### SCIENTIFIC CORRESPONDENCE

Total numbers and species composition of birds retrieved from affected areas after the Exxon Valdez oil spill

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	Area			
	Prince William Sound	Gulf of Alaska	Total	
No. retrieved	3,360	31,919	35,279	
No. identified	2,884	29,468	32,352	
Percentages:				
Loons and grebes	20.5	0.9	2.6	
Procellarids*	0.5	14.4	13.2	
Cormorants	16.0	1.3	2.6	
Seaducks	24.8	2.3	4.3	
Gulls	1.7	6.3	5.9	
Guillemots	15.1	64.9	61.7	
Other alcids†	17.2	9.7	9.1	
Other birds	4.2	0.2	0.4	

\* Includes fulmars, shearwaters and stormpetrels

† Includes pigeon guillemots, murrelets, auklets and puffins.

been much higher<sup>4</sup>. A few other locations in North America have the potential for similar bird losses, and many are the object of oil and gas exploration or development (for example, eastern Canadian Arctic, Grand Banks of Newfoundland).

Whether bird losses from the Exxon Valdez spill represent biologically significant losses in Alaska or will even be detectable in most populations remains to be seen. It will take years and even decades for some populations to return to pre-spill numbers14,15, but other natural and artificial pertubations may obscure the effects of, or recovery from, oil mortality7,9,16,17

Furthermore, even though we suspect that certain colonies were hard hit by oil, we were unable to identify where dead birds originated, and losses may therefore be spread over a larger geographical range than we surmise<sup>16</sup>. In any case, local populations may recover in 20-70 years, and the process will be accelerated if birds emigrate from unaffected colonies14-17

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predictions of secondary structure give

this region a potential a-helicoidal char-

acter. There are no residues incompatible

with  $\alpha$ -helix among the first four Leu

residues but the two prolines that flank the

fifth Leu residue should destabilize the

 $\alpha$ -helicoidal structure; we therefore pre-

protein with known sequences of func-

tionally equivalent proteins involved in

initiation of replication in plasmids of

Gram-negative bacteria, indicates that some of them<sup>6-8</sup> also have a potential

leucine zipper motif at the N<sub>2</sub>-terminal

region. The eventual absence of a leucine

or a compatible residue at the fourth posi-

tion and the presence of destabilizing resi-

dues could indicate, however, that all

Comparison of this region of the RepA

dict that the  $\alpha$ -helix has about seven turns.

# **Bacterial zipper**

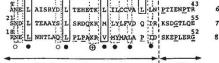
SIR-An in-phase repetition of a leucine every seven residues in an  $\alpha$ -helicoidal structure is a motif associated with the dimerization of proteins and, together with an adjacent basic region, is responsible for the interaction of eukaryotic regulators and specific DNA sequences. This structural and functional motif has been termed the 'leucine zipper'1.2. It is also present in membrane proteins that do not bind to DNA3-5.

In the course of our work on a new plasmid of Pseudomonas savastanoi (Nieto et al. in preparation) we have found that its replication protein (RepA) has a putative leucine-zipper motif in a sequence located at the N terminus. The computer

Comparison of N-terminal regions of four plasmid replication initiator proteins. RepA Coordinates of initial and RepA terminal residues are indi-Е cated. □, Leu repeats and N other compatible residues; I. other conserved positions. Average chemical character

F R6K

Protein Plasmid SNK L IESSHT L TLNEKR L VICAAS L D SRKPLPKD pPS10 pSC101



of residues; •, non-polar; O, polar; +, positively charged. Underlined: helix-destabilizing residues. HDR: helix-destabilizing region.

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## Putative Leu-zipper motif HDR

# Which Haldane?

SIR-Mark Williamson and Robert May (Nature 341, 695; 1989) in considering the Haldane beetle story appear to err by attributing it to J. B. S. Haldane, the famous geneticist. Its origin is more likely to be his father, J. S. Haldane, the distinguished physiologist, who began his work in the physiology laboratory at Oxford in 1887, or possibly his uncle, R. B. Haldane, who was Minister of War before becoming Lord Chancellor in 1912. In 1915 R.B. Haldane was excluded by Asquith from his coalition government because public opinion considered him pro-German because of his well-known enthusiasm for Kant and other German philosophers. This enthusiasm he had imparted to his young brother. Either J. S. or R. B. Haldane, as young men, might well have approached Jowett for advice on philosophy and been invited to dinner at high table at Balliol where the conversation, now a legend, could have taken place.

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these sequences may represent a leucine zipper-like motif in prokaryotes in which shorter  $\alpha$ -helices could also be functional.

Note that the reported initiator proteins share the properties of binding to DNA and of being transcriptional regulators of their own synthesis; it has been proposed that they also interact within themselves and with other proteins of the replication machinery of the cell<sup>9,10</sup>.

A computer search for the DNA-binding helix-turn-helix motif<sup>11</sup> in RepA found a C-terminal region that could fit that structure. Similar observations have been reported for the other initiation proteins<sup>12,13</sup>. The N-terminal leucine zipperlike motif described here may, therefore, be involved in protein-protein interactions.

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