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place the ssDNA-binding mouth of DnaG distal from DnaB, orienting the active site of primase inward, toward the center of the ring, where it is positioned to accept ssDNA as it is extruded from DnaB (Fig. 4, right). Alternatively, it is possible that mechanistic differences between 6:6 and 6:1 helicase-primase systems lead to different relative orientations of the primase active sites. The true relative locations of these domains awaits high-resolution study of the primase-helicase complexes in *E. coli* and phage T7.

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12. T5-overexpression plasmids encoding residues 111 to 433 of *E. coli* DnaG (DnaG-RNAP) preceded by a hexahistidine tag were constructed and overexpressed in SG13009/pREP4 cells. Cells were lysed by sonication and the extract was clarified by centrifugation. Soluble DnaG-RNAP was purified by applying the lysate to a nickel-affinity column and eluting the protein with 200 mM imidazole. His-tagged DnaG-RNAP was further purified by size-exclusion chromatography and concentrated to > 10 mg ml⁻¹. Selenomethionine-incorporated protein was expressed as described [G. D. Van Duyn, R. F. Standaert, A. P. Karplus, S. L. Schreiber, J. Clardy, *J. Mol. Biol.* **229**, 105 (1993)] and was purified as per the unsubstituted protein, except that 2 mM dithiothreitol was included in all purification buffers. Concentrated His-tagged DnaG-RNAP was dialyzed against 10 mM Hepes (pH 7.5), 100 mM NaCl, and diluted to a final concentration of ~10 mg ml⁻¹ before crystallization. Crystals of His-tagged DnaG-RNAP were formed by hanging drop vapor diffusion by mixing 1 μl of protein with 1 μl of well solution [18 to 21% polyethylene glycol (PEG) 4000, 5% PEG200, 30% ethylene glycol, 0.2 M ammonium acetate, 0.05 M sodium acetate (pH 5.0), 0.1% dioxane, 2 to 8 mM SrCl₂, YCl₂, or DyCl₃] and equilibrating the drop against 1 ml of well solution at room temperature for several days. Two nonisomorphous crystal forms were observed, depending on the divalent metal that was used; with YCl₂ or DyCl₃, small platelike crystals (~200 μm by 100 μm by 10 μm) of symmetry P2₁2₁2₁ with unit cell lengths a = 38, b = 56, c = 140 Å were formed; with SrCl₂, thicker bar-shaped crystals (~200 μm by 75 μm by 75 μm) of symmetry P2₁2₁2₁ with unit cell lengths a = 39, b = 58, c = 149 Å were formed.
13. Selenomethionine-incorporated SrCl₂-based crystals were solved by MAD phasing to 2.5 Å. Data were indexed and scaled with MOSFLM [A. G. W. Leslie, *Newsletter on Protein Crystallography No. 26* (Science and Engineering Research Council, Daresbury Laboratory, Warrington, UK, 1992)] and SCALA [W. Kabash, *J. Appl. Crystallogr.* **21**, 916 (1988)]. Selenium sites were determined with SOLVE [T. C. Terwilliger and J. Berendzen, *Acta Crystallogr. D* **52**, 749 (1996)] and refined with MLPHARE [Z. Otwinowski, *Proc. CCP4 Study Weekend* (Science and Engineering Research Council, Daresbury Laboratory, Warrington, UK, 1991),

- p. 80]. Solvent-flattening with DM [K. Cowtan, *Joint CCP4 ESF-EACBM Newlett. Protein Crystallogr.* **31**, 34 (1994)] yielded readily interpretable electron-density maps for model building (Fig. 1B) with O [T. A. Jones, J. Y. Zou, S. W. Cowan, M. Kjeldgaard, *Acta Crystallogr. A* **47**, 110 (1991)]. Elves, an automated structure solution package, was used throughout data analysis and map construction (J. Holton and T. Alber, in preparation). The initial model was refined against a high-resolution native data set to 1.6 Å resolution with an R_{work} of 23.1% and an R_{free} of 27.6% by using Refmac/ARP [G. N. Murshudov, A. A. Vagin, E. J. Dodson, *Acta Crystallogr. D* **53**, 240 (1997); V. S. Lamzin and K. S. Wilson, *Acta Crystallogr. D* **49**, 129 (1993)]. The final model includes residues 115 to 428, with the exception of residues 192 to 194 and 287, for which electron density was not observed. No bond angles for this model fall into either disallowed or generously allowed regions of Ramachandrian space.
14. The structure of the YCl₂-based crystal form was solved by molecular replacement with AMORE [J. Navaza, *Acta Crystallogr. D* **50**, 1507 (1994)] and the refined SrCl₂ structure as an initial model. The molecular replacement solution was refined to 1.7 Å resolution with an R_{work} of 20.9% and a R_{free} of 26.3% by using Refmac/ARP [G. N. Murshudov, A. A. Vagin, E. J. Dodson, *Acta Crystallogr. D* **53**, 240 (1997); V. S. Lamzin and K. S. Wilson, *Acta Crystallogr. D* **49**, 129 (1993)]. Four Y²⁺ ions were modeled, three of which bound in the putative active site of DnaG-RNAP. The occupancies of these metals were estimated by using $F_o - F_c$ difference maps until the density for these sites was appropriately accounted for. The final model included residues from 115 to 427, excluding residues 192 to 194, for which electron density was not observed. The rmsd for all common C_α atoms between the two structures is 0.6 Å. No bond angles for this model fall into either disallowed or generously allowed regions of Ramachandrian space.
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34. We thank the 5.0.2 beamline staff at the Advanced Light Source (Lawrence Berkeley National Laboratories) for assistance with measurements and J. Holton and O. Littlefield for helpful discussions. We also thank M. Botchan, R. Calendar, N. Cozzarelli, S. Gracia, R. Fennell-Fezzie, and K. DeAngelis for assistance with the manuscript and E. Egelman for providing electron micrograph reconstructions of the T7 primase-helicase. Supported by the G. Harold and Leila Y. Mathers Charitable Foundation (J.M.B.) and The Jane Coffin Childs Memorial Fund for Medical Research (J.L.K.). The crystallographic coordinates of both structures have been deposited in the RCSB Protein Data Bank (accession codes: 1DD9 and 1DDE).

