Rb-Sr dating of mylonites along major intra-cratonic and craton margin shear systems of the Precambrian Dharwar Craton, Southern India and tectonic implications

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Large-scale brittle-ductile shear zone systems, at both intra-cratonic and craton-margin settings, comprise a prominent deformation fabric of the Precambrian Dharwar Craton. Mylonites from a number of shear systems were dated by the Rb-Sr whole rock-biotite isochron method in an attempt to constrain chronology of latest deformation along the shear zones and improve our understanding of the temporal evolution of the craton in terms of deformation, magmatism and uplift events since the Archaean.

Multiple samples of mylonites from the intra-cratonic shear zones bounding the Bababudan, Chitradurga and Ramagiri greenstone belts indicate a spread of ages between 2515 Ma and 2220 Ma. The results bear evidence for recurrent Palaeoproterozoic reactivation of the boundary zones that separate large tracts of greenstone belts and granite-gneiss domains. While the older ages could relate to a terminal stage of Late Archaean thermo-tectonic events involving east-west shortening and thrusting in the Dharwar Craton, the younger ages may correspond to thermal and tectonic events such as the emplacement of mafic dyke swarms and development of large intra-cratonic sedimentary basins like the Cuddapah basin.

Unlike the intra-cratonic shear zones, an overwhelming number of Rb-Sr biotite ages of mylonites and gneisses in the vicinity of the Palghat-Cauvery shear zone system and the Eastern boundary thrust zone of the Cuddapah basin, which mark the southern and eastern margins of the Dharwar Craton, cluster around 486 Ma. These shear zones straddle the boundaries between the Archaean Dharwar Craton and the high-grade mobile belts which are generally believed to have accreted during the Proterozoic, but the chronology of their accretion has been ambiguous. The present age data constrain the latter events at late Neoproterozoic/early Palaeozoic. The results are consistent with age data on analogous tectonic settings elsewhere in the Gondwana supercontinent.

Mass dependent isotope fractionation of Hg during biotic degradation of methyl-Hg & reduction of Hg(II)

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The extent of fractionation of mercury (Hg) stable isotopes during 1) degradation of monomethyl-Hg (MMHg) via the mercury resistance (*mer*) pathway in *Escherichia coli* JM109/pPB117 and 2) Hg(II) reduction by three Hg(II) reducing strains, including a Hg(II) sensitive anaerobic strain, was investigated. It was found that MMHg and Hg(II) that remained in the reactors with microbes became progressively heavier (increasing δ^{202}Hg) with time and underwent mass dependent Rayleigh fractionation with fractionation factors $(\alpha_{202/198})_{\text{reactant-product}}$ of 1.0004 and 1.0016 ± 0.0005, respectively. We did not observe mass independent fractionation (MIF) and based on the nature of microbe-Hg interactions suggest that the nuclear spin dependent MIF is unlikely to occur during biological processes. Because of the important implications of the absence of MIF during biological processes on Hg isotope systematics, we will discuss experimental strategies that could be used to confirm this suggestion.

The *mer* mediated MMHg degradation is a multi-step process that involves two enzymes, organomercurial lyase (MerB) and mercuric reductase (MerA). The *mer* mediated Hg(II) reduction is also a multi-step process involving a dedicated Hg(II) transport system and MerA. We provide a multi-step framework for understanding the extent of fractionation seen in our MMHg degradation and Hg(II) reduction experiments and suggest which steps in the process could cause the observed extent of fractionation based on the biochemistry and kinetics of the various steps involved in the two *mer* mediated pathways. A clear effect of Hg(II) bioavailability on the extent of fractionation of Hg both during reduction of Hg(II) and degradation of MMHg via the *mer* pathway was observed and is also discussed. Knowledge of fractionation during individual steps, i.e., enzyme transformations, transport, adsorption, and diffusion, will further constrain the extent of Hg fractionation expected during various biotic processes. The framework provided in this study can guide future experiments on isotope fractionation during other transformations in the Hg biogeochemical cycle, including fractionation during Hg(II) methylation, and ultimately in the more rigorous development of Hg isotope systematics.