



HUNGARIAN UNIVERSITY OF AGRICULTURE AND LIFE SCIENCES

Doctoral School of Agricultural and Food Sciences

**MOLECULAR CHARACTERIZATION OF THE *PRUNUS FALLING*
STONES TRANSPOSON AND ITS APPLICATION IN MARKER
DEVELOPMENT**

The Thesis of the PhD dissertation

Beti Ivanovska

Budapest

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1. Background of the work and its aims

Stone fruit trees are among the most valuable perennial crops in temperate agriculture, but they remain difficult to improve. The main reasons are biological rather than merely technical: long juvenile phases delay phenotyping, many quality traits are quantitatively inherited, and perennial architecture reduces the number of selection cycles that can be completed in a breeding programme. In *Prunus* species, breeders therefore need molecular tools that shorten the path from genotype to useful cultivar.

Transposable elements (TEs) are central to this need because they generate heritable variation without requiring artificial mutagenesis. A TE insertion can be neutral, deleterious, or advantageous depending on its position and on how the host genome responds. In fruit trees, where vegetative propagation preserves somatic variants and where selection can act on stable clonal lineages, a single insertion may have disproportionate breeding value.

The *Falling Stones* (*FaSt*) element is a particularly attractive case. It was first associated with self-compatibility in apricot and later recognized as a small, gene-associated MITE with possible activity in several *Prunus* species. The hypothesis underlying this dissertation is that *FaSt* is not only a historical marker of genome change but also a current participant in transcriptional and regulatory processes.

In addition, many *Prunus* marker systems are either anonymous or only weakly connected to functional genomic regions. If *FaSt* can be integrated with Start codon targeted (SCoT) amplification, the result could be a marker system that is more informative than generic banding assays and easier to interpret in a breeding context. The dissertation therefore uses *FaSt* as a bridge between transposon biology, transcriptomics, and applied molecular marker development.

Since McClintock's pioneering work, plants have been understood as genomes in which mobile DNA shapes both structure and function. TEs are abundant, evolutionarily dynamic, and often concentrated near genes, where they can affect regulatory architecture.

A key distinction exists between autonomous and non-autonomous elements. Autonomous DNA transposons encode the transposase needed for excision and reintegration, whereas non-autonomous elements depend on helper elements but can still spread efficiently. MITEs, non-autonomous TEs are compact, numerous, and frequently located in gene-rich regions.

Prunus genomes are especially suitable for studying TE consequences because the genus combines long-standing domestication, lineage-specific divergence, and a wide range of ploidy levels. This makes it possible to compare ancestral and recent insertions, as well as to ask whether TE dynamics track breeding history and taxonomic structure.

Class I retrotransposons transpose via RNA and include LTR and non-LTR groups; Class II transposons move via DNA intermediates. Both classes can expand dramatically if host silencing is relaxed. In plants, this often happens under stress or after hybridization and polyploidization, when epigenetic control may become less stable. TE bursts can therefore leave short- and long-term genomic signatures.

TEs affect the genome at several levels. They can change gene dosage, alter local recombination, disrupt coding sequence, create new splice forms, and introduce or remove transcription factor binding sites. Their effects are therefore not limited to coding disruption. A small insertion in a regulatory region can be more consequential than a large insertion in a distant intergenic segment.

MITEs are particularly important because they combine short size with frequent gene proximity. Their abundance makes them useful as markers, while their insertion bias increases the chance that a polymorphism will be tied to a

functional locus. This combination of practical and biological value is the reason MITE-derived markers have been attractive in crop genomics.

Prunus includes major fruit trees such as apricot, peach, almond, plum, and sweet and sour cherry. These crops are economically important and widely cultivated, but they are also genetically complex. The genus includes diploids, tetraploids, and hexaploids. While some species are strongly self-incompatible, many cultivars derive from a relatively narrow base of ancestral material.

The breeding challenge is therefore not simply to select superior fruit, but to do so in a background where juvenile periods are long and segregation patterns can be difficult to interpret. In sour cherry and plum, especially, the interaction of polyploidy, hybrid origin, and cultivar history makes molecular markers indispensable for pedigree reconstruction and cultivar identification.

The genome sequence era has clarified some of this complexity, but it has also shown that structural variation is abundant. TE activity has helped distinguish closely related taxa and, in some cases, contributed to domestication traits. As a result, *Prunus* species are a strong model for studying how mobile DNA interacts with breeding history.

A large number of *Prunus* traits have already been associated with TE insertions. In peach, transposon-related changes have been linked to fruit firmness, hairlessness, and dormancy-related phenotypes. In almond, TE insertions and methylation changes can reduce expression of genes involved in bitterness-related pathways. In plum and cherry, TE footprints are associated with fruit colour, reproductive traits, and cultivar differentiation.