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Mitotic Misregulation and Human Aging

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Messenger RNA levels were measured in actively dividing fibroblasts isolated from young, middle-age, and old-age humans and humans with progeria, a rare genetic disorder characterized by accelerated aging. Genes whose expression is associated with age-related phenotypes and diseases were identified. The data also suggest that an underlying mechanism of the aging process involves increasing errors in the mitotic machinery of dividing cells in the postreproductive stage of life. We propose that this dysfunction leads to chromosomal pathologies that result in misregulation of genes involved in the aging process.

The question of why we age has intrigued mankind since the beginning of time. Extensive studies of model systems including yeast, *Caec*

norhabditis elegans, *Drosophila*, and mice as well as studies of human progerias and cellular senescence have identified a number of processes thought to contribute to the aging phenotype (1). These include the effects of oxidative damage associated with cellular metabolism and genome instabilities such as telomere shortening, mitochondrial mutations, and chromosomal pathologies. To gain greater insights into the mechanisms that control life-span and age-related phenotypes, we have studied gene

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REPORTS

regulation of normal and premature aging in actively dividing cells. Studies of fibroblasts derived from young, middle-age, and old-age humans and from humans with Hutchinson-Gilford progeria revealed sets of genes that correlate with, and hence likely contribute to, age-related phenotypes and diseases. The results also suggest that mitotic errors in dividing cells may lead to the altered expression of this collection of genes.

Ten closely matched dermal fibroblast cell lines were classified into four categories based on their chronological and diagnostic similarities: normal young (NY), normal middle (NM), normal old (NO), and Hutchinson-Gilford progeria (P) (2). Collectively, NY, NM, and NO samples allow examination of the expression levels of various genes throughout the natural aging process. Hutchinson-Gilford progeria, on the other hand, is a rare genetic disease in which those affected display at a very early age features typically associated with natural old age, including loss of or graying of hair, diminished subcutaneous fat, cardiovascular disease, and skeletal abnormalities (3). Actively dividing early passage fibroblasts from each age group were initially examined by phase contrast and fluorescence microscopy to characterize age-related morphological changes (2). For each group, the elliptical morphology characteristic of fibroblast nuclei was observed in the majority of cells. However, in contrast to fibroblasts from NY and NM individuals, whose nuclei appeared normal, the NO and P groups had a significant proportion of cells exhibiting aberrant nuclear morphology including multilobed nuclei and irregular nuclear boundaries. The NO and P populations also had a higher proportion of cells with multiple nuclei, consistent with reports of age-dependent increases in micronucleation in human lymphocytes (4). Flow-activated cell sorting (FACS) analysis of the same fibroblasts from the NY and NM groups revealed very similar populations of cells with 2N, S, and 4N DNA content. However, NO and P fibroblasts showed higher percentages of 4N DNA content (Fig. 1), consistent with the larger number of binucleated cells observed by microscopy.

To examine the transcriptional profiles (mRNA abundance) of these fibroblasts, asynchronous and actively dividing cells were cultured in vitro to about 60% confluency (2, 5). Messenger RNA levels were analyzed with high-density oligonucleotide arrays containing probes for more than 6000 known human genes. Expression patterns for each age group (NM, NO, and P) were compared with NY fibroblasts (baseline). Only those changes that were reproducible across all comparisons and all independent replicates were considered further (Fig. 2). On the basis of these conservative criteria, we found that 61 genes (~1% of the genes monitored)

showed consistent expression level changes more than twofold between young and middle age. More than half of these 61 genes can be grouped into two functional classes, (i) genes whose products are involved in cell cycle progression (25%) (Table 1) and (ii) genes involved in maintenance and remodeling of the extracellular matrix (ECM) (31%) (Table 2). The first group of genes are all involved in mitosis and are down-regulated between 2.6- and 12.5-fold. These include cyclins A, B, and F, which are typically up-regulated at the G₂-M cell cycle phase transition and control mitotic progression (6); polo kinase (pLK), which regulates both spindle assembly and cyclin-dependent ki-

nase 1-cyclin B (Cdk1-cyclin B) activation (7, 8); and p55CDC, which participates in the mitotic checkpoint (9). In addition, a group of proteins involved in spindle assembly and chromosome segregation are down-regulated, including the centromere-associated proteins CENP-A (10), mitotin (CENP-F) (11), and histone H2A.X (12), as well as the kinesin-related proteins, mitotic centromere-associated kinesin (MCAK) (13), mitotic kinesin-like protein-1 (14), and kinesin-like spindle protein (HKSP) (15). Transcription factors associated with the G₂-M transition, including B-myb (16, 17) and hepatocyte nuclear factor-3/fork head homolog (HFH-11A) (18), are also down-regulated. Myb is known to

