

三步走， 带你开始英文论文写作

魏轩 博士 Wiley学术顾问

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Agenda

看框架

论文的基本结构

如何选择合理的结构

划重点

各部分写作要点

易忽略重点解析

举例子

稿件中的实例分析

借鉴、改进

科技论文的撰写



原创论文的常见结构 (AIMRaD)

JOURNAL OF
MEDICAL VIROLOGY

Received: 25 January 2020
DOI: 10.1002/jmv.25688

RESEARCH ARTICLE

Free Access

The 2019
new coronavirus
for virus

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1 | INTRODUCTION

The family *Coronaviridae* contains
stranded RNA viruses
virologically known to cause
diseases in humans.^{1,2} In 2003, a
coronavirus outbreak,^{3,4} recently, a new coronavirus 2019-nCoV has emerged^{5,6} in the region of Wuhan (China) as a cause of severe respiratory infection in humans. Since December 2019, different cases of pneumonia of unknown origin associated with permenance at the Wuhan market in China have been reported.^{7,8} A new coronavirus, named 2019-nCoV, belonging to the *Orthocoronavirinae* subfamily, distinct

Silvia Angeletti and Massimo Ciccozzi contributed equally to this study.

The 2019-new coronavirus epidemic: Evidence for virus evolution

Domenico Benvenuto, Marta Giovanetti, Alessandra Ciccozzi, Silvia Spoto, Silvia Angeletti, Massimo Ciccozzi

First published: 29 January 2020 | <https://doi.org/10.1002/jmv.25688> | Citations: 250

Silvia Angeletti and Massimo Ciccozzi contributed equally to this study.

SECTIONS

PDF

TOOLS

SHARE

Abstract

There is a worldwide concern about the new coronavirus 2019-nCoV as a global public health threat. In this article, we provide a preliminary evolutionary and molecular epidemiological analysis of this new virus. A phylogenetic tree has been built using the 15 available whole genome sequences of 2019-nCoV, 12 whole genome sequences of 2019-nCoV, and 12 highly similar whole genome sequences available in gene bank (five from the severe acute respiratory syndrome, two from Middle East respiratory syndrome, and five from bat SARS-like coronavirus). Fast unconstrained Bayesian approximation analysis shows that the nucleocapsid and the spike glycoprotein have some sites under positive pressure, whereas homology modeling revealed some molecular and structural differences between the viruses. The phylogenetic tree showed that 2019-nCoV significantly clustered with bat SARS-like coronavirus sequence isolated in 2015, whereas structural analysis revealed mutation in Spike Glycoprotein and nucleocapsid protein.

From 2019-nCoV has emerged^{5,6} the transmission of the 2019-nCoV in distinct from SARS virus, probably transmitted

Although prompt diagnosis and patient isolation are the hallmarks for initial control of this new epidemic, molecular epidemiology, evolutionary models, and phylogenetic analysis can help estimate genetic variability and the evolutionary rate, which in turn have important implications for disease progression as

DG

In this short report,
2019-nCoV and identify
sure in distinct regions

DS

sequences have been
aligned (9) and GenBank
dataset has been built
two sequences for the
and five highly similar
percentage of similarity
ent search tool (<https://www.ncbi.nlm.nih.gov/blast/>)
duplicated sequences
The dataset including
ple sequence alignment
dit program v2.0.5.¹⁰
employed for the
arent phylogenetic hy-
gen model of evolution
ring the probabilities of
e best-fitting nucleotide
st software.¹¹ ML tree
reversible plus gamma
volutionary model using

(<http://www.datamonkey.org/>)
negative selection. For
ed fast, unconstrained
l allowed us to infer the
ic diversifying selection
fy episodic selection at
nt positive or negative
^{12,13}

elying on the website
seen searched and vali-
SwissModel environ-
been validated using the
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uctural variability of the
ir sites under selection
lied to the sequence of

1. Drosten C, Günther S, Preiser W, et al. Identification of a novel cor-
onavirus associated with severe acute respiratory syndrome. *N Engl
J Med*. 2003;348:1967-1976.

2. Chen Y, Liu Q, Guo D. Emerging coronaviruses: genome structure,
replication, and pathogenesis. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25581>

3. Chan JF-W, Yuan S, Kok K-H, et al. A familial cluster of pneumonia
among children associated with a new coronavirus of probable
person-to-person transmission – Hong Kong, 2003. *Lancet*. 2003. [https://doi.org/10.1016/S0140-6736\(03\)01345-9](https://doi.org/10.1016/S0140-6736(03)01345-9)

4. Huang C, Wang Y, Li X, et al. Clinical features of patients infected with
the 2019 novel coronavirus in Wuhan, China. *Lancet*. 2020. [https://doi.org/10.1016/S0140-6736\(20\)30183-5](https://doi.org/10.1016/S0140-6736(20)30183-5)

4 | DISCUSSION

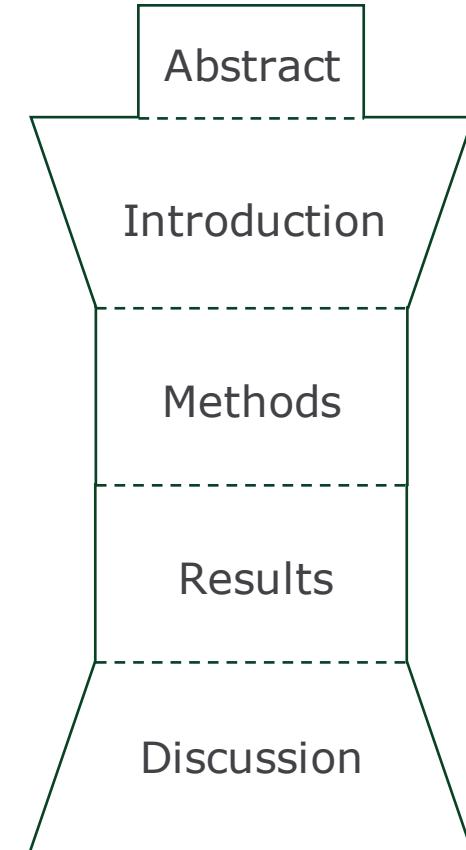
The data reported above show that the new 2019-nCoV significantly clustered with a sequence from the bat SARS-like coronavirus isolated in 2015. Moreover, in the phylogenetic tree, these two sequences are separated from the other bat SARS-like coronavirus sequences, suggesting that this bat SARS-like coronavirus is homologous and genetically more similar to the 2019-nCoV than to the other sequences of Bat SARS-like coronavirus. This supports the hypothesis that the transmission chain began from the bat and reached the human. All other genomic sequences represented in the phylogenetic tree, also including SARS and MERS coronavirus, clustered separately, thus excluding the fact that the virus involved in the actual epidemic could belong to these subgenuses. The structural analysis of two important viral proteins, the nucleocapsid and the spike-like nucleoprotein (protein S), confirmed the significant similarity of the new coronavirus with the bat-like SARS coronavirus and its difference from SARS coronavirus.

From the selective pressure and structural analysis, mutations of surface proteins, as the spike protein S, and of nucleocapsid N protein conferring stability to the viral particles have been shown. The viral spike protein is responsible for virus entry into the cell after by binding to a cell receptor and membrane fusion, two key steps in viral infection and pathogenesis. The N protein is a structural protein involved in virion assembly, playing a pivotal role in virus transcription and assembly efficiency. Mutation of these proteins could determine two important characteristics of the coronavirus isolated during the 2019-nCoV epidemic: a higher ability to infect and enhanced pathogenicity than the bat-like SARS coronavirus but lower pathogenicity than SARS coronavirus. These features can explain the 2019-nCoV zoonotic transmission and its initial lower severity than SARS epidemic. These results do not exclude the fact that further mutation could be positive selective
CONFIRMED BY RUMAN ANALYSIS, SUGGESTING THAT THE REGION COULD BE HIGHLY CONSERVED.

