mere. *Drosophila* appears to have solved the problem of ending its chromosomes by co-opting transposons, pieces of DNA that can move around the genome (5). These transposons, HeT-A and TART elements, are found in multiple copies at the end of each chromosome. Presumably, the gradual shortening of chromosomes that occurs at each cycle of replication in *Drosophila* is counteracted by the stochastic transposition of new transposon repeats to the ends. The current model for this telomeric transposition invokes a mechanism by which the RNA transposition intermediate is converted into end DNA by reverse transcriptase. As noted by Pardue (5), both mechanisms of telomere extension are similar in that telomerase is also a reverse transcriptase, and thus in both cases ends are extended by copying from an RNA template.

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Beyond their role in replication, telomeres have also been proposed to participate in meiotic pairing, in meiotic and mitotic chromosome segregation, and in the organi-

UPDATE: CHEMISTRY

Biological Nitrogen Fixation and Model Chemistry

G. J. Leigh

Nitrogenases are well known as the enzymes that biological systems such as plants and bacteria use to process N_2, yet the mechanism of their action continues to be a puzzle. In a previous Perspective (*1*), I discussed the finding that a mononuclear metal complex could split the unreactive N_2 molecule under mild conditions to give a nitrido complex (*2*) but speculated that this had no direct relevance to the way that nitrogenases fix nitrogen. Nevertheless, the discovery showed a kind of reactivity of N_2 with coordination compounds that was unexpected, if not completely unprecedented with species such as metal surfaces.

The chemistry of N_2 complexes effectively began about 30 years ago, principally with mononuclear complexes, and proceeded with the general belief (*3*) that these molecules would show us the kind of chemistry that must be used by nitrogenases. This chemistry is still the best-explored area of N_2 reactivity, although there has been a steady trickle of generally unrelated and often accidental discoveries suggesting that the protonation of N_2 in mononuclear molybdenum complexes may not represent the only reaction pathway available to nitrogenases.

The establishment of the structures of two molybdenum nitrogenases with the unusual iron-molybdenum clusters apparently containing the site of N_2 reduction (*4*) left us with the problem of identifying exactly what it might be. It is still quite feasible that mononuclear chemistry does indeed provide the key to nitrogenase reactivity, but the reports by Shan *et al.* on page 1460 (*5*) and Fryzuk *et al.* on page 1445 (*6*) in this issue open the question even wider.

Although there is disagreement as to whether the nitrogenase cluster can or cannot accommodate a N_2 molecule (*7*), this has not prevented speculations that place N_2 inside the cluster, on the surface of the cluster, or even partly inside and partly outside. Now Shan *et al.* (*5*) show us that N_2 molecules can be accommodated by six gold atoms that constitute a kind of cage. This kind of binding has little precedent in nitrogen chemistry other than a single example of a disamarium-tetralithium cage (*8*). The cluster assembles spontaneously from two trinuclear gold species and hydrazine (not N_2), and it decomposes in acids with partial or complete protonation of the N_2, depending on the supporting phosphine.

Whether the nitrogenase cluster can allow a N_2 molecule to enter it and then to be protonated inside is still a completely open question. The N-N separation in the new cluster is 1.457(14) Å (numbers in parentheses indicate error in the last digits), which should denote a single bond, and the Au-Au separations across the opposing triangles of gold atoms are greater than 3.6 Å, probably nonbonding distances. Apparently the N_2 holds the whole hexanuclear gold assemblage together. Might it not be described better as two trinuclear clusters bridged by N_2? In the nitrogenase clusters, the corresponding Fe-Fe separations, supported by bridging sulfide ions, are about 2.5 Å, and direct Fe-Fe interaction is not excluded (*4*).

The report by Fryzuk *et al.* (*6*) suggests a hitherto unrecognized possibility for nitrogenase reactivity. It has long been a mystery why all nitrogenases are apparently such prolific hydrogenases. Even in the best circumstances, they "waste" about 25% of their expensive reducing electrons as H_2. The usual rationalization is that N_2 displaces H_2 when it binds to the active site, although why that displacement should be necessary is not obvious (*9*). To date, coordinated N_2 has been shown to react with electrophiles, principally the proton, and with organic radicals (*3*). Now side-on bridging N_2 in a dinuclear zirconium complex has been shown to react with silanes and dihydrogen.

It might be argued that the final attack on the coordinated N_2 generating the coordinated N_2H is indeed electrophilic, but that is not really the point. Here we have a new class of reactions of N_2, and one that would appear to be feasible in nitrogenases and, superficially at least, analogous to the Haber process reactions used in the industrial processing of dinitrogen.

Rather than clarifying the reaction modes of nitrogenase, these reports add to the list of possibilities. Nitrogenase does indeed move in mysterious ways, and possibly in ways that we cannot yet imagine.

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