



Supplement of

Free amino acids in Antarctic aerosol: potential markers for the evolution and fate of marine aerosol

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Reagents and standard solutions

Ultra grade methanol (MeOH) was purchased from Romil LTD (Cambridge, UK), while Ultrapure water (18.2 M Ω , 0.01 TOC) was produced using a Purelab Ultra System (Elga, High Wycombe,UK). Formic acid (\geq 98%) eluent additive for HPLC system was obtained from Fluka (Sigma Aldrich®, Buchs, Switzerland) and hydrochloric acid (HCl) 37% ACS was supplied by Carlo Erba.

Each amino acid standard solution (D and L-alanine (D-/L-Ala), D and L-arginine (D-/L-Arg), D and L – asparagine (D-/L-Asn), D and L-aspartic acid (D-/L-Asp), D and L –glutamic acid (D-/L-Glu), glycine (Gly), D and L hydroxy proline (D-/L-Hyp), D and L –histidine (D-/L-Hys), D and L –isoleucine (D-/L-Ile), D and L – leucine (D-/L-Leu), D and L –methionine (D-/L-Met), D/L methionine sulfone (MetSO₂), L ornithine (L-Orn), D and L –phenylalanine (D-/L-Phe), L-proline (L-Pro), D and L –serine (D-/L-Ser), D and L –threonine (D-/L-Thr), D and L –tyrosine (D-/L-Tyr), D and L tryptophan (D-/L-Trp), and D and L –valine(D-/L-Val)) was prepared from a solid standard (purity \geq 98%), and diluted in HCl 0.1M. The solid standards were purchased from Sigma Aldrich®. Isotopically-labeled 13C amino acids (L-[¹³C₃] alanine (Ala*), L-[¹³C₄] aspartic acid (Asp*), L-[¹³C₅] glutamic acid (Glu*), and L-[¹³C₆] arginine (Arg*); purity of 98%) were purchased from Sigma Aldrich while L-[¹³C₁] leucine (Leu*), L-[¹³C₁] phenylalanine (Phe*), L-[¹³C₁] proline (Pro*), and L-[¹³C₁] valine (Val*) (purity \geq 98%) were obtained from Cambridge Isotope Laboratories Inc. (Andover, MA).

	IS	Yield	RSD	Error	RSD	Blank	MDL
		%	%	%	%	(ng abs)	(ng abs)
L-Ala	Ala*	51	10	-10	2	151	44
D-Ala	Ala*	62	7	4	3	30	22
L-Arg	Arg*	62	8	-2	9	4	2
D-Arg	Arg*	78	2	0.7	1	4	3.2
L-Asn	Val*	70	9	3	7	10	6
D-Asn	Val*	67	2	-4	9	15	6
L-Asp	Asp*	50	8	-7	6	41	30
D-Asp	Asp*	41	8	2	13	102	50
L-Glu	Glu*	58	7	-6	2	25	6
D-Glu	Glu*	57	9	-1	6	12	8
L-Hyp	Leu*	70	9	7	13	0.2	0.5
D-Hyp	Leu*	74	7	-5	10	1	1.4
L-Hys	Pro*	66	9	6	1	51	16
D-Hys	Pro*	49	7	-8	8	7	10
L-Leu/L-Ile	Leu*	60	5	-7	6	77	32
D-Leu/D-Ile	Leu*	59	5	-13	6	3	5.8
L-Met	Leu*	61	11	-2	8	2	3.2
D-Met	Leu*	65	9	-9	3	8	10
L-Orn	Arg*	43	13	2	14	249	58
L-Phe	Phe*	63	5	-3	4	5	2.8
D-Phe	Phe*	70	4	7	9	6	5.8
L-Pro	Pro*	61	9	-4	3	15	3.8
L-Ser	Phe*	38	17	-2	8	170	138
D-Ser	Phe*	56	15	6	13	98	84
L-Thr	Arg*	65	6	-1	5	10	5
D-Thr	Arg*	72	6	5	6	2	1
L-Trp	Arg*	63	10	5	6	2	5
D-Trp	Arg*	65	10	-0.2	9	1	1.2
L-Tyr	Phe*	66	13	8	10	24	16
D-Tyr	Phe*	67	9	7	10	6	8
L-Val	Val*	61	6	-6	2	57	12
D-Val	Val*	64	10	-5	5	6	3
Gly	Ala*	71	11	3	4	89	50
MetSO2	Leu*	58	8	-5	8	8	14

Table S1. Summary of yield, trueness and reproducibility expressed as a relative standard deviation (RSD%) for <u>circular quartz fiber filters</u>. For each amino acid, the internal standard (IS) used for the quantification, the amount of blank filter and the relative method detection limit (MDL) is reported.

Table S2. Summary of yield, trueness and reproducibility expressed as relative standard deviation (RSD%) for <u>backup quartz fiber filters</u> (< 0.49 μ m). For each amino acid, the internal standard (IS) used for the quantification, the amount of blank filter and the relative method detection limit (MDL) is reported.

