Amino acid racemisation in Quaternary foraminifera from the Yermak Plateau and implications for age models in the Arctic Ocean

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Introduction

Developing age models for Arctic Ocean sediments has been a long-standing problem in marine geosciences. Amino acid geochronology is a powerful tool to date Quaternary marine deposits, however it has only been applied to a limited number of sediment cores from the Arctic (Adler et al. 2008; Kaufman et al. 2008). Amino acid racemisation (AAR) studies (e. g. Kaufman et al. 2013) on the prevalent arctic foraminifera species *Neogloboquadrina pachyderma* imply that D / L values tend to be more variable than for other taxa. No studies exist from the Arctic Ocean which compare AAR rates between *Neogloboquadrina pachyderma* and benthic foraminifera species, which might have less inherent variability. To verify the applicability of AAR dating in the Arctic setting, AAR rates in *Neogloboquadrina pachyderma* and the benthic species *Cassidulina neoteretis* are compared. The Yermak Plateau provides an ideal target for sediment samples, as they generally have better preservation of microfossils and the age depth models are better constrained than in other Arctic settings.

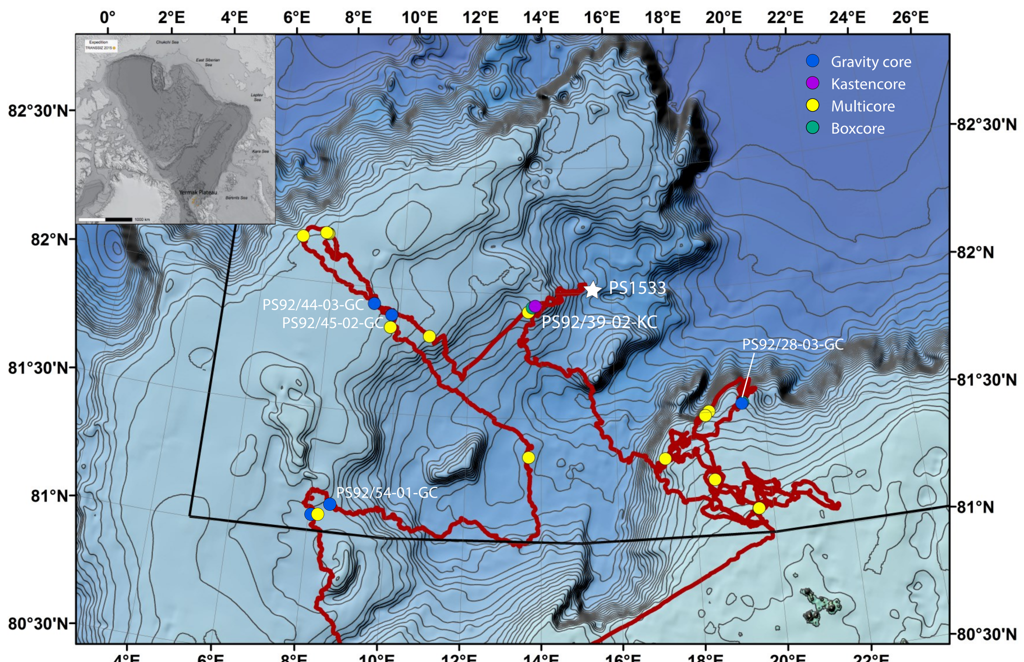


Figure 1. Study area showing the locations of sediment cores PS92/45-2 and PS92/54-1 on the Yermak Plateau (Basemap: Jakobsson et al. 2012).