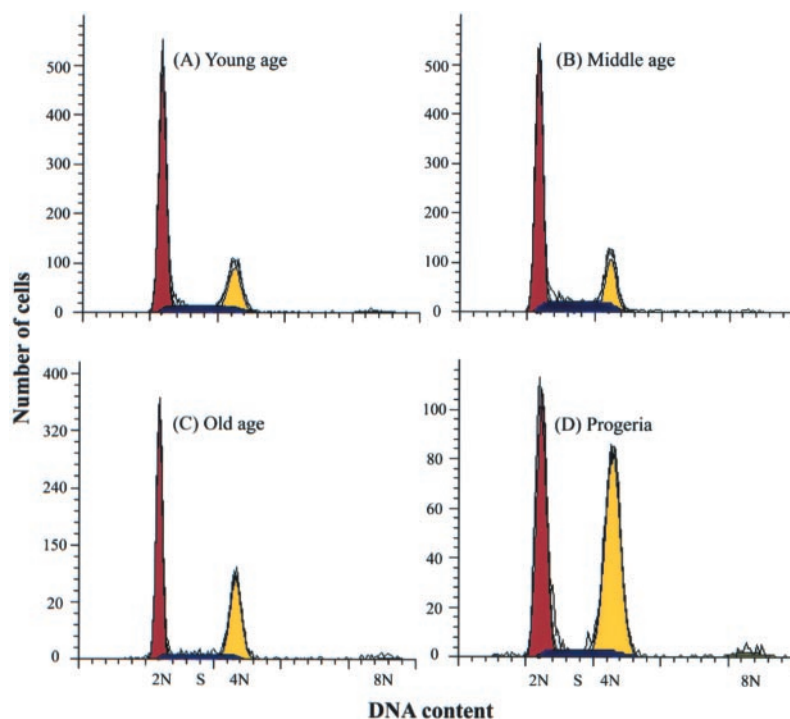


Fig. 1. Actively dividing cells were grown in culture to about 60% confluency before they were ethanol-fixed and stained with propidium iodide for DNA content. The gated histograms were generated and curve-fitted with ModFit LT (Verity Software House, Topsham, ME). (A) NY (CRL7469): 2N, 62%; S, 14%; 4N, 24%. (B) NM (CRL7581): 2N, 60%; S, 19%; 4N, 21%. (C) NO (AG04059B): 2N, 52%; S, 11%; 4N, 37%. (D) P (AG06297B): 2N, 40%; S, 8%; 4N, 52%. The cell cycle parameters for these cell lines are representative of each age group with 3% SD in NY, NM, and NO, and 6% SD in progeria. Colors indicate specific DNA content: red, 2N; blue, S; yellow, 4N; light yellow, 8N.

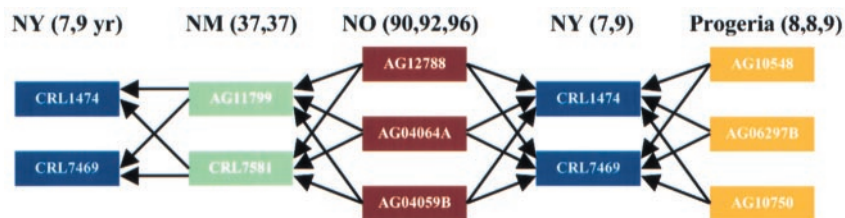


Fig. 2. A comparative analysis of gene expression in natural and accelerated human aging. Expression profiles from cells from middle- and old-age participants and participants with progeria were compared with cells from young participants. The selection criteria were set conservatively such that the selected genes were required to have the same pattern of expression (all up-regulated or all down-regulated) with a twofold change of transcriptional levels or greater in all comparisons.

Table 1. A comparison of changes in gene expression in middle age, old age, and progeria versus young. The magnitude of the changes reported was computed as the average values over the set of comparisons, where the highest and lowest values were excluded. Colors indicate genes that are common across age groups. Red, genes common across all three age groups; brown, genes common in middle and old age; blue, genes common in old age and progeria; black, genes unique to an age group.

