# Translational Genomics: Utilizing AgNORs, Chromosomal Aberrations, and the Mitotic Index in Allium cepa to Identify Targets for Salinity Resistance in Rice

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Soil Salinization accelerated by sea-level rise and salt-water intrusion poses a critical threat to global food security, significantly impacting staple crops like rice (Genua-Olmedo et al., 2016). While salinity-tolerance research traditionally focuses on ion transport and osmotic regulation, plants continue to show limited growth (Farquharson, 2009), indicating that these mechanisms alone are insufficient to prevent growth limitations. This points towards an overlooked constraint : genomic stability- which may be the decisive factor in overcoming cellular limitations that ion transport fails to address. In particular, the extent to which genomic instability and suppressed protein synthesis act as a blockade for crop resilience remains uncharacterized, necessitating the identification of novel targets capable of maintaining cellular function under saline stress. This study investigated genomic stability utilizing an Allium cepa model to identify potential targets for salinity resistance in rice. Root meristems were analyzed for mitotic index, chromosomal aberrations, and AgNOR activity. Wet-lab analysis confirmed that salinity significantly suppressed ribosomal biogenesis (AgNOR activity) and induced chromosomal damage, such as anaphase bridges. To bridge the gap between cellular damage and molecular targets, HMGB1 and Topoisomerase IIa were evaluated. While BLAST analysis confirmed high sequence conservation, AlphaFold3 structural predictions disqualified HMGB1 as a potential target due to low-confidence ipTM and pTM scores. Conversely, Topoisomerase IIa demonstrated high structural integrity and a stable DNA-interaction interface. Unlike current targets, Topoisomerase IIa as a novel target prioritizes genomic stability and protein synthesis under saline stress.

**Awards Won:**