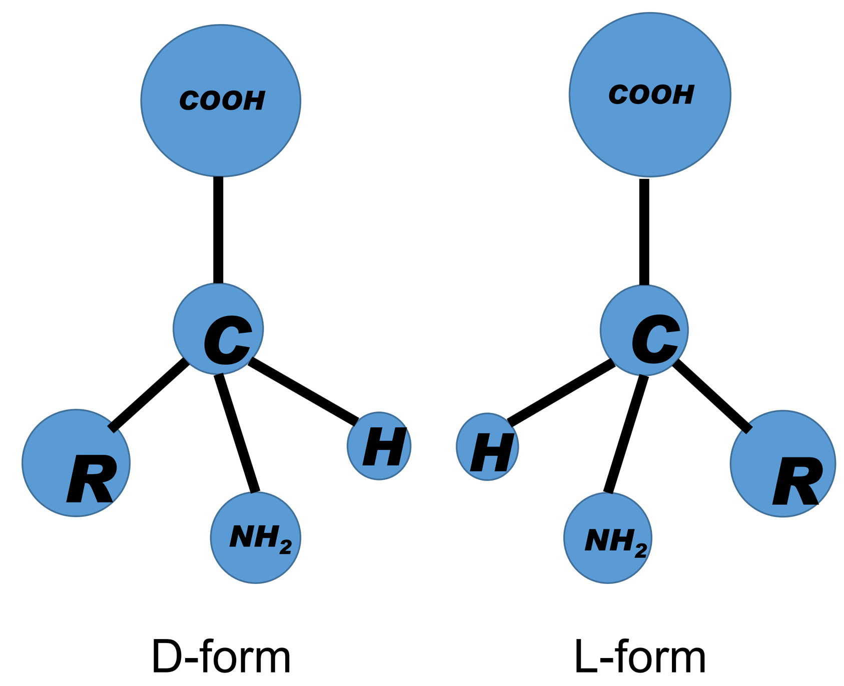
The current study investigates samples from two sediment cores from the Yermak Plateau, which were collected during the 2015 TRANSSIZ expedition: PS92 / 45-2 and PS92 / 54-1. Age models for the cores were developed using a combination of ^{14}C dating and correlation of environmental magnetic parameters with the global δ^{18}O record (Wiers et al. 2018, submitted). For core locations see Figure 1.

Methods

Amino acid racemisation dating is based on two chiral forms of the same amino acid (Figure 2): *dextro*rotatory and *laevo*rotatory. In nearly all living organisms, proteins are present in the L-form, which convert (racemise) to the D-form following death, until a 1:1 ratio is achieved. Measuring the relative proportions of the two forms, the elapsed time can be estimated.

Amino acid racemisation in foraminifera species *Neogloboquadrina pachyderma* and *Cassidulina neoteretis* from sediment cores PS92/45-2 and PS92/54-1 were analysed. 21 samples with an average of 9.3 subsamples each, resulted in 195 analyses in total.

Figure 2. Structure of a generic amino acid with the two chiral forms.



Sample preparation and analysis included the following steps:

- Light (few seconds) sonication of the foraminifera tests
- Immersion in 1 ml of 3 % H_2O_2 for 2 hours
- Rinsing three times with reagent grade water (Type I) and air drying under laminar flow
- Tests were then divided into subsamples, and placed in sterilised micro-reaction vials
- 7µl of 6M HCl was added and the vials were seal under N_2
- Hydrolysis at 110 °C for 6 hours
- Evaporation to dryness
- Rehydration in 4 µl of 0.01 M HCl with 10µM L-homoarginine (internal spike)
- High performance liquid chromatography (HPLC) analysis

