these granite-related residual fluids then infiltrate or interact with basic rocks rich in chromium, we have the unusual combination of beryllium and chromium to produce emerald in the late stages of crystallization; this is a somewhat simplistic version of the granite–greenstone genetic concept.

But the origin of emeralds from the Colombian Eastern Cordillera is now pictured rather differently. The fluids involved have been characterized as sulphate-bearing hydrothermal brines rich in the heavy oxygen isotope ^{18}O (refs 2–5, 8, 9) which were probably formed by the interaction of basinal fluids with Jurassic and Lower Cretaceous evaporites. As Ottaway *et al.*[2] describe, these fluids then interacted with organic-rich shales and limestones, resulting in oxidation of organic matter, thermochemical sulphate reduction and release of organically bound beryllium, chromium and vanadium. The black shales became characteristically bleached (they are referred to as *cenicero* zones — literally, 'ashtray') and pyrite, calcite and emerald precipitate together with accessory lode-filling phases. So sulphur is derived from the fluids, but carbon, beryllium, vanadium and chromium are derived from the shales in general and the organic matter in particular (see also refs 3–5, 8, 10, 11). The oxygen, carbon and sulphur stable-isotope data (for the brines, calcite and pyrite, respectively) are all in accord with this picture which thus neatly integrates field, mineralogical and geochemical aspects.

Fluid inclusion data[2] suggest that the temperature of homogenization and NaCl dissolution was around 330 °C. Whether this can also be considered as a trapping temperature (and so the emerald formation temperature) then depends on whether a pressure correction is required to account for the depth at which the processes occurred. The temperature would be 50 °C higher[1] for formation at 1 kilobar.

Cheilletz *et al.*[5] combined K–Ar and ^{40}Ar–^{39}Ar dating of mica associated with Colombian emerald deposits, and obtained concordant ages of 31.5–32.6 Myr before present for the Quipama–Muzo zone (although whether this includes the actual mine sampled by Ottaway *et al.* is not clear to me). At nearby Coscuez the age is slightly older, 35–38 Myr before present. With this latter age constraint and a subsidence model for the Eastern Cordillera, they then deduced a formation depth of around 4,500 m, corresponding to 1.1 kbar pressure. Taking this with their own fluid inclusion evidence resulted in a formation temperature estimate of 290–360 °C. So both research programmes converge on a moderate-temperature epigenetic model involving hydrothermal brines and sedimentary shales. The importance of thermochemical sulphate reduction is highlighted by Ottaway *et al.* and the absolute ages provided by the French team[5,12] provide a critical temporal framework. Furthermore, in other areas Ottaway *et al.* suggest that the *cenicero*-like zones may have value for exploration, as the overall new model very clearly does.

What, then, of the role of "uncorrupted youth" in the genesis of emeralds? Unfortunately, as Watson said of the Giant Rat of Sumatra, this is a story for which the world is not yet ready. □