	IS	Yield	RSD	Error	RSD	Blank	MDL
		%	%	%	%	(ng abs)	(ng abs)
L-Ala	Ala*	51	6	-8	3	226	35
D-Ala	Ala*	61	9	9	7	67	36
L-Arg	Arg*	53	7	-7	2	26	24
D-Arg	Arg*	61	8	8	3	4	3
L-Asn	Val*	55	6	-2	6	45	28
D-Asn	Val*	54	9	6	9	30	28
L-Asp	Asp*	54	6	-2	4	125	35
D-Asp	Asp*	54	9	1	8	51	28
L-Glu	Glu*	54	5	-3	4	99	18
D-Glu	Glu*	50	9	5	7	16	8
L-Hyp	Val*	56	8	3	10	3	4
D-Hyp	Val*	70	8	7	7	4	5
L-Hys	Pro*	57	32	77	15	88	114
D-Hys	Pro*	46	16	-21	10	43	64
L-Leu/L-Ile	Leu*	57	3	-8	9	31	23
D-Leu/D-Ile	Leu*	61	9	-4	2	14	12
L-Met	Leu*	56	9	-9	5	20	19
D-Met	Leu*	51	5	-9	2	11	6
L-Orn	Arg*	42	5	-3	8	275	61
L-Phe	Phe*	60	7	1	6	32	11
D-Phe	Phe*	65	9	4	8	3	2
L-Pro	Pro*	55	5	-4	3	73	42
L-Ser	Phe*	55	7	8	5	597	167
D-Ser	Phe*	42	9	-6	5	422	61
L-Thr	Arg*	63	10	9	1	46	18
D-Thr	Arg*	58	5	7	3	12	9
L-Trp	Phe*	63	9	-5	7	3	4
D-Trp	Phe*	61	9	-1	9	7	10
L-Tyr	Phe*	53	6	2	7	30	34
D-Tyr	Phe*	62	11	7	8	10	8
L-Val	Val*	58	6	-3	2	91	49
D-Val	Val*	50	8	-7	8	5	12
Gly	Ala*	56	6	-1	3	61	37
MetSO2	Leu*	51	9	-9	8	32	23

Table S3. Summary of yield, trueness and reproducibility expressed as relative standard deviation (RSD%) for <u>slotted quartz fiber filters</u>. For each amino acid, the internal standard (IS) used for the quantification the amount of blank filter and the relative method detection limit (MDL) is reported.

	IS	Yield	RSD	Error	RSD	Blank	MDL
		%	%	%	%	(ng abs)	(ng abs)
L-Ala	Ala*	72	6	-6	5	57	24
D-Ala	Ala*	346	6	450	7	-	-
L-Arg	Arg*	51	7	-9	4	8	4
D-Arg	Arg*	53	3	-1	6	2	1
L-Asn	Val*	32	5	-64	5	0.2	0.2
D-Asn	Val*	190	7	191	9	-	-
L-Asp	Asp*	71	6	1	3	102	51
D-Asp	Asp*	37	26	-3	33	348	107
L-Glu	Glu*	81	2	7	4	0.6	1.1
D-Glu	Glu*	494	10	799	9	-	-
L-Hyp	Leu*	81	4	3	5	0.5	0.2
D-Hyp	Leu	75	5	-8	5	0.5	0.8
L-Hys	Leu*	71	9	1	15	3	3
D-Hys	Asp*	45	8	-5	14	12	9
L-Leu/L-Ile	Leu*	5	65	7	-9	9	7
D-Leu/D-Ile	Leu*	7	72	13	-6	10	8
L-Met	Leu*	61	10	-8	11	5	4
D-Met	Leu*	50	8	-2	8	2.1	0.5
L-Orn	Arg*	50	9	4	8	41	23
L-Phe	Phe*	77	3	-2	3	12	10
D-Phe	Phe*	102	9	56	4	-	-
L-Pro	Pro*	61	7	-8	5	82	56
L-Ser	Phe*	88	10	57	7	-	-
D-Ser	Phe*	-18	-6	-115	-40	-	-
L-Thr	Arg*	57	6	-9	7	19	8
D-Thr	Arg*	64	8	7	4	3	2
L-Trp	Phe*	99	8	59	10	-	-
D-Trp	Phe*	93	6	54	11	-	-
L-Tyr	Arg*	61	4	6	4	12	16
D-Tyr	Arg*	63	7	-13	13	4	7
L-Val	Val*	78	3	-3	3	23	12
D-Val	Val*	174	8	140	7	-	-
Gly	Ala*	36	41	-7	3	36	15
MetSO2	Leu*	66	5	-9	5		4



Figure S1. Cluster means backward trajectories analyses at 10 m, 100m, 500m and 1000 m agl at the coastal base "Mario Zucchelli Station" (MZS) during the summer of 2010-2011. Study of the vertical stability of HYSPLIT model. The 208 back trajectories are divided into 6 clusters with the percentage of total number of trajectories that each represents reported in brackets.