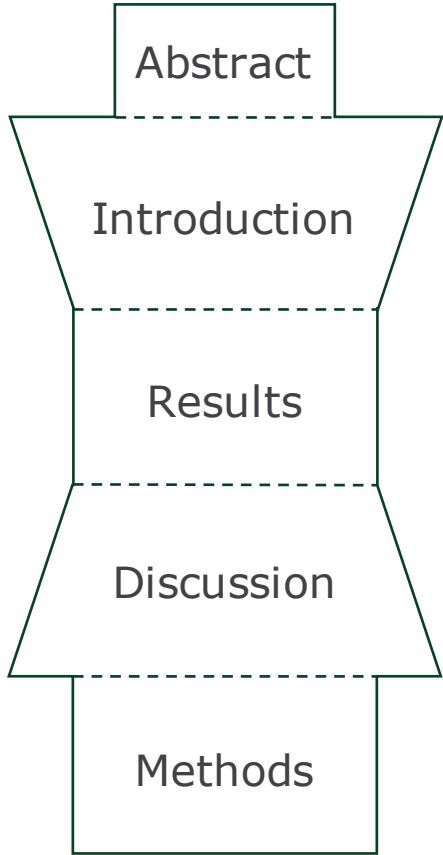
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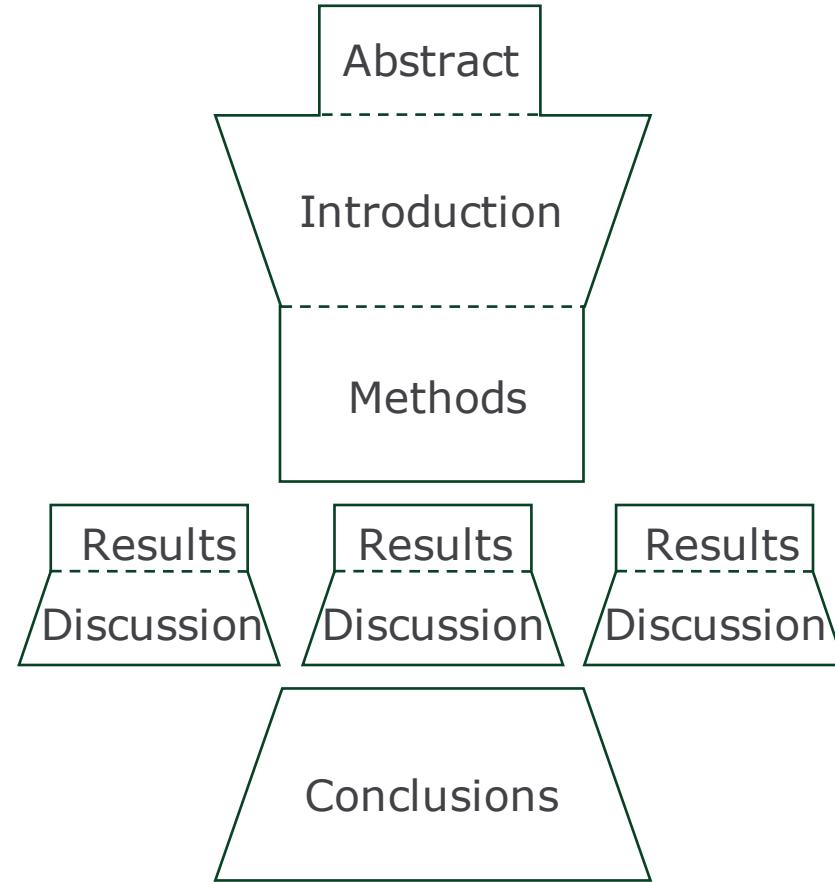
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原创论文的其他结构



AIRDaM



AIM(RaD)C

原创论文的各部分要点

题目/标题 Title

作者和单位 Author and Affiliation

摘要与关键词 Abstract and Key Words

引言 Introduction

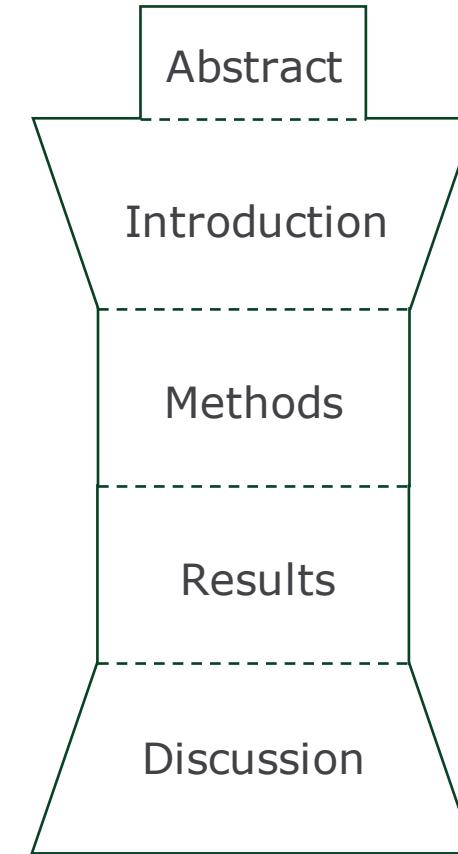
材料与方法 Methods and materials

结果 Results

讨论 Discussion

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文章标题

如何运用ABC原则撰写文章标题



标题



本篇文章要传达的最主要的信息



避免过多细节&无用的字眼



关键词！关键词！关键词！

标题的句式

名词短语式

由名词性短语构成，有效强调关键词

e.g., *Ecological responses to recent climate change*

强调研究主题和研究对象

主副式

将标题分割为两个或多个名词短语，用于希望表达的内容层次较多时

e.g., *One-dimensional nanostructures: synthesis, characterization, and application*

主标题强调研究对象，副标题强调研究目的

陈述句式

直接在题目中给出完整的研究结论

e.g., *Acrylamide is formed in the Maillard reaction*

提出结论，在文章中加以证明

疑问句式

使用探讨性的疑问句来引发读者兴趣

e.g., *Which way for genetic-test regulation?*

提出问题，在文章中回答

标题 vs 标题

Genetic vaccines against Ep-CAM break tolerance to self in a limited subset of subjects: Initial identification of predictive biomarkers

Divergent effects of IL-12 and IL-23 on the production of IL-17 by human T cells

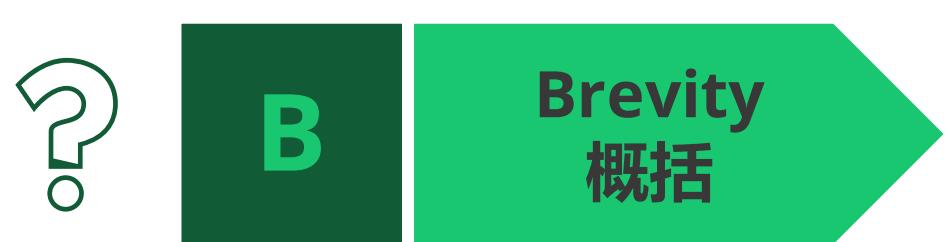
引用: 7 次

引用: 177 次

标题 vs 标题

Genetic vaccines against Ep-CAM break tolerance to self in a limited subset of subjects: Initial identification of predictive biomarkers

主副式



主标题内容不够概括，语义分散
副标题与主标题之间逻辑不够连贯

标题 vs 标题

Divergent effects of IL-12 and IL-23 on the production of IL-17 by human T cells

名词短语式



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摘要

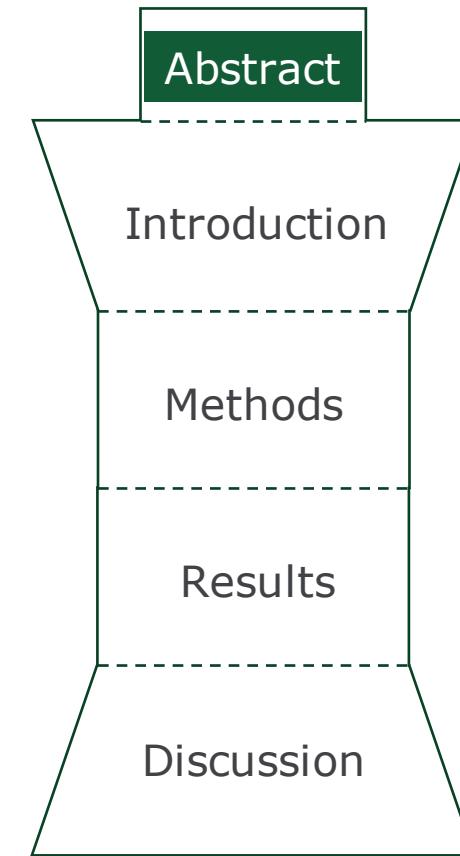
摘要的撰写原则及实例



摘要——关键词！关键词！关键词

摘要是整篇文章的高度浓缩（150-300字）：

- 背景
- 目标/假设
- 简述方法
- 主要结果
- 结论及意义



撰写摘要的原则



简短

注意摘要的字数限制



完整

摘要需涵盖文章的全部部分 (IMRaD)



满足读者需求

撰写摘要是需考虑读者希望从摘要中获得什么信息



一致性

与正文内容保持一致——不提及正文中没有提及的信息



“ ” 概括

从目标导向——摘要是“摘取要点”