Middle Age			Old Age			Progeria		
Cell Cycle Control Proteins	FoldΔ	Gene Name	Cell Cycle Control Proteins	FoldΔ	Gene Name	Cell Cycle Control Proteins	FoldΔ	Gene Name
Acc.#			Acc.#			Acc.#		
X13293	-4.8	B-myb	X13293	-4.9	B-myb	X13293	-7.0	B-myb
U74612	-3.3	Hepatocyte nuclear factor-3/fork head homolog 11A (HFH-11A)	U74612	-9.0	Hepatocyte nuclear factor-3/fork head homolog 11A (HFH-11A)	U74612	-8.7	Hepatocyte nuclear factor-3/fork head homolog 11A (HFH-11A)
Z36714	-12.5	Cyclin F	Z36714	-13.1	Cyclin F	Z36714	-8.7	Cyclin F
X51688	-5.4	Cyclin A	X51688	-5.8	Cyclin A			
M25753	-2.9	Cyclin B	M25753	-5.2	Cyclin B			
U01038	-2.8	pLK	U01038	-3.0	pLK			
U05340	-2.9	p55CDC	U05340	-4.3	p55CDC			
			S78187	-7.6	CDC25B	S78187	-3.4	CDC25B
			U56816	-8.7	Kinase Myt1 (Myt1)	U56816	-11.3	Kinase Myt1 (Myt1)
			X54941	-2.6	Cks1 Cks1 protein homologue	X54941	-4.5	Cks1 Cks1 protein homologue
			M30448	-2.2	Casein kinase II beta subunit	M30448	-2.0	Casein kinase II beta subunit
			U37022	-4.0	Cyclin-dependent kinase 4 (CDK4)	U37022	-4.0	Cyclin-dependent kinase 4 (CDK4)
			U49844	-3.0	FRAP-related protein (ATR, ATM)	U49844	-3.0	FRAP-related protein (ATR, ATM)
			X74008	-3.0	Protein phosphatase 1 gamma	X74008	-3.0	Protein phosphatase 1 gamma
Chromosomal Processing and Assembly			Chromosomal Processing and Assembly			Chromosomal Processing and Assembly		
U30872	-2.6	Mitosis (CENP-F)	U30872	-2.6	Mitosis (CENP-F)	U30872	-2.6	Mitosis (CENP-F)
X67155	-3.5	Mitotic kinesin-like protein-1	X67155	-3.5	Mitotic kinesin-like protein-1	X67155	-3.5	Mitotic kinesin-like protein-1
U37426	-3.6	Kinesin-like spindle protein (HKSP)	U37426	-3.6	Kinesin-like spindle protein (HKSP)	U37426	-3.6	Kinesin-like spindle protein (HKSP)
X14850	-2.2	Histone (H2A.X)	X14850	-2.2	Histone (H2A.X)	X14850	-6.1	Histone H2A.X
U14518	-3.3	Centromere protein-A (CENP-A)	U14518	-3.3	Centromere protein-A (CENP-A)	U14518	-4.3	Centromere protein-A (CENP-A)
U63743	-2.8	Mitotic centromere-associated kinesin	U63743	-2.8	Mitotic centromere-associated kinesin	U63743	-4.8	Mitotic centromere-associated kinesin
X13546	-2.0	Non-histone chromosomal protein HMG-17	X13546	-2.0	Non-histone chromosomal protein HMG-17	X13546	-3.0	Non-histone chromosomal protein HMG 17
			M97856	-3.0	Histone binding protein	M97856	-2.9	Histone binding protein
			D38076	-2.9	RanBP1 (Ran-binding protein 1)	D38076	-2.7	RanBP1 (Ran-binding protein 1)
			X62534	-4.3	HMG-2	X62534	-4.4	HMG-2
			Y08612	-4.1	Nup88 protein	Y08612	-3.5	Nup88 protein
			L43631	-2.5	Scaffold attachment factor (SAF-B)	L43631	-3.2	Scaffold attachment factor (SAF-B)
			U33286	-3.6	Chromosomal segregation gene homolog CAS	U33286	-2.5	Heterochromatin protein p25
			D26361	-4.3	KIAA0042 (Centromere protein-E)			
			M37583	-3.0	Histone (H2A.Z)			
			U72342	-2.3	Platelet activating factor acetylhydrolase (45 Kda subunit LIS1)			
			D43948	-2.6	KIAA0097 (36% similar to yeast Suppressor of tubulin STU2)			
Protein Processing			Protein Processing			Protein Processing		
U73379	-2.3	Cyclin-selective ubiquitin carrier protein	U73379	-3.5	Cyclin-selective ubiquitin carrier protein	U73379	-3.5	Cyclin-selective ubiquitin carrier protein
			AB003102	-2.7	26S proteasome subunit p44.5	AB003102	-2.7	26S proteasome subunit p44.5
			AB003103	-3.7	Proteasome subunit p55	AB003103	-3.7	Proteasome subunit p55
			D00760	-2.6	Proteasome subunit HC3	D00760	-2.6	Proteasome subunit HC3
			D00762	-3.2	Proteasome subunit HC8	D00762	-3.2	Proteasome subunit HC8
			D11094	-3.2	MSS1 (26S proteasome subunit)	D11094	-3.2	MSS1 (26S proteasome subunit)
			D78275	-2.4	Proteasome subunit p42	D78275	-2.4	Proteasome subunit p42

REPORTS

regulate cellular proliferation and differentiation, and HFH-11A is a homolog of *daf-16*, a protein that has been shown to regulate key metabolic and developmental genes and plays a role in regulating life-span in *C. elegans* (17).