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TRANSCRIPTION

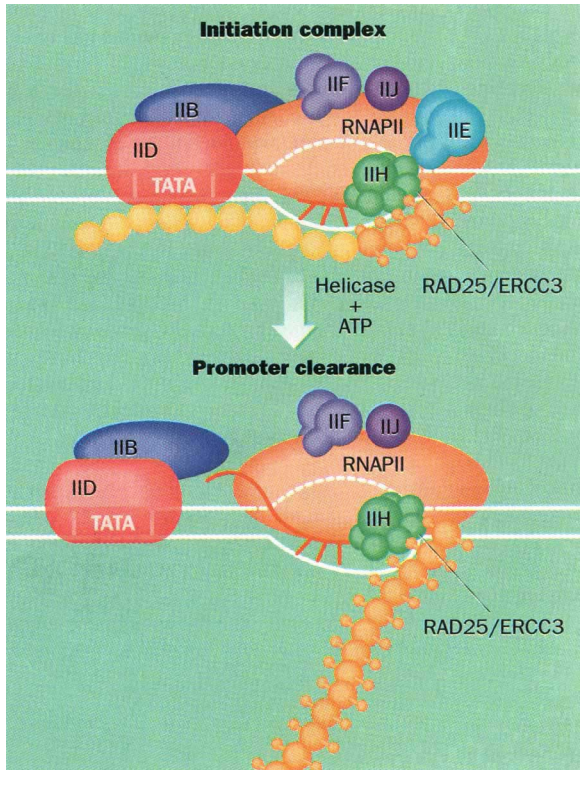
The essential twist

Ronny Drapkin and Danny Reinberg

DURING initiation of gene transcription, the DNA duplex at the promoter region melts to grant RNA polymerase access to the DNA template strand. Unlike RNA polymerases I and III, transcription initiation by RNA polymerase II (RNAPII) requires hydrolysis of the ATP (or dATP) β–γ bond[1]. Strikingly, the activity that catalyses this reaction and the precise energy-dependent step have eluded identification for years. On page 578 of this issue[2], Guzder *et al.* reveal that the yeast RAD25 DNA-repair protein possesses an ATP-dependent, DNA-unwinding activity that is essential for transcription by RNAPII. This protein, and its human counterpart ERCC3, have roused enormous interest because of their intimate connection to the basal transcription apparatus.

RNAPII requires several general factors to orchestrate transcription initiation from protein-coding genes. Most of these factors have been purified and their corresponding complementary DNAs isolated. General transcription factor IIH (TFIIH, also called BTF2) has exhibited complexity beyond expectation. Like its yeast and rat homologues, TFIIH is a multisubunit factor that has an intrinsic ATPase activity and a kinase specific for the carboxy-terminal domain (CTD) of the largest subunit of RNAPII (reviewed in ref. 3). Initial reports alluded to the possibility that CTD phosphorylation might account for the unique ATP requirement exhibited by RNAPII. The observations that the TFIIH kinase can also use GTP in the phosphorylation reaction, and that a form of RNAPII without a CTD can catalyse transcription *in vitro* yet still require ATP hydrolysis, suggested otherwise. Insight into the identity of the ATP-dependent activity came when the largest subunit of TFIIH was identified as being the ERCC3 DNA-repair protein[4].

ERCC3 was initially characterized as the gene responsible for the DNA-repair defect in xeroderma



Model for the role of the RAD25/ERCC3 subunit of TFIIH in transcription initiation. The general transcription factors (IID, IIB, IIF, IIE, IIH and IIJ) and RNA polymerase II (RNAPII) assemble on the promoter to form the complete initiation complex. TFIIH can phosphorylate (orange) the carboxy-terminal domain (CTD) of the largest subunit of RNAPII. Before it is phosphorylated, the CTD remains in contact with the TATA-binding protein of TFIID. Initiation appears to involve two energy-dependent steps, open complex formation and promoter clearance. The RAD25/ERCC3 subunit probably acts at the second of these two steps to catalyse promoter clearance in an ATP-dependent reaction. The RNA/DNA hybrid is in scarlet.

pigmentosum group B (reviewed in ref. 5), and it contains the canonical helicase motifs that typically enable proteins to unwind RNA and/or DNA duplexes in an ATP-dependent fashion. Indeed, ERCC3 allows TFIIH to unwind DNA locally in an ATP-dependent reaction[4]. Guzder *et al.* now furnish direct biochemical evidence that RAD25, the yeast equivalent to ERCC3, not only contains ATP-dependent helicase activity, like ERCC3, but also that this helicase activity is vital for RNAPII-mediated transcription[2].

A string of recent papers has revealed that *ERCC2*, the gene that corrects the DNA-repair defect in xeroderma pigmentosum group D (ref. 5), also encodes a component of human and yeast TFIIH, and that the entire TFIIH complex can function in DNA-excision repair independently of its involvement in transcription[6–9]. The yeast equivalent of *ERCC2* is *RAD3*, and like *RAD25* it encodes a DNA helicase required for DNA-excision repair. RAD3 and RAD25 are further related in that both are essential for viability in yeast.

The difference between the two proteins comes from analysis of key mutations in the nucleotide-binding domain. Such a mutation in RAD3 abolishes its ATPase/helicase activity, impairing its DNA-repair function, but not affecting cell viability, indicating that the RAD3 helicase is not required for the protein's essential function[10]. Indeed, this mutation does not affect the transcriptional role of yeast TFIIH (ref. 6). A similar mutation in RAD25, however, is lethal, implicating the ATPase/helicase activity of this protein as the essential component[9,11]. Prakash and colleagues have provided compelling evidence, both *in vivo* and *in vitro*, that RAD25 (ref. 2) and RAD3 (ref. 12) are essential for viability because of their involvement in transcription by RNAPII. The observation by Guzder *et al.*[2], that RAD25 with a mutation in the nucleotide-binding pocket is defective in transcription, clearly shows that, unlike RAD3, the ATPase/helicase activity of RAD25 is essential for its function in transcription and cell viability.