摘要

常见问题

- **背景介绍**

- 太长/没有提及

- **目标/假设**

- 假设是对整个研究意义和预期成效的阐述，但容易被忽略

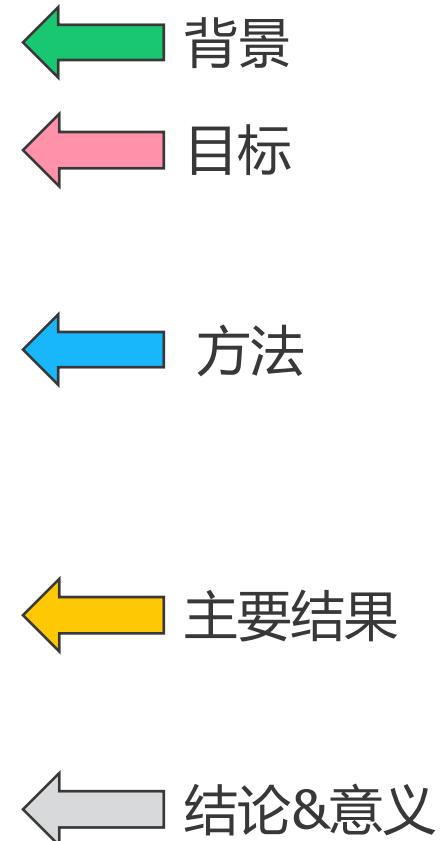
- **结论**

- 容易把结果和结论混为一谈使读者无法从摘要中获取关于研究的有效信息

摘要：优秀范例

Abstract

Dietary fiber (DF) has gained a great attention owing to its potential health benefits. *Agrocybe cylindracea* is an edible fungus with high protein and low fat contents, which is also an enriched source of DF. However, limited study has been conducted on optimizing the conditions of *A. cylindracea*-derived DF extraction and modification as well as characterizing its properties. In this study, ultrasound-assisted enzymatic method for DF extraction was optimized as the following conditions: liquid material ratio of 29 ml/g, α -amylase concentration of 1.50%, protamex concentration of 1.20%, and ultrasonic power of 150 W, which improved the DF extraction yield to 37.70%. Moreover, high temperature modification (HTM) and cellulase modification (CEM) were applied to modify *A. cylindracea*-derived DF. The results showed that HTM had more potential capacity in converting insoluble DF into soluble DF, and DF with HTM exhibited more advantages in its physicochemical properties than DF with CEM. The DF with both HTM and CEM showed antioxidant activities, reflected by the increased reducing power as well as DPPH radical, hydroxyl radical, and ABTS⁺ scavenging capabilities in vitro. These findings could offer a reference for the extraction, modification, and characterizing various properties of DF from *A. cylindracea*, which would establish the foundation for the comprehensive application of fungi-derived DF.



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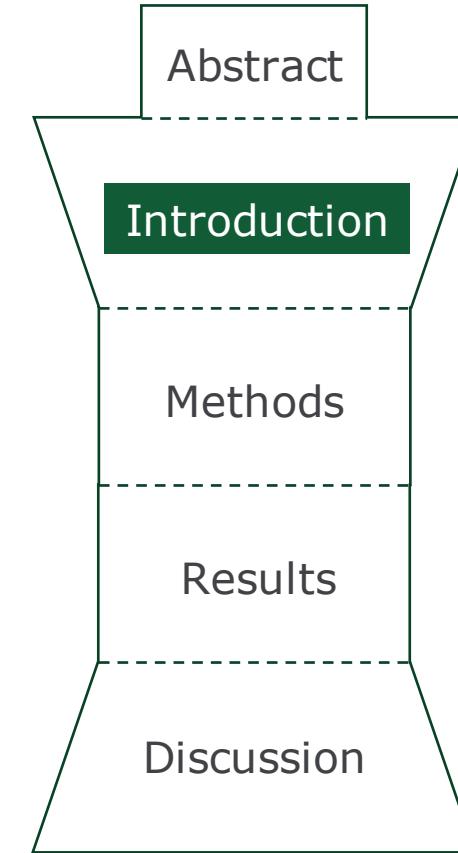
引言

强调研究的意义

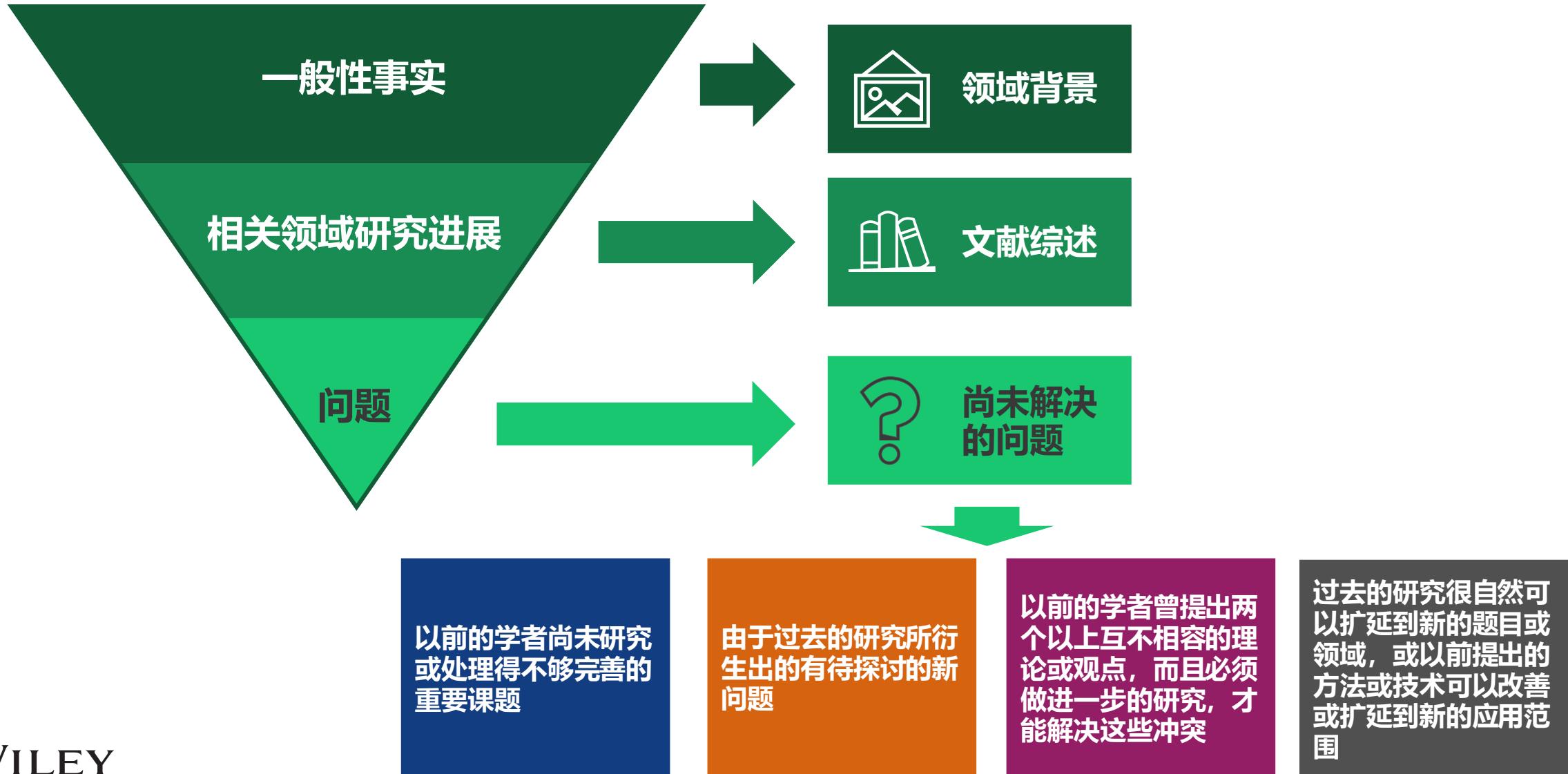


引言

- 整体研究的背景
- 详细描述研究的结果与其他相关的研究
- 阐述还未解决的问题
- 描述开展此研究的原因以及目的
- 让非此领域的专家也可以理解研究的基本原理



引言——研究背景、研究问题



引言——阐述研究目的

研究目的是将研究任务具现化

Aims

研究中希望实现的宏观目的

Objectives

研究中将达成的数条具体任务

重要性 创新性

引言

常见问题

- **背景**

- 主次不分

- **研究问题**

- 没有点出该领域尚未解决的问题-读者看不到研究的意义何在

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材料与方法

为读者提供可复现实验的信息



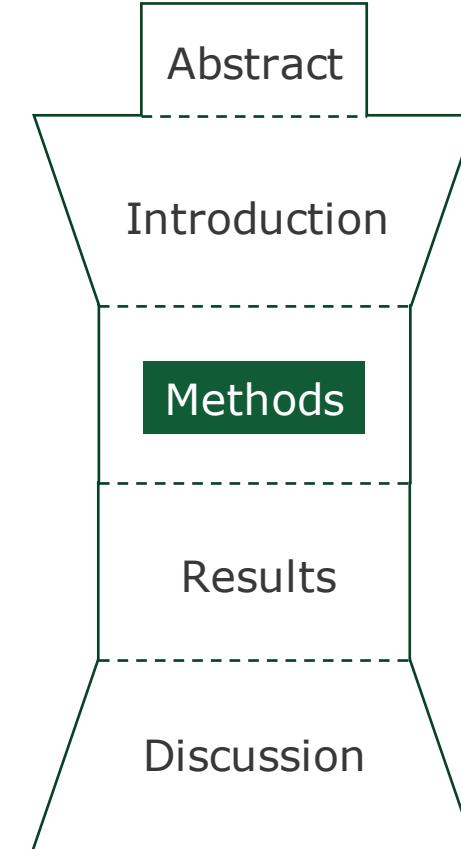
材料与方法

- **可信/可重复:**

- 提供充足的信息，使别的研究人员可以重复你的实验及结果
- 提供实验的平行/重复
- 用到的试剂要提供准确信息（比如厂商名称、产品名等）
- 提供统计学方法

- **不要复制！**

- **注意细节：只提及必要的材料与方法**



材料与方法

常见问题

统计学分析

One-way ANOVA was used in this study.