A significant number of genes involved in remodeling of the ECM also show altered expression. For example, human macrophage metalloproteinase (HME) and stromelysin 2 are increased 24- and 14-fold, respectively, whereas the protease inhibitors urokinase inhibitor (PAI-2) and cystatin M increase five- to ninefold. A number of proteoglycan cell adhesion proteins are also up-regulated, including dermatopontin, fibromodulin, and thrombospondin, as well as collagens VI and XV and cartilage oligomeric matrix protein (COMP). The preponderance of differentially expressed mitotic and ECM genes compared with genes involved in other cellular processes likely reflects some level of coordinated regulation between these classes of genes (19). The remainder of genes whose expression levels differ consistently by twofold or more include key enzymes involved in the conversion of arachidonic acids to the prostaglandins and thromboxane, such as prostaglandin endoperoxidase synthase 2, endoperoxidase synthase type II, cyclooxygenase 2, and endoperoxidase synthase (5- to 30-fold changes). Increasing levels of these enzymes with age may affect a large number of systemic physiological processes, including platelet aggregation, muscle and kidney function, bone formation, and various inflammatory processes.

Analysis of gene expression in fibroblasts isolated from old versus young individuals again revealed a down-regulation of genes involved in the G₂-M phase of the cell cycle (Table 1). Some of these same cell cycle genes that were down-regulated in middle age versus young cells are more significantly down-regulated in old-age individuals. In addition, other cell cycle genes are affected. For example, the cell cycle proteins FRAP-related protein [FRP1, a homolog of ataxia-telangiectasia mutated (ATM) and its related protein (ATR)], CKS1, and Myt1 are down-regulated three- to ninefold; all are involved in the G₂-M DNA dependent checkpoint pathway, which ensures fidelity before entry into mitosis (20). CDC25B, a key protein triggering entry into mitosis, is also down-regulated. Expression of some of these genes may be controlled by common cell cycle transcriptional control elements (21). There is also an increase in the number of down-regulated genes involved in spindle assembly and segregation, including CENP-E, HMG-2, Ran BP1 (also involved in nuclear transport and regulation of polyadenylation), and scaffold attachment factor. DNA synthesis and repair genes {e.g., thymidylate synthase, minichromosome maintenance protein, Rad

2, poly(adenosine diphosphate-ribose) [poly(ADP-ribose)] synthetase, and proliferating cell nuclear antigen} and RNA synthesis and processing genes (RNA helicases) are also down-regulated. The importance of the down-regulation of some of these repair genes has been clearly demonstrated. For example, in the case of poly(ADP-ribose) synthetase (also known as a polymerase, or PARP), partial inhibition by antisense agents or complete removal by gene knockout results in increased DNA strand breaks, recombination, gene amplification, and aneuploidy (22). Decreased expression levels are also found for proteasomal proteins, which are a core component of the anaphase-promoting complex (APC) and are responsible for the timing of the metaphase to anaphase transition (the final stage of cell division) and other key events in the cell cycle (Table 1). A significant number of genes whose products affect the ECM are again differentially expressed in fibroblasts from old-age individuals; however, the expression levels are less pronounced when compared with that of NM and NY fibroblasts. Genes involved in arachidonic acid oxidation continue to be affected, as do genes involved in lipid transport and metabolism.

Other changes in gene expression occur in old age that are not seen in middle age. For example, genes involved in the stress response and heat shock proteins are up-regulated, including $\alpha\beta$ -crystallin, which is thought to be involved in maintenance of the cellular cytoskeleton (23), and a heat shock serine protease human HtrA, which is over-expressed in osteoarthritic cartilage. Mitochondrial genes are down-regulated, which is consistent with age-related mitochondrial dysfunction (1). Similar changes in a number of stress-response and metabolic genes were observed in expression profiles of aged versus young skeletal muscle from mouse (24). Transcript levels of genes involved in oncogenesis, signal transduction, and the cellular immune response also change and may be linked with age-related diseases.

A comparison of mRNA transcript profiles between progeria and normal young cells reveals a consistent and significant change in the expression of 76 genes. Many of these genes overlap with those found in the comparison of young and old-age samples (Tables 1 and 2). In particular, genes involved in cell division and DNA or RNA synthesis and processing are commonly down-regulated in NO and P. ECM-related genes continue to represent a significant fraction of those genes whose expression levels change. Particularly in progeria, one observes changes in expression of the caldesmons, which are actin-binding proteins involved in cell cycle-dependent reorganization of the cytoskeleton (25); desmoplakin I, which plays a role in intracellular adhesive junctions (26); and auto-

taxins, which are extracellular phosphodiesterases involved in cellular chemotaxis. Transforming growth factor- β (TGF- β) expression also increases 12-fold, consistent with changes in expression of the large number of genes that affect the ECM (27). Genes involved in fatty acid transport and oxidation also vary in similar ways, as with old age and progeria.