Figure S2. Cluster means backward trajectories analyses at 10 m, 100m, 500m and 1000 m agl at the Italian-French base Dome C (DC) during the summers of 2011-2012. Study of the vertical stability of HYSPLIT model. The 172 back trajectories are divided into 6 clusters with the percentage of total number of trajectories that each represents reported in brackets.



Figure3. Cluster means backward trajectories analyses at 10 m, 100m, 500m and 1000 m agl at the Italian-French base Dome C (DC) during the summers of 2012-2013. Study of the vertical stability of HYSPLIT model. The 204 back trajectories are divided into 6 clusters with the percentage of total number of trajectories that each represents reported in brackets.



Figure S4. Matrix back-trajectories computed for each 24-h sampling at 500 m agl at the coastal base "Mario Zucchelli Station" (MZS) from the 29th November 2010 to 18th January 2011. Study of the horizontal stability of HYSPLIT model varying the source position of one degree of latitude and longitude from the real coordinates of source.



Figure S4. continued



Trajectory Direction: Backward Duration: 240 hrs Vertical Motion Calculation Method: Model Vertical Velocity Meteorology: 0000Z 1 Dec 2010 - reanalysis

Figure S4. continued

lat.: -73.

Trajectory Direction: Backward Duration: 240 hrs Vertical Motion Calculation Method: Model Vertical Velocity Meteorology: 0000Z 1 Dec 2010 - reanalysis

1 lat.: -73

Trajectory Direction: Backward Duration: 240 hrs Vertical Motion Calculation Method: Model Vertical Velocity Meteorology: 0000Z 1 Dec 2010 - reanalysis



Figure S4. continued



Figure S4. continued



Figure S4. continued



Figure S5. Matrix back-trajectories computed for each 24-h sampling at 500 m agl at the Italian-French base Dome C (DC) 19^{th} December 2011 to 28^{th} January 2012. Study of the horizontal stability of HYSPLIT model varying the source position of one degree of latitude and longitude from the real coordinates of source.



Figure S5. continued



Figure S5. continued



Figure S5. continued







NOAA HYSPLIT MODEL ectories ending at 1000 UTC 27 Jan 12 CDC1 Meteorological Data Backward traje



Figure S5. continued

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Figure S6. Matrix back-trajectories computed for each 24-h sampling at 500 m agl at the Italian-French base Dome C (DC) from 07th December 2012 to 26th January 2013. Study of the horizontal stability of HYSPLIT model varying the source position of one degree of latitude and longitude from the real coordinates of source.



NOAA HYSPLIT NODEL ectories ending at 1000 UTC 17 Dec 12 CDC1 Meteorological Data

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NOAA HYSPLIT MODEL ectories ending at 1000 UTC 13 Dec 12 CDC1 Meteorological Data

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Figure S6. continued

NOAA HYSPLIT MODEL Backward trajectories ending at 1000 UTC 16 Dec 12 GDG1 Meteorological Data

Source * at multiple locations

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Figure S6. continued



Figure S6. continued



Figure S6. continued



Figure S6. continued



Figure S7. Wind rose of the sample collected from 27 December to 06 January at the Italian-French base "Concordia Station" (Dome C) during the summer in Antarctica 2012-13.



Figure S8A. 5-day back-trajectories of the first sample (from 13 to 18 January) collected during the oceanographic cruise on the R/V Italica during the summer of 2011-12 on the Southern Ocean. The trajectories were computed for each 24-h sampling using a vertical velocity model at 100 m above sea level.



Figure S8B. 5-day back-trajectories of the second sample (from 18 to 23 January) collected during the oceanographic cruise on the R/V Italica during the summer of 2011-12 on the Southern Ocean. The trajectories were computed for each 24-h sampling using a vertical velocity model at 100 m above sea level.



Figure S8C. 5-day back-trajectories of the third sample (from 25 to 29 January) collected during the oceanographic cruise on the R/V Italica during the summer of 2011-12 on the Southern Ocean.. The trajectories were computed for each 24-h sampling using a vertical velocity model at 100 m above sea level.



Figure S8D. 5-day back-trajectories of the fourth sample (from 31 January to 6 February) collected during the oceanographic cruise on the R/V Italica during the summer of 2011-12 on the Southern Ocean. The trajectories were computed for each 24-h sampling using a vertical velocity model at 100 m above sea level.



Figure S8E. 5-day back-trajectories of the fifth sample (from 7 to 9 February) collected during the oceanographic cruise on the R/V Italica during the summer of 2011-12 on the Southern Ocean. The trajectories were computed for each 24-h sampling using a vertical velocity model at 100 m above sea level.



Figure S8F. 5-day back-trajectories of the sixth sample (from 13 to 18 February) collected during the oceanographic cruise on the R/V Italica during the summer of 2011-12 on the Southern Ocean.. The trajectories were computed for each 24-h sampling using a vertical velocity model at 100 m above sea level.



Figure S8G. 5-day back-trajectories of the seventh sample (from 18 to 19 February) collected during the oceanographic cruise on the R/V Italica during the summer of 2011-12 on the Southern Ocean. The trajectories were computed for each 24-h sampling using a vertical velocity model at 100 m above sea level.