One-way ANOVA was used **on XXX study between samples**. Significant differences between samples were assessed by **Fisher's LSD pairwise comparison**, and significance level was set **at $p \leq 0.05$** . One-way ANOVA was carried out **using XLSTAT software (2012, Addinsoft, Paris, France)**.

材料与方法

常见问题

统计学分析的表述

2.6 Statistics

Data are expressed as mean±standard error mean (SEM) from at least 3 independent experiments. Kaplan-Meier curves were used for analysis of survival followed by Log-rank (Mantel-Cox) test. Statistical analysis, other than for RNA-seq results, was performed using Student's t-test with Welch's correction (if applicable). For multiple comparisons, one-way ANOVA followed by Tukey multiple comparisons analysis between the group of interest and all other groups was used. Volcano plot and differential expression analysis of miRNAs were generated using the edgeR Bioconductor package in R. Differences between the experimental groups were considered statistically significant (*) or highly significant (**) (***)¹, when the p-value was <0.05, <0.01, or <0.001, respectively. Graphs were generated using GraphPad Prism software version 6.0 (GraphPad, La Jolla, CA).

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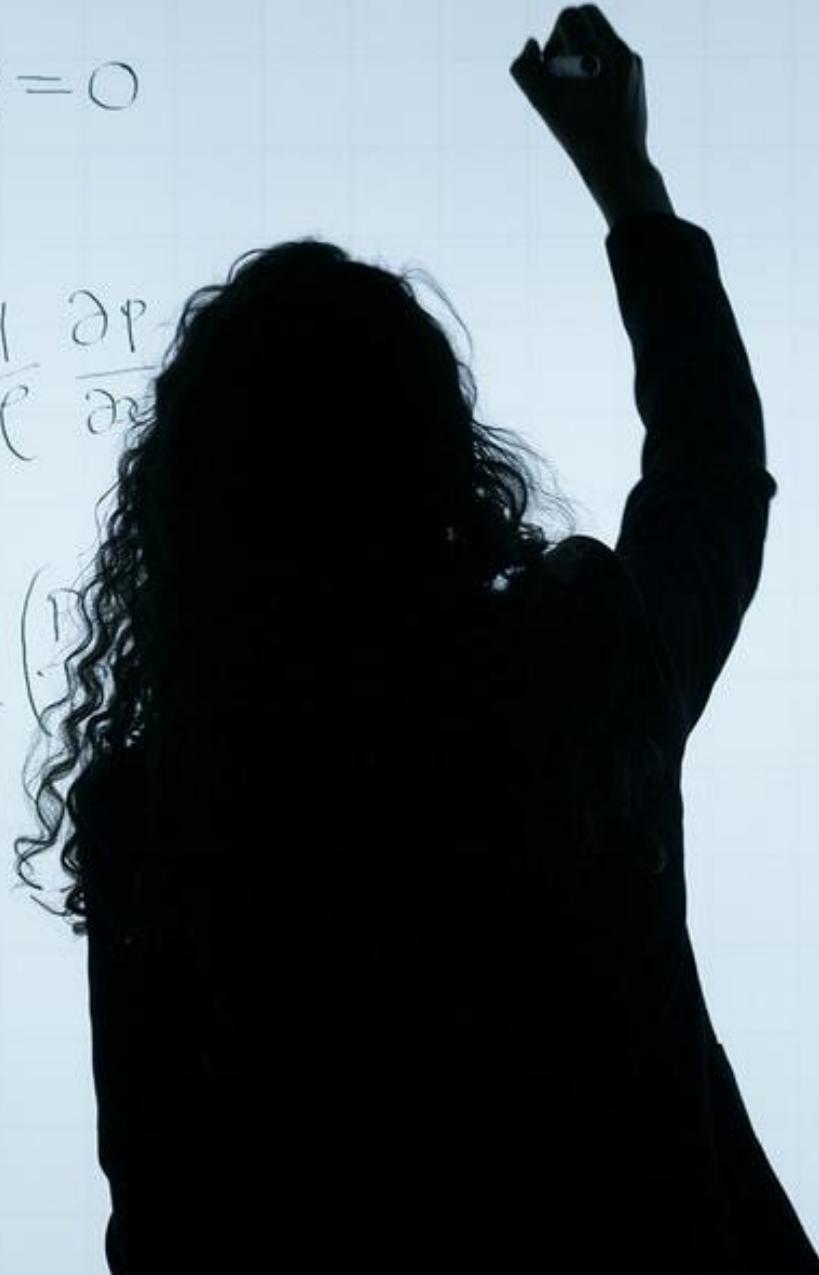
结果

展示研究中的发现

$$\frac{\partial}{\partial x} (e^u) = 0$$

$$u \frac{\partial u}{\partial x} = -\frac{1}{c} \frac{\partial p}{\partial x}$$

$$u \left(\frac{\partial u}{\partial x} \right) + u \frac{\partial}{\partial x} \left(\frac{\partial u}{\partial x} \right)$$



结果

- **逻辑**

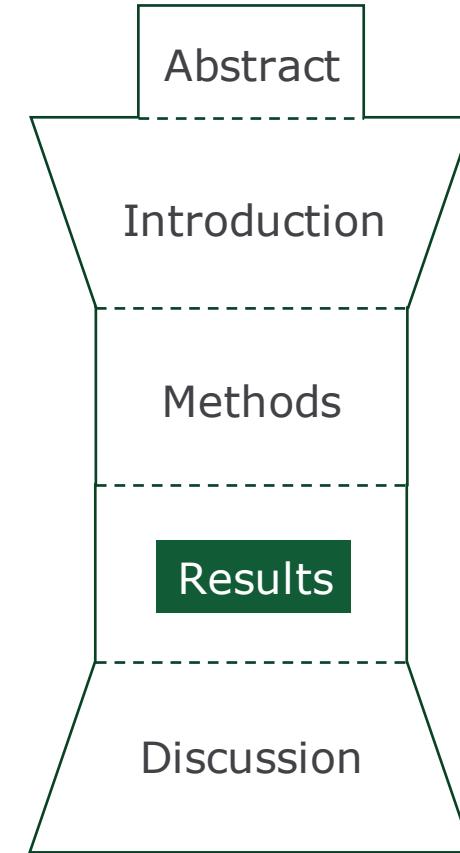
- 以逻辑和清晰的方式，展示和解释实验

- **关注细节**

- 务必要引用**每个/所有**图表并描述实验结果

- **可信/可重复**

- 提供**统计分析**以及清晰地阐述重要的数据



结果

常见问题

- 结果的表述要一致且逻辑清晰

Up to 2300 cars an hour use each lane of the M4 while figures show that Victoria Rd is flooded with more than 93,000 vehicles a day.

