PERSPECTIVES: COGNITION

# An Innate Basis for Language?

Dorothy V. M. Bishop

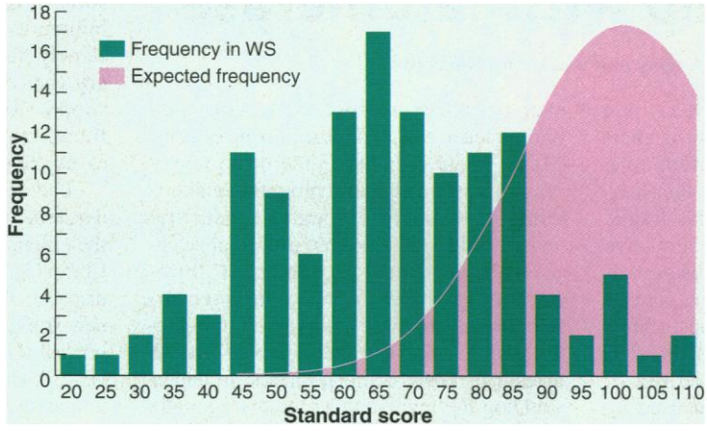
"It is an established opinion amongst some men, that there are in the understanding certain innate principles; some primary notions, characters, as it were stamped upon the mind of man: which the soul receives in its very first being, and brings into the world with it. It would be sufficient to convince unprejudiced readers of the falseness of this supposition, if I should only show...how men... may attain to all the knowledge they have, without the help of any innate impressions; and may arrive at certainty, without any such original notions or principles...." Some 300 years after the British philosopher John Locke wrote these words in his *Essay Concerning Human Understanding*, a report by Paterson *et al.* on page 2355 of this issue (*1*) emphasizes that there is still a lively debate about how much "innate" linguistic knowledge an infant is born with.

Enhanced online at www.sciencemag.org/cgi/content/full/286/5448/2283

We know from patients with neurological impairments and from neuroimaging studies that the adult brain is a modular system, that is, different regions perform specific functions. But how does the brain get that way? One view is that distinct brain regions govern particular functions—such as, the processing of language or numbers—from the outset, a notion in keeping with the idea of innate principles. An alternative view is that the embryonic brain is not specialized and that the emergence of distinct brain regions governing particular functions becomes apparent only during postnatal development. Locke's antipathy to "innate principles" appears vindicated by research showing that modularity (distinct brain regions governing particular functions) is a property that emerges during postnatal development and is dependent on both biological maturation and interactions with the environment.

There is, however, a persistent fly buzzing around in the ointment of the emergent modularity theory. Williams syndrome (WS) is a genetic disorder in which complex language skills can develop despite general mental deficits. This syndrome differs from specific language impairment (SLI) in which language acquisition is selectively impaired but development is otherwise normal. To explain this pattern of dissociation, it has been argued that the brain must have an innate language module that is selectively impaired in SLI but is spared in WS.

Paterson and colleagues (*1*) present data that question this interpretation. They argue that cognitive profiles of very young children with WS look different from those reported in older children and adults with the disorder. Their study breaks new ground by applying state-of-the-art methods that use the preferential looking test (in which the tester infers, for example, whether infants understand a word by measuring the time they spend looking at a named object compared to that for a distracting object) to measure cognitive abilities. On a vocabulary recognition test, toddlers with WS did worse than age-matched controls, and no better than toddlers with Down syndrome, who have a similar IQ. However, on a test of number skills, toddlers with WS did well, outperforming those with Down syndrome. It is well established that adult patients with WS do better (relatively speaking) on language tasks than on those involving numbers. So, the message from the new work seems simple: Just because a person with congenital brain impairment shows an uneven intellectual profile, one cannot assume that this profile has been present from birth.




**Vocabulary proficiency in Williams syndrome (WS).** Distribution of standard scores on the PPVT-R (a vocabulary test in which the child has to point to a named picture from an array of four). The vocabulary test was administered to a sample of 127 individuals with WS aged from 4 to 52 years. The bar graph shows the frequency of individuals with WS achieving a particular standard score. The expected distribution in the general population is superimposed as a normal curve. Paterson *et al.* (*1*) suggest that the poor verbal proficiency they found in infants with WS would improve with age, but these data show that only a minority of older individuals with WS have age-appropriate vocabulary. Furthermore, the correlation between age and PPVT-R scaled score was not significant in this sample. [Redrawn from (*5*)]