The most directly relevant context for this thesis is self-incompatibility. In *Prunus*, SI is governed by the S-locus and the interaction of pistil and pollen factors. When a transposon interrupts the *S-haplotype-specific F-box* gene or changes its promoter environment, the result can be self-compatibility. *FaSt*

entered the literature in exactly this context: a small insertion with large compatibility consequences.

Therefore, TE biology in *Prunus* should not be treated as a purely descriptive subject. TE insertions can be causal, can be useful markers, and can illuminate the genome regions where selection has acted. The *FaSt* transpositional movement sits at the intersection of evolutionary genomics and breeding relevance.

RNA-seq made it possible to investigate whether *FaSt* is only a DNA-level variant or also part of the transcriptome. This is important because transcription is one of the first signs of activity, but the interpretation of RNA data in repeat-rich genomes is not trivial. Repeats, paralogs, and low-complexity regions can all complicate alignment, multi-mapping, and downstream differential expression analysis.

The marker-development literature in *Prunus* shows that utility depends on the balance between technical simplicity and interpretability. SSRs and SNPs are highly informative, but not always easily tied to function. SCoT markers are reproducible, and adjacent to genes. TE-based primers can anchor markers to a defined sequence motif, producing a more interpretable banding profile.

This dissertation takes advantage of that logic by combining a start-codon-targeted primer with a *FaSt*-specific primer. In principle, this should enrich for fragments in or near genes, increase polymorphism, and provide a marker set that can be sequenced and interpreted rather than merely scored as a gel band.

TE-based markers are already familiar in plant genetics. They can exploit retrotransposon insertion structure, while DNA-transposon-based approaches use terminal inverted repeats or family-specific motifs. The advantage of such markers is that they sample genomic variation accumulated

through insertion history, which often correlates with evolutionary or breeding lineages.

In *Prunus*, several marker systems have been used to clarify diversity and pedigree, but the majority are either not anchored in function or are restricted to a narrow genomic class. A *FaSt*-anchored system is different because the transposon itself has biological relevance. It can therefore be used not only to estimate relatedness but also to generate hypotheses about how a particular region evolved.

The literature on fruit-tree TE insertions also shows that regulatory effects can be surprisingly local. A promoter insertion can create a new expression pattern without causing dramatic downstream transcriptome changes, and an insertion in a UTR can alter stability or translation without changing coding sequence.

FaSt is small enough to be PCR-friendly but structured enough to be biologically informative. As a Mutator-like MITE, it sits in a class of elements known for gene proximity and dynamic copy-number evolution. Its repeated appearance in *Prunus* literature, especially in self-compatibility and promoter contexts, made it an ideal target for a thesis focused on both mechanism and application.

2 . Objectives

1. Structural and functional characterization of a recently discovered transposon (*FaSt*) in the *Prunus* genome.
2. Analysis of the transcriptome for the expression of *FaSt* elements in diploid and polyploid *Prunus* species.
3. Quantitative analysis of *FaSt* expression in different tissues and across different phenological stages.
4. Identification of genes whose expression might correlate with *FaSt* elements.
5. Development of a new molecular marker system for *Prunus* species based on *FaSt* transposon.

3. Materials and methods

The study combined molecular laboratory work with bioinformatics and statistical analysis. Plant material was collected from a *Prunus* germplasm collection and from selected apricot tissues used for RNA-seq comparison. DNA and RNA isolation followed established protocols, and cDNA was prepared for transcript detection and expression analysis.

PCR and qRT-PCR were used to detect and quantify *FaSt*-related transcripts. Genome-wide and transcriptome-wide *in silico* analyses were then carried out to determine copy number, genomic location, and phylogenetic distribution. Finally, a SCoT-FaSt marker system was developed, scored, sequenced, and analysed with diversity and phylogenetic tools.

Statistical evaluation included ANOVA, correlation analysis, principal component analysis where appropriate, and marker-efficiency calculations such as PIC, resolving power, and diversity indices. RNA-seq analysis used standard quality control, alignment, counting, and DESeq-based differential expression testing.

3.1 Plant material and sampling

The transcriptional analyses covered multiple *Prunus* species and tissues. The inclusion of leaves, floral organs, and reproductive tissues was also important because transposon activity often varies by developmental stage.

For the marker work, the accessions were chosen to represent a broad set of *Prunus* taxa and cultivar histories.

For RNA-seq, the key comparison was between self-compatible and self-incompatible apricot reproductive tissues. This comparison allowed the thesis to ask whether *FaSt*-related variation is associated with the transcriptome state of tissues directly relevant to compatibility.