—Daily Telegraph (18 April 2001)

- 数据及数据单位要一致
 - 保留有效数字 vs 精确到小数点后
 - 使用国际标准单位/期刊规定单位制

结果——数据单位

Kind	Sample	5'-GMP g/ kg (L)	5'-IMP g/ kg (L)	5'-AMP g/ kg (L)	Asp g/ kg (L)	Glu g/ kg (L)
1		841 ± 15.6 ^{fgh}	981 ± 48.7 ^{cd}	2710 ± 264 ^{gh}	3001 ± 362 ^{cd}	1025 ± 141 ^d
		1735 ± 76.5 ^d	27317 ± 1721 ^b	4017 ± 139 ^e	962 ± 240 ^{def}	2010 ± 587 ^d
		1347 ± 12.7 ^e	2050 ± 192 ^c	2190 ± 49.0 ^{hi}	5120 ± 282 ^c	50500 ± 2433 ^c
		68.4 ± 5.2 ⁱ	N.D.	153 ± 0.51 ^{2j}	61.7 ± 3.00 ^f	278 ± 8.43 ^d
		1072 ± 2.39 ^f	32343 ± 717 ^a	2862 ± 0.678 ^{fg}	91.3 ± 8.59 ^{ef}	97.5 ± 11.3 ^d
		3549 ± 45.3 ^b	N.D.	7262 ± 201 ^c	2450 ± 580 ^{de}	5277 ± 1498 ^d
		4702 ± 72.4 ^a	1676 ± 275 ^{cd}	41177 ± 301 ^a	880 ± 29.1 ^{def}	5430 ± 72.2 ^d
		N.D.	362 ± 132 ^{cd}	3514 ± 45.9 ^{ef}	62284 ± 1657 ^a	219533 ± 12325 ^a
		2572 ± 249 ^c	1734 ± 250 ^{cd}	2991 ± 6.50 ^{fg}	336 ± 146 ^{ef}	85000 ± 4390 ^b
		86.1 ± 0.60 ⁷ⁱ	29.7 ± 3.20 ^d	N.D.	N.D.	1924 ± 20.3 ^d
2		644 ± 9.05 ^h	555 ± 13.9 ^{cd}	9382 ± 161 ^b	32827 ± 1573 ^b	62302 ± 3282 ^c
		N.D.	N.D.	1640 ± 19.0 ⁱ	165 ± 64.1 ^{ef}	1257 ± 600 ^d
		974 ± 41.2 ^{fg}	N.D.	2591 ± 163 ^{gh}	968 ± 186 ^{def}	2248 ± 435 ^d
3		741 ± 27.7 ^{gh}	N.D.	4760 ± 417 ^d	141 ± 74.4 ^{ef}	2834 ± 1085 ^d

结果

常见问题

结果的表述没有统计学分析的支持

Example:

The intensity of A was increased from 2.0 to 2.5 by adding 1 mL of 0.2 mg/mL B.

↓ $p = 0.01$

Modified:

The intensity of A was increased **significantly** from 2.0 to 2.5 by adding 1 mL of 0.2 mg/mL B ($p = 0.01$).

从2.0到2.5是不是显著 (significant) 的增加?

if

$p < 0.05$, 可以说 significant increase, 并给出 p 值



if

p 接近 0.05 (e.g. $p=0.051$), 可以说 “the intensity of A has an increasing trend when 0.2 mg/mL of B was added”

if

p 远高于 0.05 (e.g. $p=0.12$), 不可以说加入 B 后 A 有增加

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讨论

总结、升华

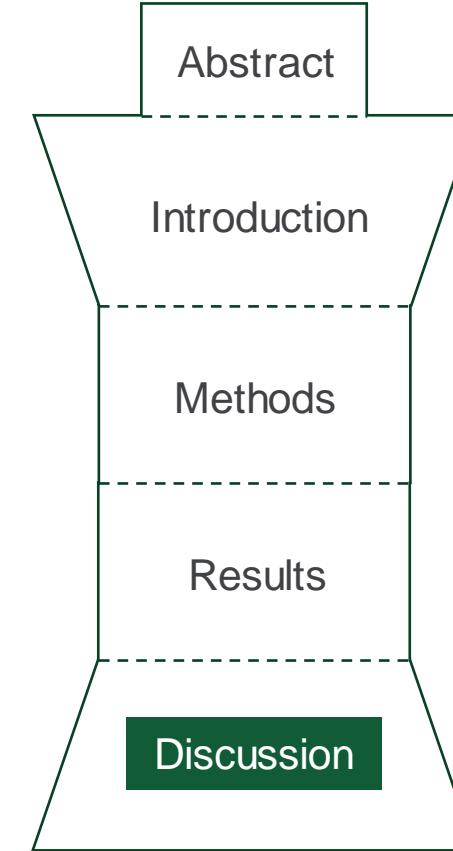


讨论——写作要点

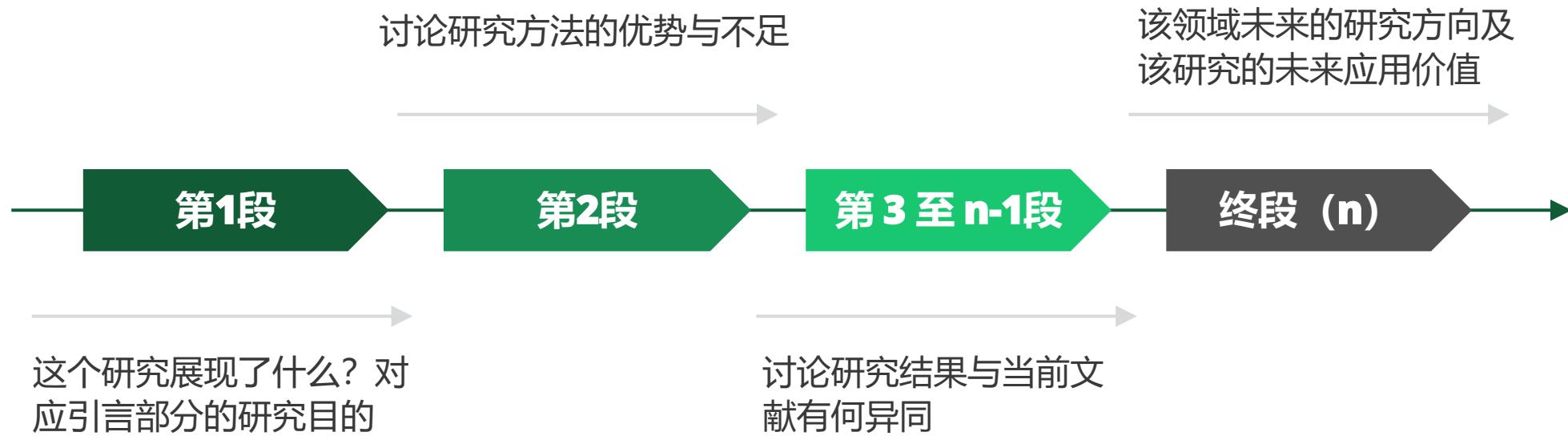
- 快速总结研究发现
- **不要**重复“结果”
- 结果需要结合更广的背景、范围展开讨论
- 结果是否否定了前人的研究？为什么？
- 结论是如何促进这一领域进展的？
- 研究的局限性，对未来研究的影响？

实事求是，不要过度解读，也不要妄自菲薄。

撰写“讨论”是一种艺术，不要吝于请教他人寻求帮助！



讨论——推荐结构



讨论

常见问题一对比

- 与其他文章对比要言之有物，对比要具体
- 不仅要对比**是否一致**，也要分析**是否一致的原因**
- 如果研究领域缺乏文章可对比，选择相近的topics：
 - 同样研究主题的**不同研究对象**

讨论

常见问题—文献引用

讨论中不要漏掉重要文献

审稿人的观点：



作者可能并不了解该研究领域

- 实验设计可能需要改进



作者可能故意隐瞒相关研究

- 该研究结果可能与文献相反，但作者无法解释
- 该研究并非原创

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图表

独立展示数据信息



图表——要点

图表需要在没有文章的辅助下也可以独立的展现其所表达的完整内容

- **布局**

- 清晰，准确

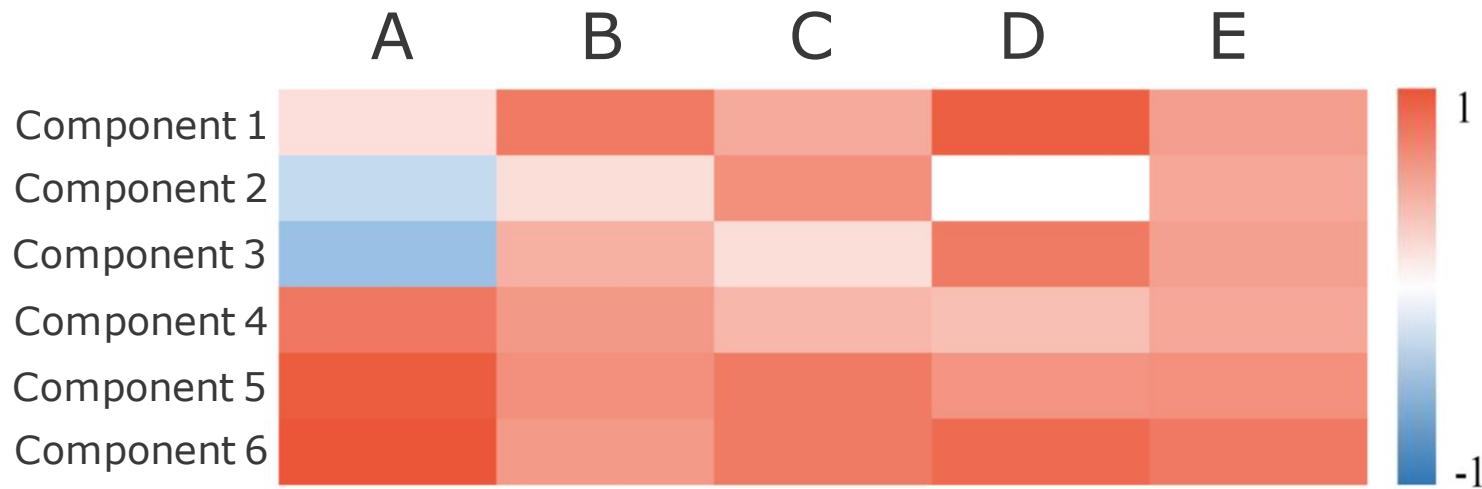
- **图表的标注**

- 表明图表的含义（什么数据分析所得），各简称的意义，实验进行了几次重复，etc.

