

My research focused on non-autonomous transposable elements, their genomic impact, evolution, and use as molecular markers for plant breeding.

**Potatoes** are among the most consumed crops with varieties specifically developed for different purposes and adapted to varying environmental conditions. Accordingly, a clear distinction of potato cultivars is crucial to protect the rights of breeders and customers. In cooperation with the German potato breeder NORIKA GmbH, I have developed a **molecular marker** system to genotype potato cultivars, landraces, and wild species during three projects funded by the German Federal Ministry of Education and Research (BMBF) [1]. The markers are based on insertional polymorphisms of short interspersed nuclear elements (SINEs). For the practical application of the markers by the NORIKA GmbH, I established a fingerprint database. Based on this work, the research group is currently searching for resistance trait-associated markers in potato using my R workflow to identify candidate marker bands for site-specific markers. Such trait-associated markers enable the cost-saving and accelerated breeding of new varieties with desired traits.

To study the genomic basis of our molecular markers, I comparatively analyzed five nightshade genomes using bioinformatics tools and customized Python scripts [2]. **Nightshade SINEs** are enriched in distal, euchromatic chromosome regions, with individual SINE families associated with genes to a varying extent. Thereby, they potentially contribute splice sites, regulatory and coding sequences. Remarkably, 10% of the annotated genes in the five nightshade genomes harbor at least one SINE insertion. The presence of young copies implies a recent SINE amplification in potato, contrasting tomato and pepper. In addition to their mere insertional activity, SINEs can affect the genome through their involvement in sequence rearrangements, evident from tandem-like arrangements and the transduction of flanking sequence regions upon SINE transposition.

Previous studies in plants have indicated a rather narrow phylogenetic distribution of SINE families. In contrast, my computational analysis of a hundred genome assemblies revealed the occurrence of a highly conserved 3' SINE domain in at least 24 SINE families, widespread across the plant kingdom in a patchy manner [3]. This led us to the postulation of the **Angio-SINE superfamily**. Using multiple complementary approaches, I investigated and visualized the modular relationships within this SINE superfamily. When considering all full-length copies, Angio-SINEs are frequently enriched in and nearby genes with a potential impact on the expression or splicing of these genes.

To study repetitive sequences, traditional dotplot visualizations are helpful, but available tools either lacked specific features or their use could not be automated. Due to this, I developed the **cross-platform software FlexiDot**, with novel features like the visualization of sequence annotations to generate highly informative and customizable dotplots [4]. This has been published in the journal *Bioinformatics*. Other **bioinformatics pipelines**, that I designed and implemented during my work, have been applied to other transposable element types and species leading to co-authorships in multiple publications from our research group.

[1] Seibt *et al.* (2012) Theoretical and Applied Genetics

[2] Seibt *et al.* (2016) The Plant Journal

[3] Seibt *et al.* (2020) The Plant Journal

[4] Seibt *et al.* (2018) Bioinformatics