

# 評估 SARS-CoV-2 複本感染所造成之 piRNA 表現暨基因體 穩衡的改變

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## 摘要:

細胞或外泌體中 piRNA 表達的改變, 除了能夠改變基因的表達外, 現亦被指出其能維護基因體的穩定性, 進而衍生出疾病更進一步之進程。各類外界能改變 piRNA 表達的因子中, 病毒因其來源及序列相似之特性, 亦被指出其能影響 piRNA 之表達。適以, 我們將借由 SARS-CoV-2 複本的表達來瞭解其對 piRNA 的調節, 和對基因體穩衡的影響。我們的合作者在人類肝癌細胞 T7-Huh7 中表達 SARS-CoV-2 複本以模擬受 SARS-CoV-2 感染的細胞, 並證實了 piRNA 交互作用蛋白, PIWIL4, 於複本表達前後的存在, 進一步, 我們計算出與複本可能有直接作用的 piRNAs, 並篩選複本表達前後具明顯改變的 piRNAs。而由普查已發表之基因序列, 我們發現了 SARS-CoV-2 複本的表達實際上是限制了基因變異的產生, 而其對基因體穩衡之影響則待更進一步闡明。先前的研究證明, 在小鼠細胞內剔除 PIWIL2 會降低外泌體對 SARS-CoV-2 的免疫作用調節, 我們則證明相對於 PIWIL2, PIWIL4 在人體內扮演著相似的角色, 現則正於適用的人類細胞中對其進行剔除。

## Assessment of SARS-CoV-2 infection affected piRNA expression and genome instability

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### Abstract:

Changes of piRNA expression in cell and exosome not only affect global gene expression, maintain the genomic stability but also might prevent the diseases' progression. Due to the sequence homology and evolutionary history, the viral infection was listed among the environmental factors that interfere the piRNA expression. Therefore, we are going to assess the piRNA-regulated genome stability by expressing SARS-CoV-2 replicons. We found that, the expression of SARS-CoV-2 replicons does not change the expression of piRNA interacting protein, PIWIL4. Specific putative piRNAs expressional changes were detected before and after the expression of replicons. From the downloaded RNA-sequencing data, we found that the transcriptional variations were limited after the viral infection. Since PIWIL2-knockout in mice cells limited immuno-induction capability of the secreted exosome, we are currently knocking-out the functional similar PIWIL4 and L1TD1 genes in order to recapitulate these observation in human cells.