- **一致性**

- 文章中的所有图表所用的简称/缩写需要一致

图表一准确性



Pearson Correlation

分析两组数据之间的相关性

r : 相关系数

p : 显著性

Fig. 1 Heatmap based on the Pearson correlation coefficients between results and each component. Values close to 0 and 1 (-1) correspond to low and high correlation of result, respectively. A represented XXX. B represented XXX. C represented XXX. D represented XXX. E represented XXX.

图表一准确性

Table 6.2: Pearson's correlation coefficient (r) of 16 amino acids and 2-AP in 13 fragrant rice samples.

	Pro	GABA	Glu	Ala	Gly	Val	Leu	Ile	Thr	Ser	Asn	Asp	Phe	Lys	Tyr	Trp	2-AP
proline	—	0.718**	0.490 ^{nc}	0.914***	0.860***	0.809***	0.064 ^{nc}	0.408 ^{nc}	0.912***	0.728**	0.558*	0.176 ^{nc}	0.369 ^{nc}	0.730**	0.192 ^{nc}	0.371 ^{nc}	0.123 ^{nc}
GABA	—	—	0.829***	0.775**	0.907***	0.425 ^{nc}	-0.285 ^{nc}	-0.060 ^{nc}	0.703**	0.963***	0.845***	0.434 ^{nc}	0.043 ^{nc}	0.801**	-0.144 ^{nc}	0.276 ^{nc}	-0.075 ^{nc}
glutamic acid	—	—	—	0.663*	0.767**	0.267 ^{nc}	-0.537 ^{nc}	-0.404 ^{nc}	0.573*	0.823***	0.895***	0.845***	-0.226 ^{nc}	0.678*	-0.339 ^{nc}	0.208 ^{nc}	0.002 ^{nc}
alanine	—	—	—	—	0.950***	0.780**	-0.126 ^{nc}	0.228 ^{nc}	0.931***	0.760**	0.790**	0.420 ^{nc}	0.214 ^{nc}	0.772**	0.096 ^{nc}	0.432 ^{nc}	-0.101 ^{nc}
glycine	—	—	—	—	—	0.628*	-0.237 ^{nc}	0.096 ^{nc}	0.877***	0.895***	0.874***	0.425 ^{nc}	0.109 ^{nc}	0.817***	-0.038 ^{nc}	0.341 ^{nc}	-0.164 ^{nc}
valine	—	—	—	—	—	—	0.424 ^{nc}	0.686**	0.857***	0.435 ^{nc}	0.389 ^{nc}	0.138 ^{nc}	0.673*	0.726**	0.531 ^{nc}	0.738**	-0.061 ^{nc}
leucine	—	—	—	—	—	—	—	0.837***	0.116 ^{nc}	-0.210 ^{nc}	-0.455 ^{nc}	-0.565*	0.925***	0.026 ^{nc}	0.894***	0.592*	0.189 ^{nc}
isoleucine	—	—	—	—	—	—	—	—	0.362 ^{nc}	-0.052 ^{nc}	-0.228 ^{nc}	-0.547 ^{nc}	0.885***	0.207 ^{nc}	0.802**	0.553*	-0.024 ^{nc}
threonine	—	—	—	—	—	—	—	—	0.766**	0.665*	0.335 ^{nc}	0.421 ^{nc}	0.838***	0.272 ^{nc}	0.561*	-0.017 ^{nc}	
serine	—	—	—	—	—	—	—	—	—	0.797**	0.447 ^{nc}	0.102 ^{nc}	0.816***	-0.087 ^{nc}	0.309 ^{nc}	0.017 ^{nc}	
asparagine	—	—	—	—	—	—	—	—	—	—	0.680 ^{nc}	-0.147 ^{nc}	0.707**	-0.252 ^{nc}	0.259 ^{nc}	-0.271 ^{nc}	
aspartic acid	—	—	—	—	—	—	—	—	—	—	—	-0.357 ^{nc}	0.399 ^{nc}	-0.371 ^{nc}	0.176 ^{nc}	0.046 ^{nc}	
phenylalanine	—	—	—	—	—	—	—	—	—	—	—	—	0.323 ^{nc}	0.932***	0.771**	0.188 ^{nc}	
lysine	—	—	—	—	—	—	—	—	—	—	—	—	—	0.120 ^{nc}	0.618*	-0.244 ^{nc}	
tyrosine	—	—	—	—	—	—	—	—	—	—	—	—	—	—	0.747***	0.202 ^{nc}	
tryptophan	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	-0.069 ^{nc}	
2-AP	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, nc: no correlation, ≥ 0.05

