**EVALUATION OF THE ACTIVITY OF BIOACTIVE PLANT’S METABOLITE ON THE ALZHEIMER’S DISEASE PROTEINS (BETA-AMYLOID & TAU PROTEINS)**

**BACKGROUND**

Alzheimer's disease (AD) is a neurodegenerative disorder where the affected brain exhibits astroglyosis (high number of astrocytes in the brain), nerve cell atrophy and neuronal loss. This then manifests as loss of cognitive functions and memory in elderly patients (Fuyuki *et al*, 2018). Excessive accumulation of the β Amyloid Protein (Aβ) and Tau Proteins (TP) have been identified as major contributor of this damage (Siddhartha *et al*, 2012). AB is produced from the β Amyloid protein precursor (APP) in the brain by an enzymatic cleavage of β and γ secretase and it exists in large amount in the brain and important in neurodevelopmental stages of human (Siddhartha *et al*, 2012). Tau proteins exist in the brain and stabilizes cell’s microtubules shape, undue phosphorylation along this protein structure makes them weak and eventually fall off. These fallen Tau proteins thus polymerizes to form plaques implicated in AD (Fuyuki *et al*, 2018). There is no known therapeutic agent for AD. Bioactive plant’s metabolite are currently being used locally to manage the disease. There is need to explore the activities of these natural metabolites on major precursors of AD, thereby establishing their potential as novel drug candidates (Selvaraj, J et al, 2020).

**GENERAL OBJECTIVE**

To check for the activities of some bioactive plant metabolites on both precursors and major proteins implicated in AD

**METHOD**

The plants currently used locally for managing AD will be identified and their profile downloaded from online databases such as NPASS. Plants to be used include: drumstick tree (*Moringa oleifera*), tumeric (*Curcuma longa*), garlic extract (*Alium sativum*), cattle stick (*Carpalobia lutea)* and lemon balm (*Melissa officinalis*).

The APP protein (1AAP), will be downloaded from protein data bank including the TP (20N9). The enzymes secretase (α, β and γ) structure will also be gotten from the enzyme bank. The downloaded plant compounds and proteins will be prepared, docked and visualize using Chimera, Pymol, Pyrx or Auto Dock Vina, discovery studio and Ligplot to observe binding affinities and interactions. These affinities are compared to current accepted binding affinities for therapeutic management of AD which will be docked along the plant phytochemicals to establish their potential as drug candidates

The homologs of these proteins and enzymes will be carefully studied to check for conservative areas and the above procedure repeated for these areas to have a progressive research

**EXPECTED RESULT**

One or more plant metabolite will have a high binding affinity for any of these proteins which can establish their use as an inhibitor or enhancer in managing AD

**REFERENCES**

1. Fuyuki, K., Masato, H. (2018). Reconsideration of Amyloid Hypothesis and Tau Hypothesis in Alzheimer's Disease. Frontiers in Neuroscience, 12, 25. <https://doi.org/10.3389/fnins.2018.00025>
2. Selvaraj, J., Sardar, H., Vishnupriya, V., Balakrishna, J. P., Mohan, S. K., Nivedha, R. P., Vijayalakshmi, P., & Ponnulakshmi, R. (2020). Molecular docking analysis of amyloid precursor protein with compounds from the Australian cowplant. Bioinformation, 16(7), 561–566. <https://doi.org/10.6026/97320630016561>
3. Siddhartha, M.R., George, P., Zhu, X., Boehm,J. (2012). Amyloid Beta and Tau Proteins as Therapeutic Targets for Alzheimer’s Disease Treatment: Rethinking the Current Strategy. International Journal of Alzheimer’s Disease, 7, 2012. <https://doi.org/10.1155/2012/630182>