INDUCED AMINO ACID CHIRALITY FROM STRONG MAGNETIC FIELDS IN INTERSTELLAR ENVIRONMENTS. M. A. Famiano[1,2], R.N. Boyd[3,4], T. Kajino[2,5], T. Onaka[5], K. Koehler[6], and S. Hulbert[3] [1]Western Michigan University, Kalamazoo, MI, USA, [2]National Astronomical Observatory of Japan, Mitaka, Tokyo, Japan, [3]Department of Physics, The Ohio State University, Columbus, OH, USA, [4]Department of Astronomy, The Ohio State University, Columbus, OH, USA, [5]Department of Astronomy, Graduate School of Science, University of Tokyo, Tokyo, Japan, [6]Los Alamos National Laboratory, Los Alamos, NM, USA.

Introduction: Recent work [1,2] has suggested that the chirality of the amino acids could be established in the magnetic field of a nascent neutron star from a core-collapse supernova via processing by the neutrinos that would be emitted. This model, the Supernova Neutrino Amino Acid Processing Model, or SNAAP model, not only appears to produce a small chiral imbalance, but always produces the same sign of the chirality. This is also consistent with evidence that the origin of amino acid chirality may be non-terrestrial in nature.[3-5]

We have studied the capability of the SNAAP model for selective destruction of one molecular chirality. This extends previous work [2] to include the dynamical effects that would be produced on the amino acids that were included in meteoroids that were large enough to escape destruction by the supernova photons as they passed by a nascent neutron star. This model has many similarities to nuclear magnetic resonance, even though it is essentially classical. The study does show that the amino acids contained in a large meteoroid could undergo orientation from the magnetic field of the neutron star, subsequent chiral sub-state selection from the combination of that field and the rotation of the meteoroids, and finally chiral selection by the neutrinos emitted as the neutron star produced by a core-collapse supernova cools over its characteristic few second cooling time.

Method: A Monte Carlo code was written to simulate strong neutrino interactions with amino acids in the vicinity of neutron stars.[6] This model assumes that the neutrinos emitted from the nascent neutron star would interact with the amino acids, which had been oriented by the neutron star's magnetic field. These molecules would have to be contained in large meteoroids that happened to be passing by the star as it became a supernova, so that they could survive the high temperature environment existing near the star. The crucial interaction that destroys ^{14}N is $^{14}N + \nu_e \rightarrow {}^{14}C + e^+$ where ν_e is an electron antineutrino and e^+ is a positron. It was also assumed that some imbalance in the total angular momentum of the molecules would be achieved, perhaps by the Buckingham effect[7,8], so that the conversion of ^{14}N to ^{14}C would, because of a spin selection effect on the strength of the interaction, selectively destroy one orientation compared to the other. These amino acids would have to be contained in large meteoroids that happened to be passing by the star as it became a supernova, so that they could survive the high temperature environment existing near the star.

Conclusions: In order for an effective production of an enantiomeric excess of polar atoms/molecules via the SNAAP model, three things are required: 1) a strong external magnetic field, 2) a nuclear species with a non-zero magnetic moment (gyromagnetic ratio), and 3) an external polarized weak interaction mechanism. All three of these are satisfied by introducing a meteoroid containing a molecular species which can be polarized with respect to the magnetic field produced by a nascent neutron star from a core-collapse supernova. The meteoroid acts as the substrate carrying the molecular or atomic species, and the neutron star provides both the external magnetic field and the polarized weak interaction in the form of selective destruction of the molecule via neutrinos, which are naturally polar, since they have a definite helicity. The differential in interaction cross sections between the neutrino-nucleus collisions in which the reactants are aligned parallel or anti-parallel, together with the asymmetric emission of the neutrinos, provides a selective destruction of one of the orientations of the polar molecule, and an enantiomeric excess is created.

Although some aspects of the SNAAP model are speculative, tests could be done on amino acids in an intense neutrino beam to at least check the capability of this most basic aspect of the model.[9]

References:

[1] Boyd R.N. et al. (2010) *Astrobiology, 10*, 561. [2] Boyd R.N. et al. (2011) *Int. J. Mol. Sci., 12*, 3432. [3] Kvenvolden K. et al. (1970) Nature, 228, 923. [4] Cronin J.R. et al. (1997) Science, 275, 951. [5] Glavin D.P. et al. (2010) Met. Plan. Sci, 45, 1948. [6] Famiano M.A. et al. (2014) Symmetry, 6, 909. [7] Buckingham A.D. (2004) Chem. Phys. Lett., 398, 1. [8] Buckingham A.D. and Fischer P. (2006) Chem. Phys., 324, 111. [9] Boyd R.N. (2012) Stardust, Supernovae and the Molecules of Life, Springer (New York).