

ORIGINAL ARTICLE

tRFs as Potential Exosome tRNA-Derived Fragment Biomarkers for Gastric Carcinoma

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SUMMARY

Background: Gastric Carcinoma (GC) is one of the common diseases induced by the interaction of genes and environment. Exosomes are potential markers for several health problems, which contain lipids, proteins, long non-coding RNAs, microRNAs (miRNAs), and tRNA-derived fragments (tRFs). The roles of mRNAs and miRNAs in GC have been studied comprehensively; however, little research was focused on the function of plasma exosomal tRFs.

Methods: We collected plasma samples from fifty healthy controls and fifty GC patients, and all exosomes were isolated with a combined centrifugation and characterized by electron microscopy, western blot, and flow cytometry. The small RNA sequence was performed to detect the plasma exosomal tRFs, and tRFs markers were validated by real-time quantitative PCR. Three exosomal diagnostic tRFs were confirmed by receiver operating characteristic analyses.

Results: In this study, we found higher plasma exosomal tRF-25, tRF-38, tRF-18 expression in GC than in controls. Plasma exosomal tRF-25, tRF-38, and tRF-18 showed better accuracy for GC diagnosis.

Conclusions: Our results suggest that plasma exosomal tRF-25, tRF-38, and tRF-18 were biomarkers for GC detection; tRF-25, tRF-38 and tRF-18 might be predictive of GC prognosis.

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Supplementary Tables

Table S1. Summary of cleaning data and length distribution of tags produced by small RNA sequencing.

	Total reads	Clean reads (%)	Total base	Clean base (%)	GC (%)
Control group 1	14,200,746	13,762,444 (96.91)	710,030,711	396,783,254 (55.88)	50
Control group 2	13,019,091	9,410,704 (72.28)	650,948,789	266,376,255 (40.92)	52
Control group 3	8,272,662	5,670,613 (68.55)	413,609,999	145,298,849 (35.13)	51
<u>Gastric carcinoma 1</u>	13,921,677	12,930,629 (92.88)	696,077,453	368,666,816 (52.96)	52
<u>Gastric carcinoma 2</u>	13,607,345	13,035,544 (95.80)	680,361,116	364,830,917 (53.62)	51
<u>Gastric carcinoma 3</u>	7,707,255	4,101,087 (53.21)	385,341,343	112,843,965 (29.28)	51

Table S2. Summary of mapping data by small RNA sequencing.

	Control group 1	Control group 2	Control group 3	<u>Gastric carcinoma 1</u>	<u>Gastric carcinoma 2</u>	<u>Gastric carcinoma 3</u>
1. MiRNAs mapping data						
All reads	13,762,444	9,410,704	567,0613	12,930,629	13,035,544	4,101,087
Unmapped reads	9,938,248	7,126,500	330,4189	9,524,099	8,584,913	3,363,785
Mapped reads	3,824,196	2,284,204	2,366,424	3,406,530	4,450,631	737,302
Unique mapped reads	3,141,126	124,778	1,462,411	2,915,706	3,540,412	527,882
Repeat mapped reads	683,070	1,036,415	904,013	490,824	910,219	209,420
Insert size	51	52	52	54	51	51
2. tRFs mapping data						
All reads	9,843,696	6,942,463	3,187,383	9,299,747	8,388,647	3,242,028
Unmapped reads	9,794,575	6,911,146	3,159,501	9,241,037	8,327,881	3,228,119
Mapped reads	49,121	31,317	27,882	58,710	60,766	13,909
Unique mapped reads	4,572	1,003	562	722	2,172	148
Repeat mapped reads	44,549	30,314	27,320	57,988	58,594	13,761
Insert size	29	30	29	29	30	29

Table S3. Summary of piRNA mapping data by small RNA sequencing.

	Control group 1	Control group 2	Control group 3	<u>Gastric carcinoma 1</u>	<u>Gastric carcinoma 2</u>	<u>Gastric carcinoma 3</u>
1. Potential piRNA (mapped to piRNA cluster)						
All reads	8,859,997	5,315,485	2,128,763	8,220,699	6,996,165	1,672,178
Unmapped reads	8,811,163	5,236,259	2,082,606	8,119,364	6,882,084	1,623,290
Mapped reads	48,834	79,226	46,157	101,335	114,081	48,888
Unique mapped reads	42,597	38,228	19,478	43,664	56,369	22,094
Repeat mapped reads	6,237	40,998	26,679	57,671	57,712	26,794

Table S3. Summary of piRNA mapping data by small RNA sequencing (continued).

	Control group 1	Control group 2	Control group 3	Gastric carcinoma 1	Gastric carcinoma 2	Gastric carcinoma 3
2. Known piRNA (mapped to piRBase)						
All reads	48,834	79,226	46,157	101,335	114,081	48,888
Unmapped reads	47,464	73,188	43,302	96,715	110,094	47,035
Mapped reads	1,370	6,038	2,855	4,620	3,987	1,853
Unique mapped reads	179	1074	712	1112	1091	530
Repeat mapped reads	1191	4964	2143	3508	2896	1323
Insert size	28	29	29	29	29	29
3. rRNA derived piRNA						
All reads	5,353	21,338	6,603	14,851	5,770	9,029
Unmapped reads	4,780	21,043	6,379	14,239	5,461	8,879
Mapped reads	573	295	224	612	309	150
Unique mapped reads	49	203	113	130	62	95
Repeat mapped reads	524	92	111	482	247	55
Insert size	24	27	26	25	26	27
4. tRNA derived piRNA						
All reads	21,079	30,979	31,373	28,854	31,082	16,729
Unmapped reads	15,891	25,247	24,623	25,393	27,784	12,650
Mapped reads	5,188	5,732	6,750	3,461	3,298	4,079
Unique mapped reads	443	1,538	385	327	456	289
Repeat mapped reads	4,745	4,194	6,365	3,134	2,842	3,790
Insert size	30	29	30	29	29	30