图表一标注

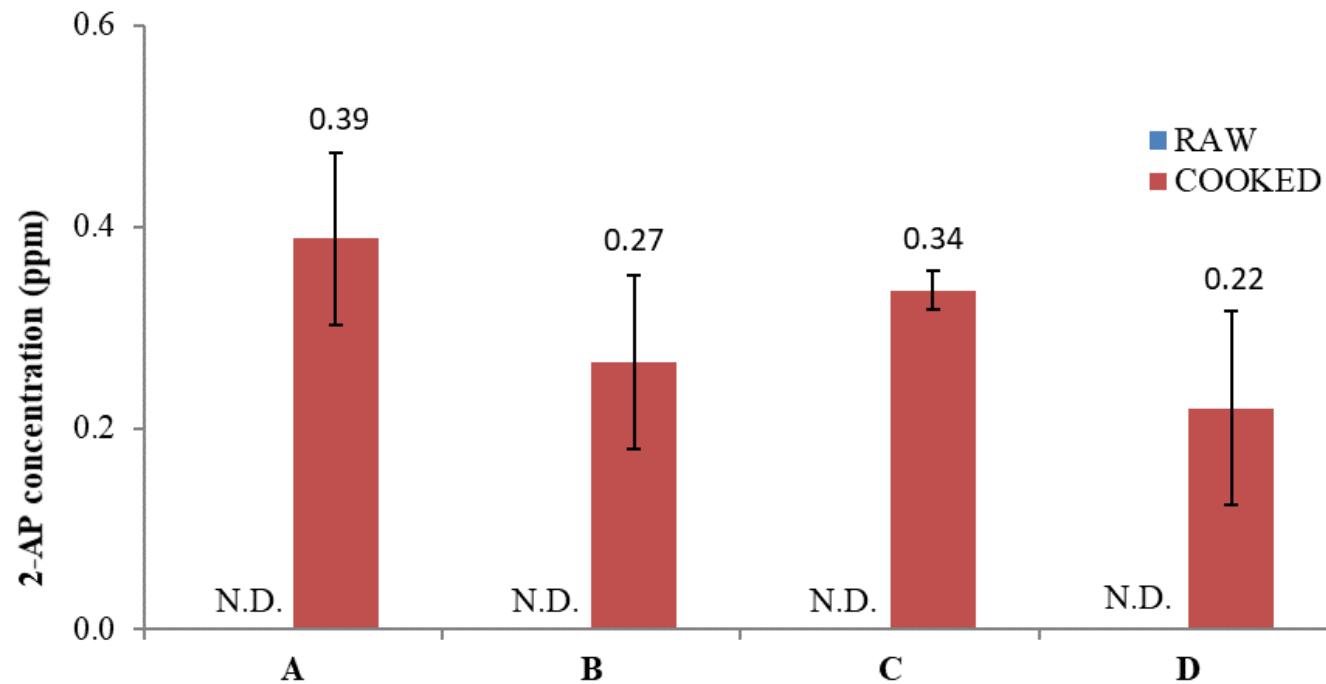
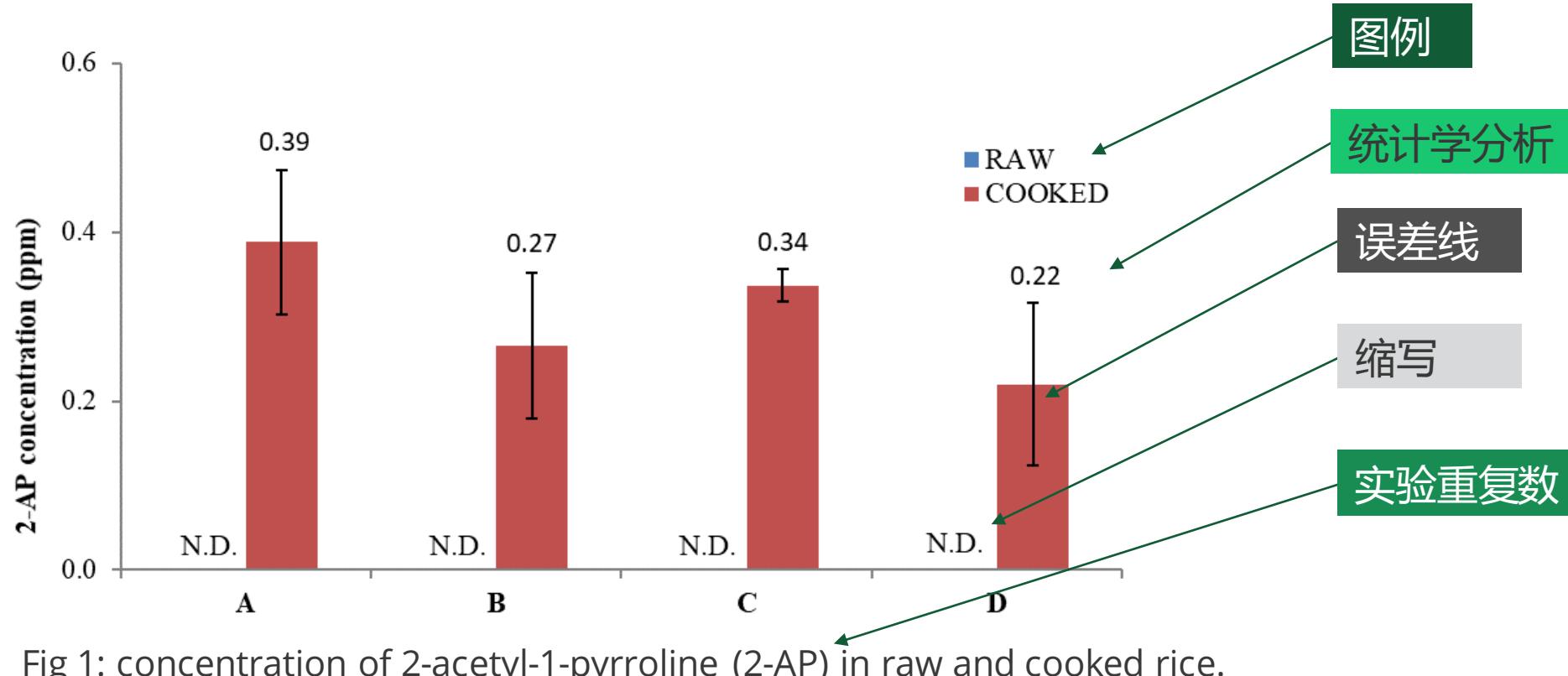


Fig 1: concentration of 2-acetyl-1-pyrroline (2-AP) in raw and cooked rice.

图表一标注



图表一标注

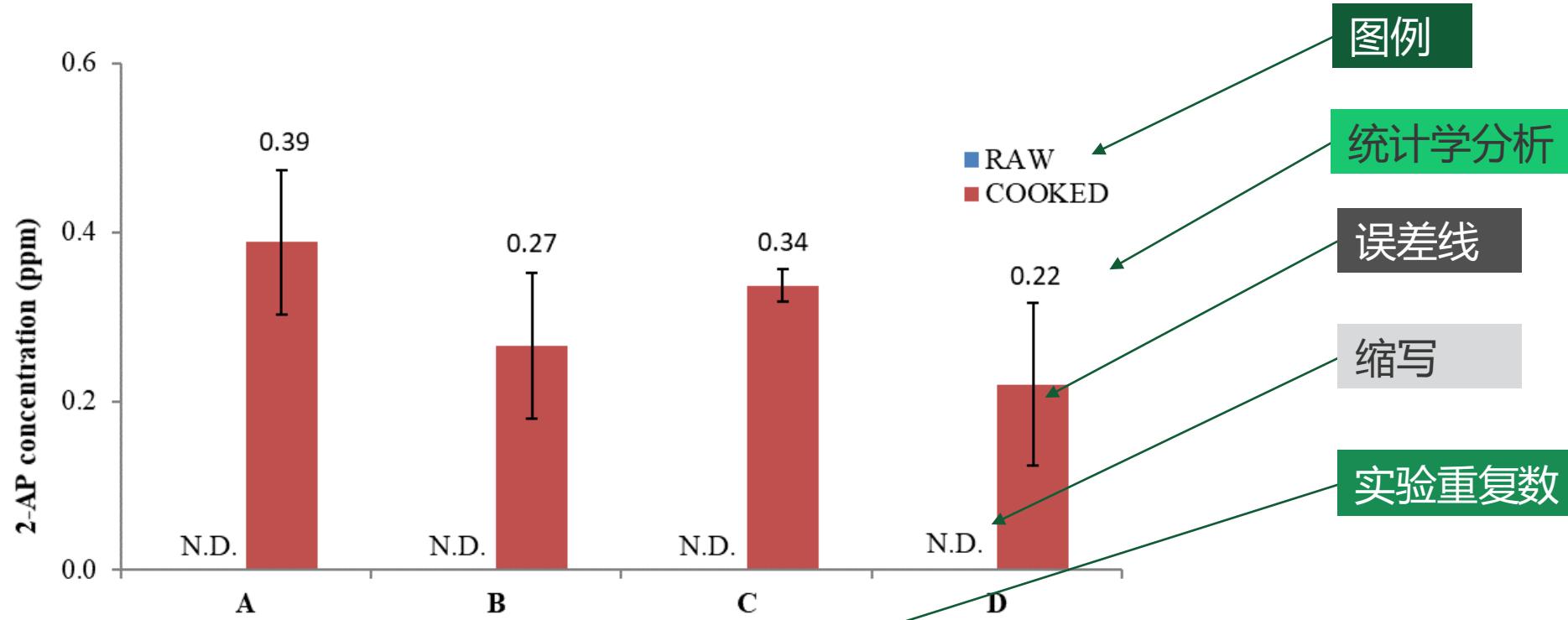


Fig 1: concentration of 2-acetyl-1-pyrroline (2-AP) in raw and cooked rice ; **blue bars represent raw rice, red bars represent cooked rice**

