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Yong Loo Lin School of Medicine

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UNDERSTANDING THE DOUBLE-STRANDED RNA (dsRNA) STRUCTURE OF *ANTIZYME-INHIBITOR 1 (AZIN1)* TRANSCRIPT AND ITS THERAPEUTIC POTENTIALS

WEDNESDAY
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3PM – 3.30PM

ANATOMY SEMINAR ROOM L2, MD10, DEPARTMENT OF ANATOMY, NUS.

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RNA editing is a co- or post-transcriptional process which results in sequence variation in the RNA molecule, and the most common type of RNA editing is the conversion of adenosine to inosine (A-to-I) in human, which is catalyzed by adenosine deaminases acting on RNA (ADARs).

Inosine is read as guanine by most cellular translational machineries, therefore the A-to-I editing has a great impact on edited RNAs, no only affecting the base pairing properties, but also altering codon after translation. Our previous study has reported that the over-editing of *antizyme inhibitor 1* (AZINI1) has been observed in approximately 50% of hepatocellular carcinoma (HCC) patients, which predicts much worse prognosis than patients without the over-editing. The editing complementary sequence (ECS) is essential for the formation of dsRNA structure for ADARs to bind and catalyse the deaminase reaction. Thus elucidating the ECS of the *AZIN1* transcript allows us to understand the precise dsRNA structure required for *AZINI1* editing. By generating minigene constructs and detection of the presence of editing, the sequences required for complementary base-pairing that forms the dsRNA structure was elucidated. We found that the proximal portion (8bp) of sequence within the exon 12 is essential for the formation of dsRNA structure and subsequent *AZINI1* editing. Based on the understanding of the precise dsRNA structure for the *AZIN1* editing, we aim to develop RNA-based therapeutics to block the editing of *AZINI1* for HCC treatment.

Address enquiries Dr Hu Qidong at 66013730 or Ms Carolyne Ang at 65163200. All are welcome.