What precisely does RAD25/ERCC3 helicase do in transcription? Open complex formation is ATP dependent[13], as is the helicase activity of RAD25/ERCC3. So, most logically, it functions in open complex formation during transcription initiation. Interestingly, this step is not entirely specific for ATP: it appears that at high enough concentrations, any nucleotide can provide the β–γ energy bond, with ATP having the lowest K_m (J. Gralla, personal communication). Because the helicase activity of RAD25/ERCC3 is specific for ATP, it is unlikely that it catalyses open complex formation.

What else might the RAD25/ERCC3 helicase do? Studies on the composition of the RNAPII ternary complex have excluded the involvement of RAD3/ERCC2, RAD25/ERCC3 and TFIIH in elongation, as none of these factors has been detected in the ternary complex (P. Kumar, L. Zawel and D. Reinberg, unpublished results). TFIIH and ATP may act at a stage subsequent to open complex formation yet before elongation[14], a phase called promoter clearance. This phase is akin to a functional roadblock, bypass of which requires energy in the form of ATP. Once the polymerase forges through this roadblock, the TFIIH helicase activity (provided by RAD25/ERCC3) and the ATP cofactor are no longer required. Moreover, the use of a pre-melted linear template (a template already in the open conformation) that extends over the transcription start site circumvents the requirement for ATP in RNAPII transcription[15]. This bypass probably encompasses the open complex and promoter clearance phases of initiation and obviates the requirement for the TFIIH (RAD25/ERCC3) helicase.

This study may also shed light on the observation that superhelicity of the DNA template circumvents the requirement for TFIIH and ATP hydrolysis[16,17]. Superhelical tension perhaps provides the energy for a stable open complex, similar to the pre-melted heteroduplex, thereby bypassing the ATPase requirements for open complex and promoter clearance.

On current understanding, it seems that open complex formation and promoter clearance are two energy-dependent steps. It is likely that the RAD25/ERCC3 subunit of TFIIH functions at the second step, but the activity involved in open complex formation remains unknown. We will have the answer, in mechanistic terms, only after nucleotide and factor requirements are biochemically correlated. It should not be long in coming. □

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DAEDALUS

Lagging ahead

THE gas butadiene is an ingredient of synthetic rubber. It has a nasty tendency to polymerize prematurely. The interior of a pipe or tank of the gas often becomes coated with a mass of frothy polymeric solid. Once initiated, this 'popcorn polymer' grows at the expense of the gas. It can jam valves, block pipes and even burst containers. The higher the temperature, the more luxuriantly it grows. The infestation has to be cleared away mechanically, and the installation 'disinfected'.

Daedalus sees opportunities in this nuisance. He points out that, like foamed polystyrene, butadiene popcorn polymer is an excellent heat insulator. Imagine, he says, a boiler room or industrial plant with a wide range of complex hot vessels and pipes. Conventional lagging would be expensive to apply, and tricky to manoeuvre into all the little corners. But release butadiene into the room, and it would polymerize spontaneously to popcorn polymer on all the hot parts. It would lag the whole installation, including all the tricky and inaccessible details. Furthermore, the process would be self-optimizing. A very hot object would acquire a thicker coating before its lagged surface was cool enough not to attract further polymerization. Every part would thus receive just enough insulation for its temperature.

DREADCO's chemists are now exploring the popcorn reaction. They argue that a reaction so hard to prevent must be very easy to encourage. By adding copolymers and modifiers, they hope to perfect an autolagging vapour whose strongly temperature-dependent polymerization gives an ideal foamy or whiskery thermal insulator. Released among the steam pipes and heat exchangers of chemical works and generating stations, 'Vapourlag' will coat their most complex recesses with perfectly proportioned insulation. Blown under the floorboards of a house, it will insulate the longest and most labyrinthine central-heating and hot-water pipes. Expensive, labour-intensive lagging will be a thing of the past.

The converse problem, that of insulating cold surfaces, defeats this elegant chemistry. But Daedalus recalls that α-methylstyrene does not polymerize above 0 °C; for a long time it was thought not to polymerize at all. The DREADCO team hopes to devise an analogous Vapourlag monomer which can only polymerize on cold surfaces. The world's deepfreezes and refrigerators, and its more weather-beaten houses, could then also gain the benefits of cheap, easily renewed Vapourlagging. David Jones