Results

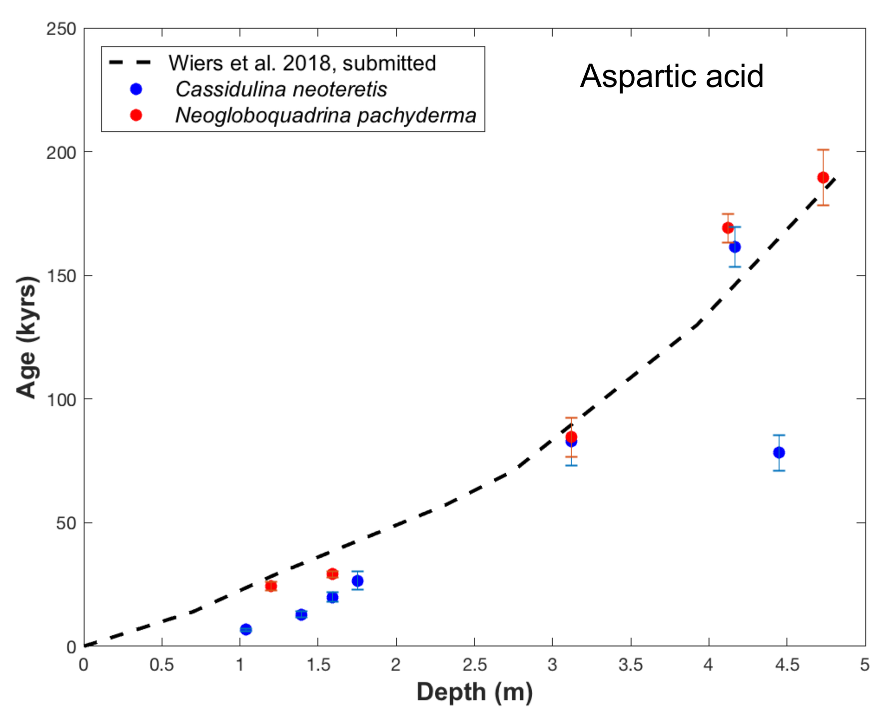


Figure 3. Age depth relationship for core PS92 / 45-2 based on on aspartic acid D / L ratios and the global calibrated age equation of Kaufman et al. (2013). The dashed line represents the age-depth model proposed by Wiers et al. (2018, submitted).

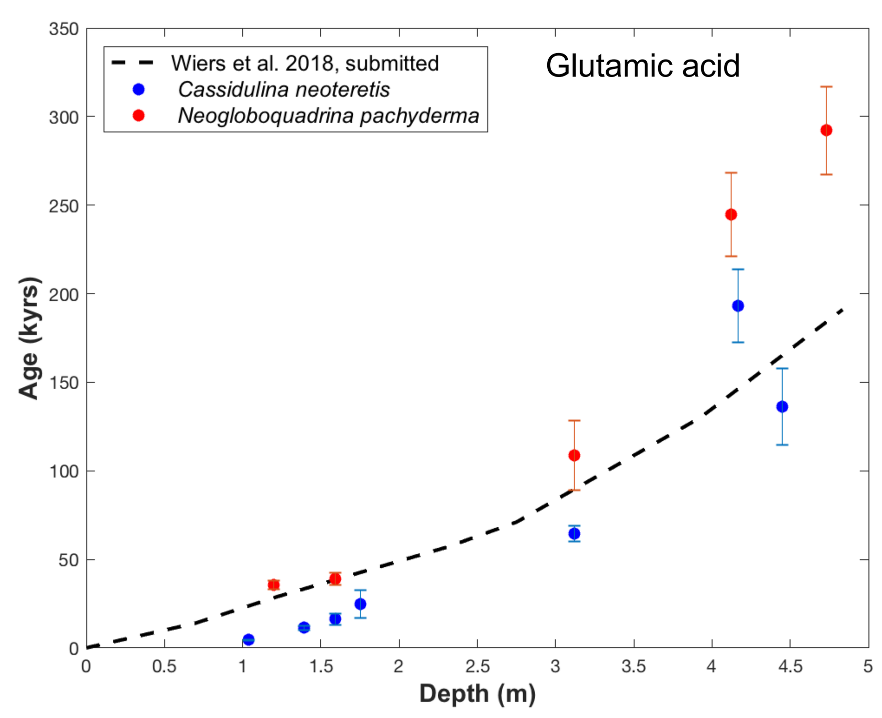


Figure 4. Age depth relationship for core PS92 / 45-2 based on on glutamic acid D / L ratios and the global calibrated age equation of Kaufman et al. (2013). The dashed line represents the age-depth model proposed by Wiers et al. (2018, submitted).