These investigators provide good evidence that it is an oversimplification to characterize the WS phenotype as "language good, number poor" based on observations of adults with WS. But, should we conclude that the balance of cognitive abilities undergoes a radical shift during postnatal development? Williams syndrome is often cited as a condition in which language is spared in the face of other mental deficits, but this sparing is relative rather than absolute. Language is reliably better than visuospatial construction, but both are typically well below average. Cases with normal vocabulary exist, but they are not typical (see the figure). In a study in which parents were asked to check off on a list those words that they heard their child say (*2*), 2-year-olds with WS were reported to have larger vocabularies than those with Down syndrome. However, with the exception of two children with WS whose vocabularies were in the 75th percentile for age, early language acquisition in both groups was much slower than normal. As for number skills, Klein and Mervis (*3*) found no difference between children with WS and those with Down syndrome on quantitative reasoning, whereas studies assessing mental arithmetic revealed that children with WS had very low scores (*4*). This suggests that children with WS may show less impairment on number skills if these are assessed by concrete methods rather than by more abstract tests. Paterson and co-workers contest the description of toddlers with WS as "language good, number poor." However, I would argue that this profile is a caricature of the WS phenotype at any age. Individuals with WS who have age-appropriate language skills do exist, but they are in the minority. In most cases, language is an area of relative strength but is, nevertheless, below the level expected for that age. As for number skills, the level of deficit in WS may depend on the type of task used for assessment.

The theoretical importance of WS may lie less in what it tells us about the independence of different domains of the brain than in what it reveals about how different

The author is in the Department of Experimental Psychology, University of Oxford, South Parks Road, Oxford OX1 3UD, UK. E-mail: dorothy.bishop@psy.ox.ac.uk

cognitive capacities affect the process of language development. For instance, auditory short-term memory is an area of particular strength in WS, and an area of particular weakness in both Down syndrome and SLI. Klein and Mervis (*3*) suggested that children with WS do best on language tests that involve memory, and others (*5*) have noted that within a WS sample, language level is closely linked to auditory short-term memory. This suggests that one important factor determining language proficiency in different clinical groups could be the capacity for auditory short-term memory. This idea meshes well with the proposal that a specialized system for remembering speech evolved in humans as a prerequisite for learning language (*6*).

The newborn brain is not a homogeneous mass. Differentiation of sensory areas is established early, and some parts of the brain are implicated in language learning more than others. It is not surprising that genetic disorders affecting the brain can yield characteristic behavioral phenotypes. We must beware, however, of jumping to the conclusion that different language profiles reflect the status of specialized innate brain areas that mediate complex functions such as syntax. Different profiles could reflect the status of, for example, simple auditory memory. To understand just how this might occur, we need to study the process of development in genetic disorders, as well as its final outcome. The Paterson study has made a promising start, and its findings suggest that our assumptions about developmental disorders may be radically challenged by tracing cognitive development from its earliest manifestations.

**References and Notes**


1. S. J. Paterson *et al.*, *Science* **286**, 2355 (1999).
2. C. B. Mervis and B. F. Robinson, *Dev. Neuropsychol.*, in press.
3. B. P. Klein and C. B. Mervis, *Dev. Neuropsychol.* **16**, 177 (1999).
4. P. Howlin *et al.*, *J. Appl. Res. Intellect. Disabil.* **11**, 207 (1998).
5. C. B. Mervis *et al.*, in *Neurodevelopmental Disorders*, H. Tager-Flusberg, Ed. (MIT Press, Cambridge, MA, 1999), pp. 65–110.
6. A. Baddeley *et al.*, *Psychol. Rev.* **105**, 158 (1998).


PERSPECTIVES: MOLECULAR BIOLOGY

# Mutant Dyskerin Ends Relationship with Telomerase

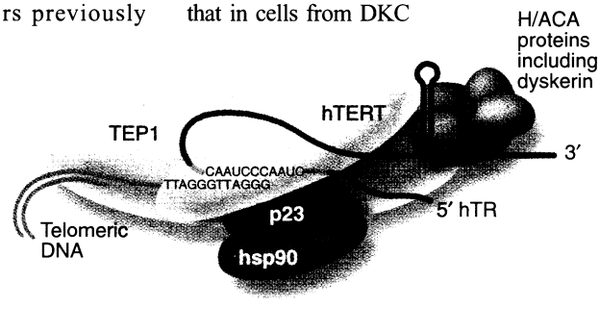
**Jerry W. Shay and Woodring E. Wright**