Comparison of the genes whose transcript levels change as a function of natural and premature aging reveals classes of genes that can be linked to aging-related phenotypes and diseases. For example, osteoblast (OB)-specific factor 2 (osteoprotegerin) (28) and OB-cadherin (29) play key roles as transcriptional activator and adhesion molecules in bone formation, respectively. Their down-regulation in old age may be linked to bone diseases such as osteoporosis. HME (30) is up-regulated with age and has been shown to be associated with joint destruction in rheumatoid arthritis. Down-regulation of the hyaluronic acid (HA) synthase may also contribute to joint disease; depletion of HA is observed in early experimental osteoarthritis in dogs (31). Cartilage oligomeric matrix protein is significantly up-regulated in old age and has been shown to correlate with disease activity in rheumatoid arthritis and is also arthritogenic when expressed in rat cartilage (32). Cathepsin C, an oligomeric lysosomal protease whose loss of function results in periodontal disease and palmoplantar keratosis, is down-regulated 10-fold in old age (33). In general, the altered expression of a large number of genes that influence the ECM may contribute to age-related changes in the derma.

Expression of other genes possibly linked to age-related diseases is also observed. The breast cancer susceptibility protein-1 (BRCA-1) associated Ring domain protein (BARD1), which binds the NH₂-terminus of BRCA-1, a protein implicated in DNA repair and cell cycle checkpoint regulation, is down-regulated in old-age and progeria cells (34). Down-regulation of BARD1 may deleteriously affect BRCA-1 function and may be linked with age-related sporadic breast cancer; mutations of BARD1 have been identified in breast, ovarian, and uterine cancers (35). The hFRP-1 gene, which is also down-regulated in old age, is a homolog of the gene *ATM* mutated in ataxia-telangiectasia (A-T). A-T is an autosomal recessive disorder characterized by progressive neurodegeneration, immune deficiencies, premature aging, chromosomal instability, and radiation sensitivity (36). ATM, like BRCA-1, plays a key role in the cellular response to DNA breaks, including activation of cell cycle checkpoints and DNA repair. Down-regulation of genes involved in these pathways would result in an increase in genetic instability and sensitivity to reactive oxygen species. $\alpha\beta$ -crystallin expression increases with old age (37). It is also overexpressed in a number of neurolog-

Table 2. A comparison of changes in gene expression in middle age, old age, and progeria versus young. Methods and colors are as in Table 1.

Middle Age			Old Age			Progeria		
Acc.#	FoldΔ	Gene Name	Acc.#	FoldΔ	Gene Name	Acc.#	FoldΔ	Gene Name
Fatty Acids Synthesis			Fatty Acids Synthesis			Fatty Acids Synthesis		
D28235	-5.3	Prostaglandin endoperoxidase synthase-2	D28235	-3.0	Prostaglandin endoperoxidase synthase-2	D28235	-4.1	Prostaglandin endoperoxidase synthase-2
L15326	-7.1	Endoperoxidase synthase type II	L15326	-3.1	Endoperoxidase synthase type II	L15326	-4.1	Endoperoxidase synthase type II
U04636	-29.7	Cyclooxygenase-2 (hCox-2)	U04636	-7.1	Cyclooxygenase-2 (hCox-2)	U04636	-11.8	Cyclooxygenase-2 (hCox-2)
M59979	11.6	Prostaglandin endoperoxidase synthase	M59979	8.0	Prostaglandin endoperoxidase synthase	D50840	-2.5	Ceramide glucosyltransferase
Extracellular Matrix (ECM)/Cytoskeleton			Extracellular Matrix (ECM)/Cytoskeleton			Extracellular Matrix (ECM)/Cytoskeleton		
U05291	9.7	Fibromodulin	U05291	8.2	Fibromodulin	U05291	4.9	Fibromodulin
D87258	2.6	Cancellous bone osteoblast serine protease	D87258	3.0	Cancellous bone osteoblast serine protease	D87258	2.3	Cancellous bone osteoblast serine protease
M31551	8.5	Urokinase inhibitor (PAI-2)	M31551	-3.0	Urokinase Inhibitor (PAI-2)	M31551	-4.7	Urokinase Inhibitor (PAI-2)
L23808	23.5	Metalloproteinase (HME)	L23808	5.7	Metalloproteinase (HME)	HG174-HT174	5.9	Desmoplakin 1
L32137	7.6	Germline oligomeric matrix protein (COMP)	L32137	15.4	Germline oligomeric matrix protein (COMP)	HG2743-HT2845	3.3	Caldesmon 1, Alt. splice3, non-muscle
U62800	5.3	Cystatin M (CST6)	U62800	21.0	Cystatin M (CST6)	HG2743-HT2846	3.4	Caldesmon 1, Alt. splice4, non-muscle
L10035	3.3	Crystallin beta-B2	S45630	2.9	Alpha B-crystallin=Rosenthal fiber component	M83216	5.7	Aorta caldesmon
L12350	4.4	Thrombospondin	U03272	-4.5	Fibrillin-2	HG2743-HT3926	5.1	Caldesmon 1, alt splice 6, Non-muscle
Z22865	5.8	Dermatopontin	D13666	-7.2	Osteoblast specific factor 2 (OSF-2os)	X05232	-29.5	Stromelysin
U94332	4.9	Osteopontin	U54804	-9.5	HAS2 (hyaluronan synthase)	U54804	-6.5	HAS2 (hyaluronan synthase)
X07820	13.5	Metalloproteinase stromelysin-2	D21255	-3.4	OB-cadherin-2			
HG4480-HT4833	7.7	Collagen, type VI, alpha 2	U50939	-2.6	Amyloid precursor protein-binding protein 1 (APP-BP1)			
L25286	4.3	Collagen, type XV, alpha 1	X87212	-5.9	Cathepsin C			
Growth Factors			Growth Factors			Growth Factors		
Y00787	5.0	MDNCF	Y00787	-4.1	MDNCF	Y00787	-4.1	MDNCF
			D50683	-2.8	TGF-beta IIR alpha	AB00584	11.6	TGF-beta superfamily protein
			Tumor Suppressors			Tumor Suppressors		
			U76638	-4.5	BRCA1-associated RING domain (BARD1)	U76638	-3.5	BRCA1-associated RING domain protein (BARD1)
			Protein Synthesis/processing			Protein Synthesis/processing		
			L35594	-14.8	Autotaxin	L35594	-14.8	Autotaxin
			L46720	-12.0	Autotaxin-t (atx-t)	L46720	-12.0	Autotaxin-t (atx-t)