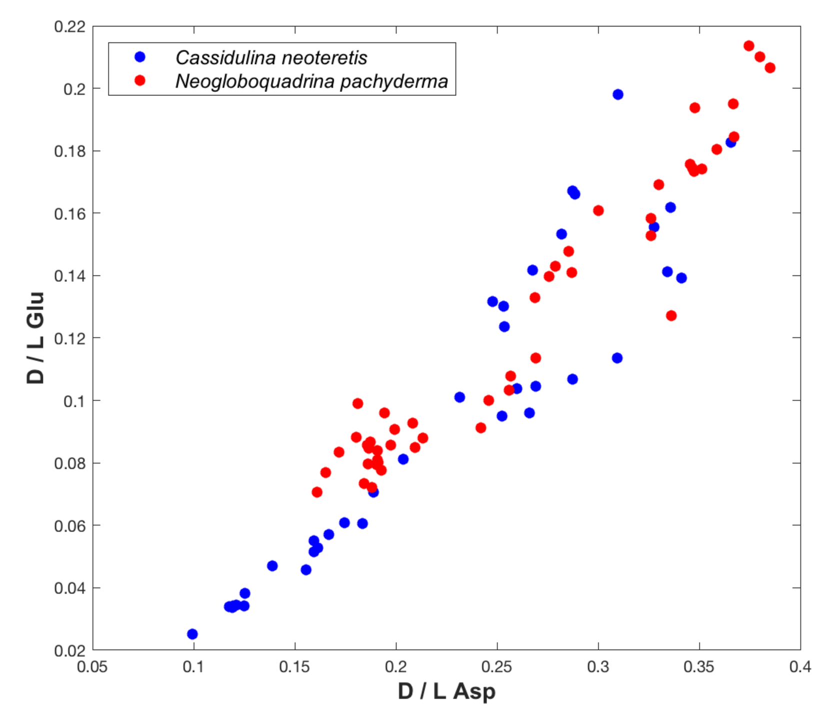


Figure 5. Extent of racemisation (D / L) in aspartic acid (Asp) and glutamic acid (Glu) in individual subsamples of *Cassidulina neoteretis* and *Neogloboquadrina pachyderma* from sediment core PS92 / 45-2.

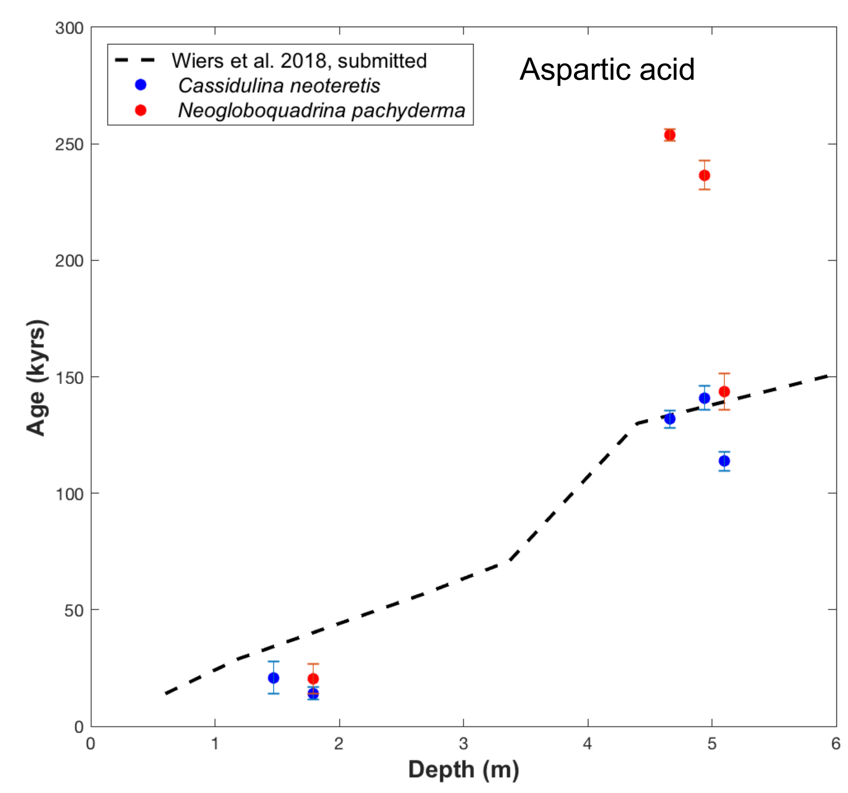


Figure 6. Age depth relationship for core PS92 / 54-1 based on aspartic acid D / L ratios and the global calibrated age equation of Kaufman et al. (2013). The dashed line represents the age-depth model proposed by Wiers et al. (2018, submitted).

