instantaneous OAWRS areal density (fish/m²) images illustrating initiation and along-bank shoal growth over tens of kilometers in tens of minutes. (G to L) Spatial and temporal evolution of massive herring shoals during the evening of 3 October 2006. Instantaneous OAWRS images taken over 6 hours illustrate shoal thickening in the across-bank direction and gradual migration of its southern edge. Roughly 250 million herring (50,000 tons) are imaged in (L), or 5 to 20% of the entire Georges Bank stock based on NMFS CFFS line-transect surveys (Fig. 4E) and combined CFFS, bottom trawls, and catch landings (12). Our simultaneous capture trawl surveys show that over 99% of the fish imaged by OAWRS within the dense shoals are Atlantic herring, combined with a small fraction of Acadian redfish (*Sebastes fasciatus*) and haddock (*Melanogrammus aeglefinus*). The moored OAWRS source is the coordinate origin in all OAWRS images, at 42.2089°N, 67.6892°W on 3 October. The positive vertical axis in all OAWRS images points 16° counter-clockwise of true north. The dashed lines indicate water depth contours.

Fig. 2. Time-depth profile of fish volumetric density (fish/m³) measured by CFFS along: (A) the V-shaped line transect shown in Fig. 1, D to F, and (B) the J-shaped line transect through the shoal shown in Fig. 1, H and I. Black dashed vertical lines correspond to transect start (alpha) and end (omega) points.



transect of Fig. 1H to the 150-m contour 2 to 4 km to the south in Fig. 1L, is evident in the most populous region and quantified in Fig. 3A. The migration is slow, roughly 0.2 m/s (Fig. 3A), which is consistent with the average swimming speed of

herring in a school (15). Another example of a southern migration appears in Fig. 4 for 29 September. Shoals first form as usual by sunset (Fig. 4, A and B). Massive portions of their southern edges then migrate upslope from depths greater than 50 m

(Fig. 4B) to spawning grounds 2 to 3 km to the south where depths are less than 50 m (Fig. 4D). The migration speed is similar to that observed on 3 October, following that expected for the material displacement of millions of swimming herring. Dense evening shoals sometimes developed a diffuse northern component (Fig. 1, H to L), which could indicate a north-south migration route for spawning herring from offshore regions of the Gulf of Maine to Georges Bank. The southern edge of the shoals, in contrast, was typically sharp (Fig. 1, G to L), following the general bathymetric contour of the spawning grounds of Georges Bank, indicating the leading edge of a synchronous mass migration.

We found the overall process of rapid shoal formation, triggered by attainment of a critical density of 0.2 fish/m² near sunset, and subsequent migration toward spawning grounds to define a regular diurnal behavioral pattern that was consistently observed (22) during our roughly 1-week measurement period as shown in Figs. 1 to 4 and Figs. S1 to S4. The