图表一标注

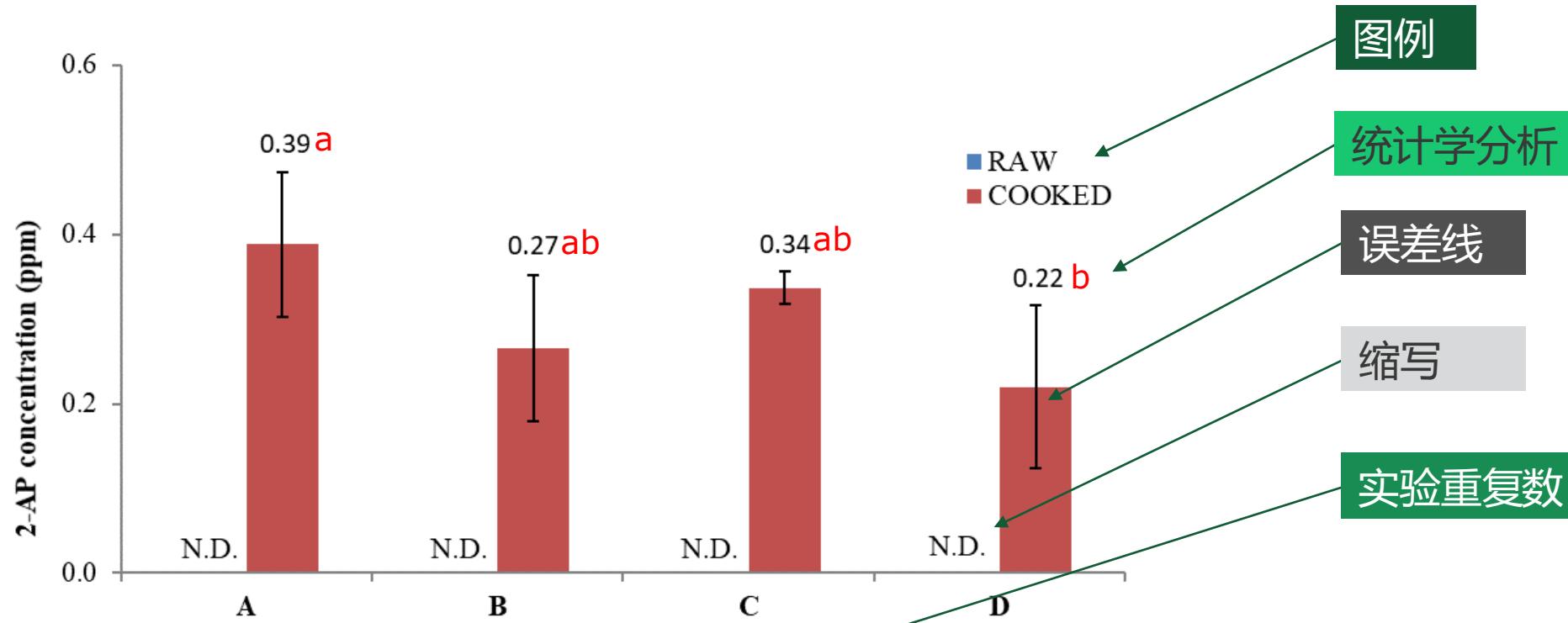


Fig 1: concentration of 2-acetyl-1-pyrroline (2-AP) in raw and cooked rice ; blue bars represent raw rice, red bars represent cooked rice; **bars not sharing the common letter are significant different ($p < 0.05$)**

图表一标注

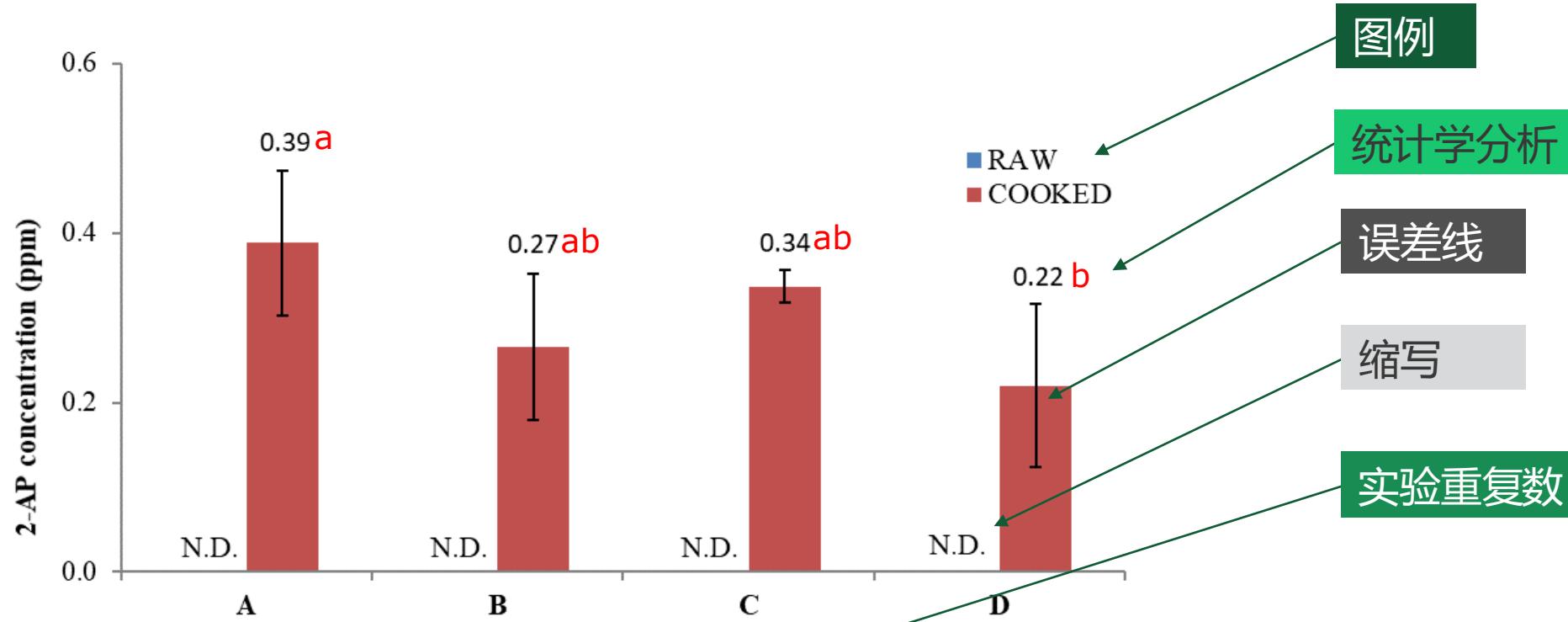


Fig 1: concentration of 2-acetyl-1-pyrroline (2-AP) in raw and cooked rice ; blue bars represent raw rice, red bars represent cooked rice; bars not sharing the common letter are significant different ($p < 0.05$); **error bar represents standard deviations of triplication of experiment.**

图表一标注

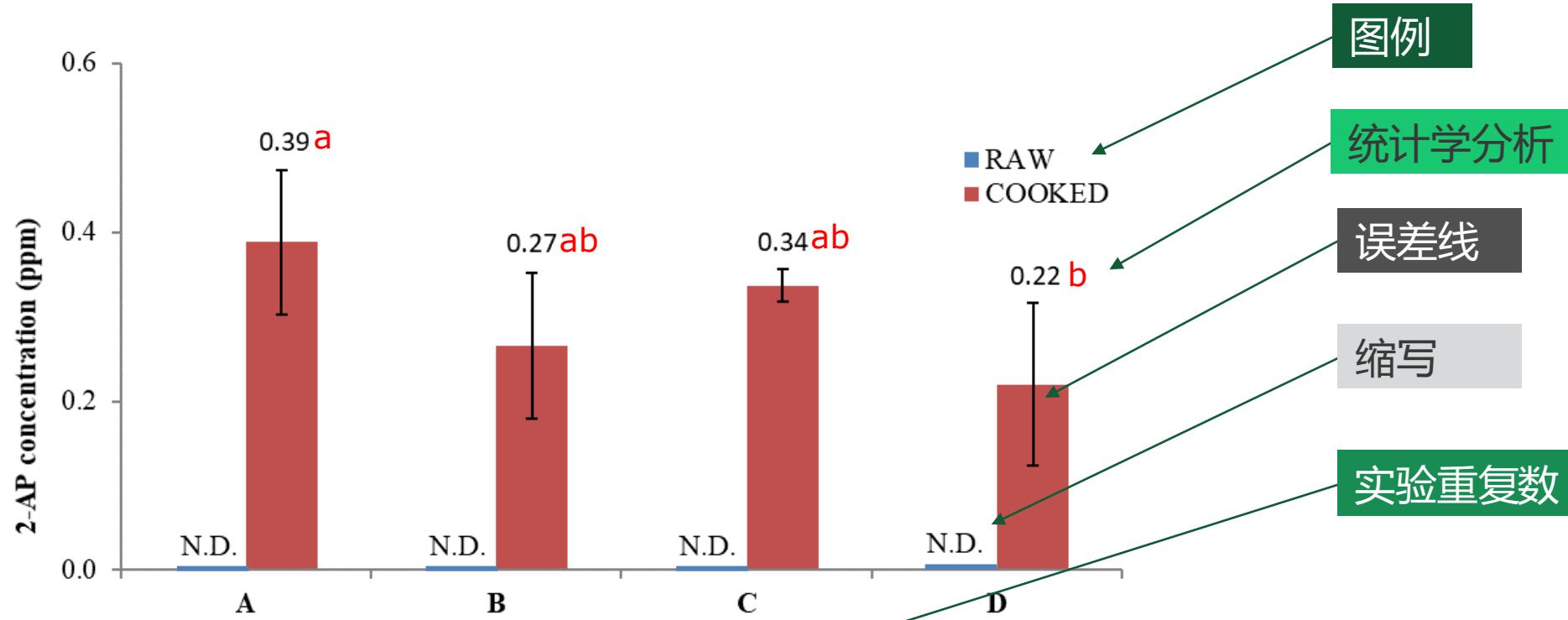


Fig 1: concentration of 2-acetyl-1-pyrroline (2-AP) in raw and cooked rice ; blue bars represent raw rice, red bars represent cooked rice; bars not sharing the common letter are significant different ($p < 0.05$); error bar represents standard deviations of triplication of experiment. **N.D.: the concentration lower than LoD of instrument (10^{-5} ppm).**

图表——无效表格/数据

- 图表中列举的大量的信息，然而在文章中没有提及或仅部分提及
- 注意期刊要求，是否有图表**数量限制**

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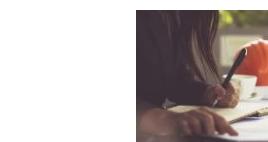
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