REPORTS

ical disorders such as Alzheimer's disease, Diffuse Lewy Body disease, and Alexander's disease, suggesting a possible link between this protein and age-related neurologic disease. $\alpha\beta$ -Crystallin has also been implicated in the formation of age-related nuclear cataracts (38). The amyloid precursor protein (APP)-binding protein, which binds at the COOH-terminal of APP, the proteolysis site in the generation of β amyloid peptides, is down-regulated with age (39). TGF- β , a key growth factor that regulates tissue homeostasis and whose sustained expression is responsible for tissue fibrosis, is highly up-regulated in progeria, consistent with the biopsies from the progeria patients. COX-2 expression is down-regulated in NM, NO, and P samples. COX-2 knockout mice exhibit abnormalities in the kidney, heart, and ovaries that result in renal dysplasia, cardiac fibrosis, cancer, gastric insufficiency, and female infertility—all of which are related to aging (40). Thus, analysis of gene expression across a larger collection of human genes and in a number of different tissues specifically affected by these and other age-related diseases may allow the identification of key genes associated with diseases of aging, which may provide potential points for therapeutic intervention. Clearly, it will be of interest to carry out similar studies with cell types associated with specific diseases such as breast epithelial cells.

In addition to identifying genes that contribute to the aging phenotype, the analysis of gene expression in natural aging and progeria may also provide insights into the underlying mechanisms of the aging process. A comparison of cells from middle- and old-age humans reveals a common set of genes with altered expression levels. These genes are principally involved in the G₂-M phase of the cell cycle and in remodeling the ECM; they are likely linked through changes in the cellular cytoskeleton that occur during cell division. A comparison of gene expression in old age and progeria also reveals dysregulation of many of the same genes, as well as additional genes involved in DNA or RNA synthesis and processing. The large number of mitosis-related genes that are down-regulated in middle-age, old-age, and progeria fibroblasts does not simply reflect altered cell cycle populations resulting from differential growth rates. This is supported by the fact that the G₀-G₁ and G₂-M populations in young and middle age are virtually identical and that the cells also grow at the same rate. In old-age and progeria cells, the 4N DNA content is even higher, reflecting either a larger number of cells in G₂-M or an increased incidence of tetraploidy. The genes whose expression is altered in middle-age, old-age, and progeria also do not correspond with those observed in cellular senescence (41). Indeed, a recent re-examination of fibroblast culture replicative life-span does not show a correlation with donor age (42). In

addition, the transcript profiles described here do not resemble those of quiescent (19), contact-inhibited (43), or G₁-arrested cell populations (44), nor do the changes in gene expression observed here correspond to those observed in the aged hypothalamus (43) or skeletal muscle (24). In the latter case, a marked stress response was observed along with a lower expression of metabolic and biosynthesis genes. Although a number of the same changes were observed here, the majority of changes we observe in cell cycle, ECM, fatty acid oxidation, and disease-related genes were not observed in muscle or hypothalamus. The altered expression of these genes observed at middle age and elaborated in old age and progeria are likely specific to mitotic versus postmitotic cells.

We suggest that an altered expression of genes involved in cell division occurs with age. These changes result in increased rates of somatic mutation, leading to numerical and structural chromosome aberrations and mutations that manifest themselves as an aging phenotype. Previous studies have demonstrated an increase in aneuploidy with increased age (45), and down-regulation of mitotic genes has been shown to lead to aneuploidy in experimental models. For example, both a motorless mitotic centromere-associated kinesin (MCAK) and antisense inhibition of MCAK lead to chromosome lagging during anaphase (13). It has also been argued that mutations in presenilin 1 and 2, which are associated with both the interphase kinetochore and centrosome and account for most early onset familial Alzheimer's disease, may result in chromosome pathologies (46). Aneuploidy associated with chromosome 21 is involved in Down syndrome, a disease characterized by some features of premature aging. Misregulation of genes involved in cell division may be the result of an intrinsic lack of fidelity that arises in the absence of selection in the postreproductive stage. Alternatively, the growing loss of fidelity may result from the cumulative effects of oxidative damage associated with metabolism, which are slowed by caloric restriction (24). In fact, there may be multiple entry points into this process. For example, Werner syndrome, which is characterized by the premature appearance of aging in young adults (47), shows an increased rate of chromosomal abnormalities caused by mutations in a DNA helicase or exonuclease enzyme known as WRN.