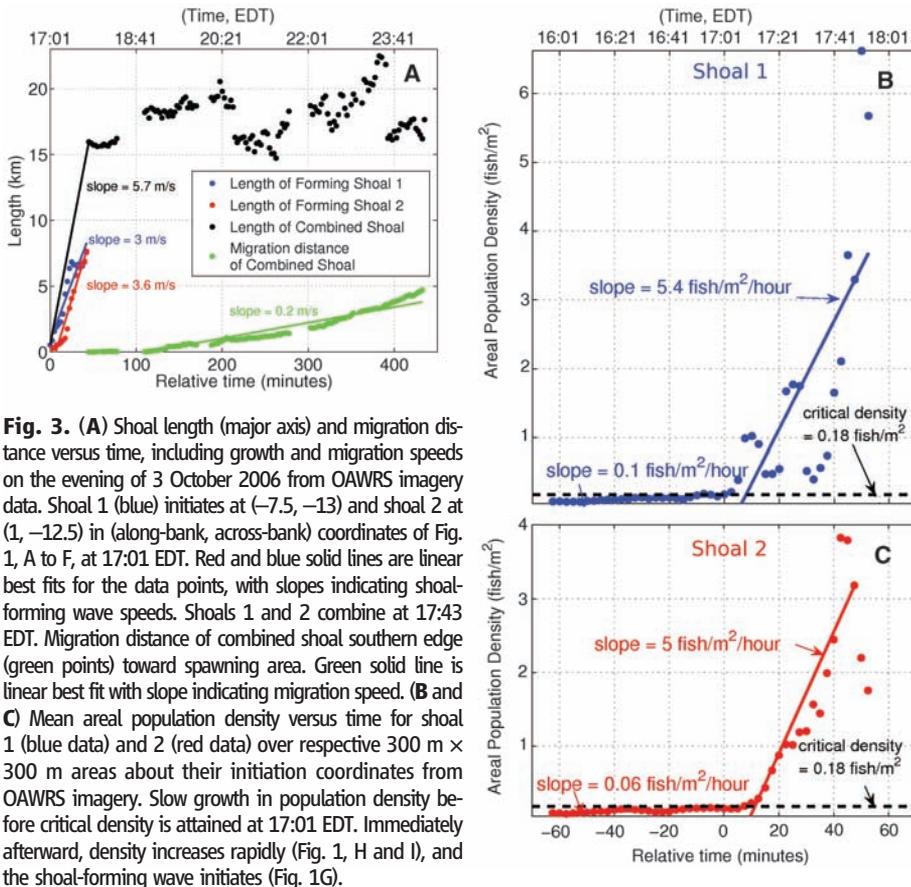
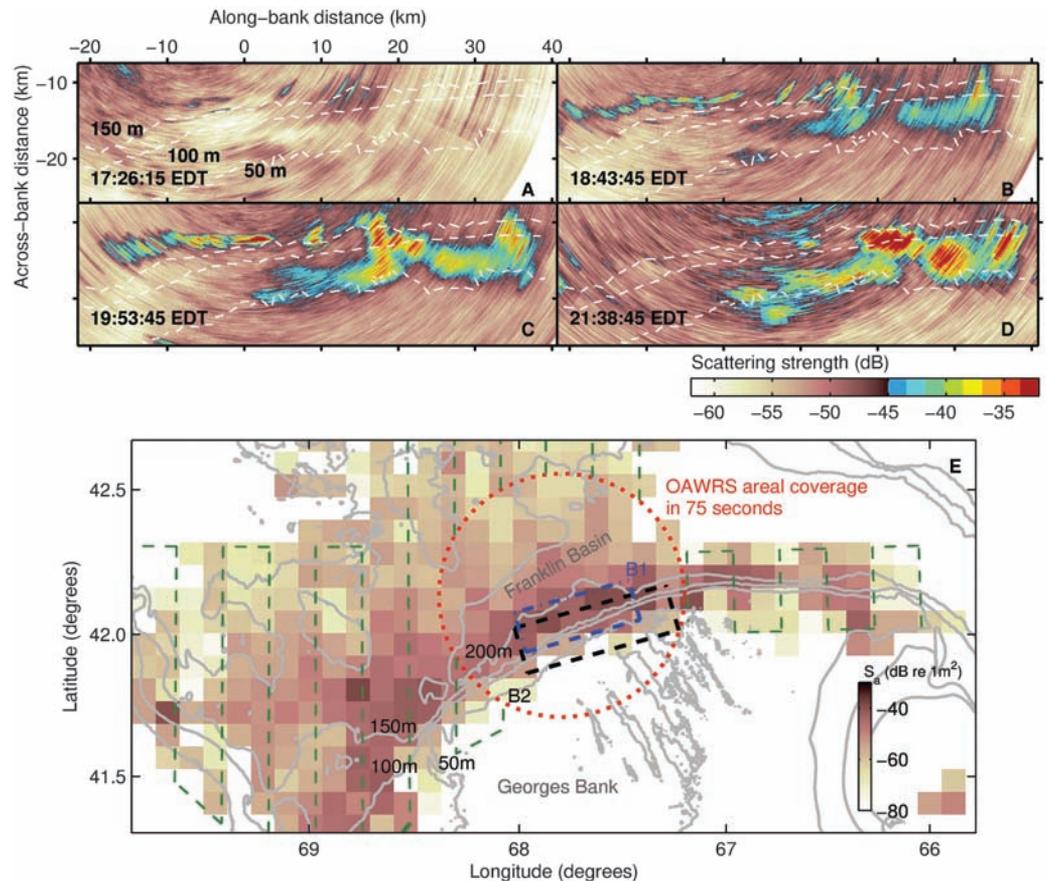


Fig. 4. (A to D) Sequence of OAWRS scattering strength (32) images illustrates formation, growth, and subsequent southern migration of herring shoals toward the Georges Bank spawning grounds on the evening of 29 September 2006. Sunset was at 18:15 EDT. Same region as Fig. 1, G to L. **(E)** Backscattering strength s_a (33) at 5 by 5 nautical miles (1 nmi = 1852 m) grid obtained by averaging CFFS line-transect data from 1999 through 2005 NMFS Annual Fall Herring Surveys (34). Boxes B1 and B2 are regions shown in Fig. 1, G to L, and Fig. 4, A to D, respectively. Regions of maximum herring concentration are consistent between OAWRS 2006 imagery (Fig. 1) and NMFS 6-year average (Fig. 4E). Red circle indicates OAWRS areal coverage in 75 s. Green dashed line indicates the line transect of a typical 2-week NMFS survey, not shown within red circle.



