Modern agriculture increasingly relies on crops that are easier to grow, harvest, and adapt to changing climate conditions. In cucumber, a globally important crop with great cultural and economic value in Poland, bushy plant growth habit is a highly desirable trait, particularly for field cultivation and mechanical harvesting. However, most cucumber varieties grow as long, vining plants, which complicates large-scale production. A unique cucumber line called **W-19**, developed in Poland, grows in a compact, bushy form and is promising for breeding new varieties. This growth habit is controlled by a single recessive gene, named ***bushy*** **(*bu*)**, but its molecular identity and function remain unknown.

The goal of this project is to identify the ***bu*** gene and understand how it influences plant architecture at the genetic and molecular levels. We will use a method called **Bulked Segregant Analysis combined with sequencing (BSA-seq)** to pinpoint the genomic region responsible for the trait. By analyzing DNA from a mapping population derived from a cross between W-19 and a standard cucumber line (B10), we will identify DNA sequence differences linked to the bushy phenotype.

Once the candidate region is identified, we will use additional genetic and comupational analyses to narrow it down to a specific gene. These analyses will include comparing gene sequences from bushy and wild-type plants, annotating gene models using public databases, and predicting protein structure and function using tools like **InterProScan**, **Pfam**, and artificial intelligence – **AlphaFold3**. Structural modeling will help us assess how the mutation might alter the protein's activity or stability. To understand how the gene functions in different parts of the plant, we will perform **gene expression profiling using RT-qPCR** in various tissues such as shoot apices, stems, roots, and tendrils. Other computational analyses will conducted to predict function of this gene and its protein product e.g., promotor analysis to determine gene activity or phylogenetic analysis to follow evolutionary changes.

The broader motivation behind this work is to support the development of cucumber cultivars better suited to **mechanized agriculture**, which is becoming increasingly important as labor costs rise and environmental pressures mount. Identifying the ***bu*** gene could also provide valuable molecular markers for **marker-assisted selection (MAS)**, enabling faster breeding of bushy cucumber varieties.

Beyond breeding applications, this project will expand our fundamental understanding of how plant architecture is regulated in cucurbits like melon, pumpkin or zucchini, in which the genetic basis of growth habit is still poorly understood.