Dyskeratosis congenita (DKC) is a rare inherited disorder that is characterized by early death from bone marrow failure or pulmonary complications (*1*). Other symptoms include fragile bones, the absence of hair, progressive nail dystrophy, darkening or absence of skin color, underdeveloped testes, precancerous cells in mucous membranes, abnormalities of the gastrointestinal tract, pulmonary fibrosis, and an increased risk of skin cancer (*1*). The defect is caused by mutations in the *DKC1* gene that encodes the protein dyskerin. This protein resembles the yeast protein Cbf5p, believed to be involved in the production of ribosomal RNA (rRNA) (*2*). In a recent issue of *Nature*, Collins and colleagues (*3*) now demonstrate that DKC may not be caused by a deficiency in rRNA, but rather by a defect in the maintenance of telomeres (the repeat DNA sequences at the ends of chromosomes).

The enzyme telomerase is responsible for adding DNA sequences to the ends of chromosomes, replacing the terminal repeats lost during replication. Telomerase, a cellular reverse transcriptase, is a ribonucleoprotein (RNP) composed of both RNA and protein components (see the figure). It adds TTAGGG repeats to the ends of telomeres by copying a template within its own RNA (*4*). Telomerase activity is present in the cells of the early mammalian embryo, in germ line cells, in certain proliferating stem cells (such as those of the hematopoietic system), and in almost all cancer cells. Most normal cells have little or no telomerase activity and show progressive shortening of telomeres throughout their lifespan, resulting in a limited proliferative capacity and eventual growth arrest. Introduction of the catalytic component of telomerase into these cells results in telomere maintenance and the bypass of growth arrest (*5*). There is much interest in understanding the regulation of telomere length, the identification of telomere-binding proteins, and the elucidation of the functions of the different telomerase components.

Collins and co-workers previously showed that the 3′ end of the RNA component of telomerase (hTR) has structural and functional similarities to the H/ACA family (hairpin-hinge-hairpin-tail) of small nucleolar (sno) RNAs (*6*). Sequence elements in H/ACA snoRNAs that are also found in hTR are required for RNA maturation and stability. In their new study, the investigators demonstrate that dyskerin, itself a component of H/ACA snoRNAs, interacts with the telomerase hTR (see the figure). Why should human telomerase associate with a protein component of the snoRNP complex that is thought to guide uridine modifications of rRNA? It is possible that dyskerin promotes the interaction of telomerase with the nucleolus (the site of rRNA and ribosome production). This might facilitate telomerase RNA processing or RNP assembly through the same cellular machinery that evolved to make ribosomes. In support of this hypothesis, it has been found that mammalian telomerase RNA associates with the nucleolus (*6*).

The sequence homology between dyskerin and yeast Cbf5p (*7*), together with the phenotype associated with a lack of Cbf5p (*2*), led to the proposal that DKC is a disorder of ribosome production (*8*). In the new work, Collins and colleagues show that normal dyskerin is a component of human H/ACA snoRNPs. But, they discovered that mutant dyskerin is evidently still able to carry out snoRNP functions, as it has no discernible impact on rRNA processing. Instead the authors found that in cells from DKC




**End game.** The human telomerase RNP complex. The RNA component of telomerase (hTR) contains a template region that directly binds to the G-rich overhang of telomeres at the ends of chromosomes (*4*). In association with the catalytic reverse transcriptase protein subunit (hTERT), telomeric repeats are synthesized. Telomerase-associated proteins (TEP1, a vault protein that physically associates with both hTR and hTERT) and p23/hsp90 (molecular chaperones that physically and functionally associate with hTERT) are also components of the telomerase RNP (*9, 10*). The protein components of snoRNPs including dyskerin—which associate with the H/ACA portion of hTR—may be important for the biogenesis, processing, or turnover of the telomerase RNP (*3*). Telomere-binding proteins that might interact with the hTERT complex are not shown.

The authors are at the University of Texas Southwestern Medical Center, Dallas, TX 75390, USA. E-mail: shay@utsw.swmed.edu

## References and Notes

[1] **Cognitive Modularity and Genetic Disorders**
S. J. Paterson; J. H. Brown; M. K. Gsödl; M. H. Johnson; A. Karmiloff-Smith
*Science*, New Series, Vol. 286, No. 5448. (Dec. 17, 1999), pp. 2355-2358.
Stable URL:
http://links.jstor.org/sici?sici=0036-8075%2819991217%293%3A286%3A5448%3C2355%3ACMAGD%3E2.0.CO%3B2-F