

Plants are an unrivaled source of medicines and bioactive molecules. However, the complexity of plants has hindered our ability to elucidate and engineer the metabolic pathways that are responsible for synthesis of these important molecules. Using a range of bioinformatic and experimental methods, S.E.O.'s research group has contributed to our understanding of the enzymatic and mechanistic basis for a wide variety of plant-derived molecules. A few recent examples include the discovery of the enzymes for quinine (1), vinblastine (2), strychnine (3), ibogaine (4) and kratom alkaloid (5) biosynthesis. Her group has developed new methodologies to streamline the discovery of these enzymes; recent examples include development of single cell mass spectrometry methodology (6) and single cell transcriptome-metabolomic multiplexing (7). Moreover, her work reveals the divergent evolutionary mechanisms by which chemical diversity in plants arises (*e.g.* 8, 9). Conversely, she has also shown the mechanistic basis by which the same molecular scaffold can independently evolve (*e.g.* 10, 11). Collectively, her work provides a basis for metabolic engineering of these compounds (1), thereby enabling sustainable access to these important molecular scaffolds.

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