evidence suggests the primary biological function of the shoals is a prelude to synchronized spawning. Close proximity of individuals can induce synchronous reproductive development through visual and olfactory stimulus (17). Synchronous development is often critical because each female must typically produce a large number of eggs within very tight time constraints to enable group spawning (17, 23). Shoal formation at greater depths allows these activities to proceed with reduced risk of attack from predators (24), such as pilot whales, porpoise, and tuna, that prefer to hunt in the shallower spawning grounds (4, 25). Evening formation allows matching and subsequent migration to spawning grounds to occur under cover of darkness, with more safety from predator attack. The shoaling behavior we observed is evidently unrelated to diurnal feeding (4) activities, because trawl samples obtained during our survey show 99% of the herring have empty stomachs and have not yet spawned. This is consistent with historic observations showing that herring do not feed during the spawning period (26). More generally, our observations during the spawning period show the formation processes of large oceanic fish shoals (i) require initial conditions on population density and external stimuli, such as light level; (ii) follow the actions of a small number of leaders; (iii) rely upon extremely rapid and efficient time-space convergence events that propagate as coherent waves over great distances by chain reaction; and (iv) involve extensive horizontal structures that evolve in a highly organized and predictable

manner. The rapidity with which these shoal-forming waves spread once the initial conditions are satisfied is indicative of the advantage the group has over the isolated individual in transferring information over great distances. Our observations also provide ecosystem-scale evidence that a critical population density triggers rapid transition from disordered to highly synchronized behavior, and small groups of leaders often play crucial roles in affecting the actions of much larger groups, as has recently been predicted in general theoretical investigations (19, 21, 27–29), simulations, and laboratory experiments (26, 27) about animal group behavior (20, 30, 31). These findings provide information essential to the conservation of marine ecosystems that vast oceanic fish shoals inhabit.

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Supporting Online Material

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Materials and methods

Figs. S1 to S6

References

Movie S1

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Genetic Contribution to Variation in Cognitive Function: An fMRI Study in Twins

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Little is known about the genetic contribution to individual differences in neural networks subserving cognition function. In this functional magnetic resonance imaging (fMRI) twin study, we found a significant genetic influence on brain activation in neural networks supporting digit working memory tasks. Participants activating frontal-parietal networks responded faster than individuals relying more on language-related brain networks. There were genetic influences on brain activation in language-relevant brain circuits that were atypical for numerical working memory tasks as such. This suggests that differences in cognition might be related to brain activation patterns that differ qualitatively among individuals.

The direct link between genes, brain, and behavior can be difficult to establish (1). Structural and functional investigations in the human and mouse brain suggest that some genes are expressed in highly specific brain regions, whereas other genes have more global effects (1–4). The

total heritability of individual differences can be examined with twin studies (5–8). Functional magnetic resonance imaging (fMRI) studies investigating specific brain regions assumed to subservise some cognitive function did not demonstrate high heritability of brain activity (9–14). Genetic influences on brain activation in areas that typically subservise a cognitive function might be modest because these areas will be activated similarly among humans. By contrast, brain regions activated in some individuals only might be better candidates for genetic analysis. Thus, genetic effects should be tested cortex-wide.

Structural and functional brain investigations suggest that brain areas that are similarly activated among humans may be embedded in larger brain networks that vary among individuals (1, 4), possibly causing individual differences in cognition. An attractive candidate for the study of genetic influ-

ences on brain networks is working memory for digits under arithmetic distraction. Heritability estimates for behavioral measures in this task are high (15), and stable individual differences in the spatial organization of function-carrying areas were shown (16). A distractor task causes an interruption of verbal rehearsal, leading to rapid forgetting (17). The decay model of working memory (18, 19) states that numbers can be retained without explicit verbal rehearsal, but it does not specify neural correlates of these memory processes. The triple-code model (20) claims that number processing and arithmetic require both magnitude and language-related number representations in inferior parietal cortex, angular gyrus, and perisylvian cortex. Individuals holding numbers in memory in a language-related or magnitude code suffer from code interference when executing arithmetic tasks. Employing early motor coding routes protects memory traces from distraction (21), which corresponds to the importance of finger representations for number processing also in adulthood (22).

For genetic fMRI studies, appropriate brain alignment, sufficient individual differences, reliability, and statistical power are of core importance (6, 23–25). We used an extended twin design consisting of male monozygotic (MZ) twins with an additional nontwin brother, where every brother is related to both twins. We examined reaction times (RT) as a measure of proficiency and blood oxygen level-dependent (BOLD) response as a measure of relative brain (de)activation (26) during two identical scanning sessions in all participants. These two observations of the phenotypes of interest were entered into a genetic structural equation model (SEM) that estimates additive genetic effects corrected for measurement error (23). Heritability h^2 was expressed as the percentage of reliable variance accounted for

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