Chromosome pathologies that begin to occur in dividing cells relatively early in life (postreproductive stage) may then lead to misregulation of key structural, signaling, and metabolic genes associated with the aging phenotype, such as osteoporosis, Alzheimer's disease, arthritis, and so forth. Misregulation of this sort is expected to increase in each round of cell division. It may be propagated to other normal mitotic (e.g., leu-

kocytes, epithelial cells, glial cells, and so forth) and postmitotic (e.g., neurons, muscles, and so forth) cells through changes in the ECM and oxidized fatty acid derivatives that affect signaling pathways. Aging, therefore, may occur gradually and in mosaic patterns, rather than as a uniform phenomenon as in cancerous growth, which is clonal. Additional studies are required before we can understand the aging process in complex organisms, both in mitotic and postmitotic tissue, but the studies reported here highlight important mechanisms that may contribute to aging and age-related problems.

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Similar Requirements of a Plant Symbiont and a Mammalian Pathogen for Prolonged Intracellular Survival

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Brucella abortus, a mammalian pathogen, and *Rhizobium meliloti*, a phylogenetically related plant symbiont, establish chronic infections in their respective hosts. Here a highly conserved *B. abortus* homolog of the *R. meliloti* *bacA* gene, which encodes a putative cytoplasmic membrane transport protein required for symbiosis, was identified. An isogenic *B. abortus* *bacA* mutant exhibited decreased survival in macrophages and greatly accelerated clearance from experimentally infected mice compared to the virulent parental strain. Thus, the *bacA* gene product is critical for the maintenance of two very diverse host-bacterial relationships.

Rhizobia establish agriculturally important symbioses with leguminous plants (1), whereas brucellae are highly infectious pathogens of animals and cause the human disease brucellosis (2, 3). Despite leading to exceedingly different outcomes in interactions with their respective eukaryotic hosts, the in-host life-styles of these closely phylogenetically related bacteria (4) show striking parallels. In the establishment of chronic infection, both rhizobia and brucellae are endocytosed by host cells, where they then undergo adaptive changes and ultimately live for prolonged periods in intracellular, acidic, host-membrane-bound compartments (1–3, 5, 6).

Rhizobium meliloti *bacA* mutants invade

alfalfa nodules like wild-type bacteria, but lyse upon release into plant cells before they can differentiate and establish a chronic host infection (7). *BacA* is predicted to be a cytoplasmic membrane transport protein with seven transmembrane domains (7, 8). *BacA* is 64% identical to, and functionally interchangeable with, the *Escherichia coli* *SbmA* protein inferred to be a transporter of bleomycin and microcins B17 and J25 (9). *R. meliloti* *bacA* mutants also have increased resistance to bleomycin (9).

We identified a *B. abortus* DNA fragment that included a monocistronic 1248-nucleotide open reading frame (ORF) (GenBank AF244996) (10) that encodes a predicted protein of 47.3 kD with 68.2% identity to *R. meliloti* *BacA*. In both *B. abortus* and *R. meliloti*, *bacA* is flanked by an upstream gene for a putative transporter and a downstream gene, transcribed in the opposite direction, that has similarity to a putative bacterial secreted protein. We constructed an allele (*bacA1*) of the *bacA* gene in which 41% of the *bacA* ORF was

replaced with a drug resistance cassette (strain KL7) (11). As with *R. meliloti*, disruption of *bacA* function resulted in increased resistance to bleomycin (Fig. 1) (12).

The capacity of the brucellae to survive and replicate in host macrophages is critical to their ability to produce disease (2). The *bacA1* mutant and its wild-type parent were opsonized and used to infect cultured murine macrophages (13). During the first 24 hours post infection (p.i.), both strains showed net intracellular killing by the phagocytes (Fig. 2). The virulent wild-type strain showed characteristic net replication in macrophages at 36 hours p.i. and beyond, but the *bacA1* mutant did not appear to recover after the initial period of killing.

To determine if this defect in intracellular replication in macrophages correlated with an inability to establish a chronic infection in the host, we experimentally infected BALB/c mice with the *bacA1* mutant and its wild-type parent (14). BALB/c mice represent the classic model for chronic *B. abortus* infection in the host (15): Substantial numbers of brucellae can be recovered from the spleens and livers of mice infected with virulent strains

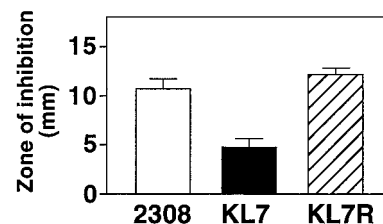


Fig. 1. Increased resistance of the *B. abortus* *bacA* mutant to killing by bleomycin. Strains 2308 (wild-type), KL7 ($\Delta bacA$), and KL7R (reconstructed $\Delta bacA$) were spread onto Schae-dler agar plates and overlaid with filter paper disks containing bleomycin. The diameter of cleared zones of *B. abortus* growth inhibition in response to the drug was measured after 72 hours. Data are presented as the mean \pm SD ($n = 5$).

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