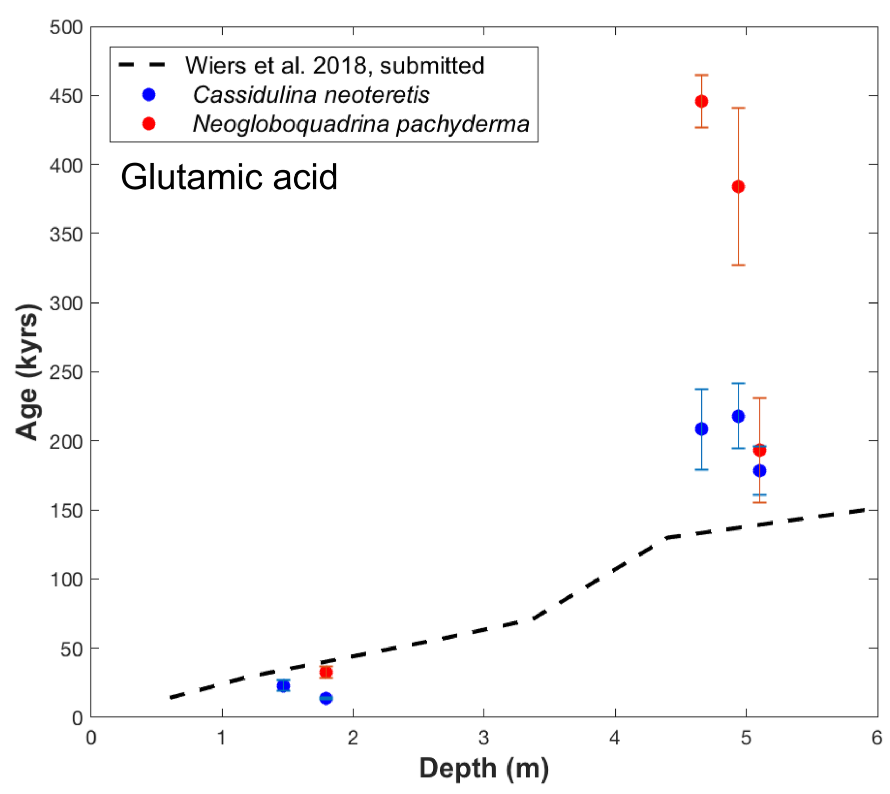


Figure 7. Age depth relationship for core PS92 / 54-1 based on glutamic acid D / L ratios and the global calibrated age equation of Kaufman et al. (2013). The dashed line represents the age-depth model proposed by Wiers et al. (2018, submitted).

Key findings

- Amino acid racemisation rates analysed in planktic (*Neogloboquadrina pachyderma*) and benthic (*Cassidulina neoteretis*) foraminifera from the Yermak Plateau conform to the global rate of racemisation as predicted by the model of Kaufman et al. (2013).
- The extent of racemisation for both aspartic and glutamic acids increases with sample age both in the planktic species *Neogloboquadrina pachyderma* and in the benthic species *Cassidulina neoteretis* from multiple cores.
- Aspartic acid racemisation results from sediment cores PS92/45-1 and PS92/54-1 support the age-depth model proposed by Wiers et al. 2018 (submitted) for the cores.
- Depth versus age trends for *Neogloboquadrina pachyderma* are more scattered than for *Cassidulina neoteretis.*
- Depth versus age trends for glutamic acid generally show more scatter than for aspartic acid, confirming previous findings by Kaufman et al. (2013).
- The results indicate the applicability of amino acid racemisation in the dating of Arctic Ocean sediments, however, further research is required to establish its relevance in the central Arctic.

References

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- Kaufman et al (2008) Paleoceanography and Paleoclimatology 23.3 (2008).
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