3.2 PCR, qRT-PCR and cloning

Conventional RT-PCR was used as an initial qualitative assay. qRT-PCR then provided relative expression measurements, enabling comparison among tissues and genotypes. Because transposon transcripts can be less abundant than conventional gene transcripts, careful normalization and replicate consistency were essential.

For marker analysis, primers were used in SCoT-only and SCoT-FaSt combinations. The resulting fragments were separated, visualized, and scored. Selected amplicons were then cloned and sequenced to confirm that the marker actually represented the intended genomic region rather than a PCR artefact.

This cloning step is especially important in marker systems that rely on repeat-rich DNA. Without sequence confirmation, one cannot easily know whether a band comes from a true transposon-associated locus or from an unrelated fragment of similar size.

3.3 Bioinformatic and statistical analyses

The *in silico* analyses used sequence similarity searches to identify *FaSt* copies in genomes and transcript datasets. The genomic location of each copy was examined to determine whether it lay in a promoter, UTR, intron, exon, or intergenic region. This context was used later to interpret likely regulatory consequences.

RNA-seq data were pre-processed, aligned, quantified, and tested for differential expression. The analysis was focused on whether the presence of *FaSt* at compatibility-related loci corresponded to broad transcriptome shifts or

to a much narrower local effect. The latter possibility would indicate that *FaSt* acts more as a cis-regulatory modifier than as a global pathway regulator.

Marker data were analyzed with diversity and phylogenetic methods. The aim was to judge whether the combined primer system produces a robust signal at both the interspecific and intraspecific level, and whether the resulting clustering patterns reflect known botanical history.

4. Results and discussion

The results consistently point to a single interpretation: *FaSt* is an active and biologically meaningful component of *Prunus* genomes. It is detectable at the RNA level, it is not randomly distributed at the DNA level, and it can be exploited as an informative marker source. At the same time, its effect appears to be context dependent rather than globally disruptive.

This dual character is important. *FaSt* is not just an interesting TE from an evolutionary standpoint. It is also a practical genomic feature that can be leveraged in applied horticulture. The following subsections move from expression evidence to genomic distribution and finally to marker performance and evolutionary inference.

4.1 RT-PCR detection of *FaSt*-related transcripts

The RT-PCR results demonstrated that *FaSt*-related transcripts are present across the species and tissues sampled. The presence of the transcript in leaves, floral organs, and reproductive tissues indicates that *FaSt* is not transcriptionally silent under normal growth conditions.

Broad tissue detection suggests that *FaSt* may be transcribed from multiple genomic copies or from copies embedded within transcribed loci. Given its insertion preference for gene-rich regions, both possibilities are plausible. In either case, transcription increases the chance that *FaSt* may influence the host transcriptome through local RNA processing or chromatin effects.

The qualitative RT-PCR data therefore provide the first line of evidence for activity. They justify the subsequent quantification and support the notion that *FaSt* copies are not merely dormant relics inherited from an ancient insertion event.

4.2 qRT-PCR analysis of tissue-specific expression

qRT-PCR refined the qualitative picture. The strongest expression was observed in anther tissue, and the anther of the self-compatible apricot cultivar 'Pannónia' showed a higher *FaSt* signal than the anther of the self-incompatible plum cultivar 'Hanita'. This result is consistent with reproductive tissue being a major site of transcriptional activity and with compatibility-related loci being especially informative.

The difference between the two genotypes should not be over-interpreted. The data do not prove that *FaSt* expression causes self-compatibility or that it is always upregulated in compatible tissues. What they do show is that expression varies in a biologically meaningful way and that reproductive tissues deserve priority in future functional work.

A useful interpretation is that *FaSt* transcription may reflect a balance between local chromatin openness and the developmental state of the tissue. Anthers are particularly dynamic, and many regulatory events converge there. A transposon that is active in that environment could contribute to tissue-specific regulatory noise or to stable cis-effects on nearby genes.

4.3 *In silico* analysis of *FaSt* distribution in *Prunus* species

The *in silico* analyses revealed clear structural patterns. *FaSt* copies are abundant and non-randomly distributed across *Prunus* genomes, with particularly strong representation on chromosomes 1 and 6. The copy number and integrity differ among species, with polyploid taxa carrying more copies overall and *Cerasus* species containing a larger proportion of fragmented elements.

A useful way to read the data is as a spectrum of element age and genomic retention. Complete copies likely represent relatively recent or better preserved insertions, whereas fragmented copies suggest older, partially degraded insertions. The fact that cherries tend to carry more fragmented copies indicates that their *FaSt* landscape may be older or more heavily eroded than that of peach and almond.

The data also support a lineage-specific evolutionary scenario. Some insertions appear to predate the major subgeneric splits, whereas others are restricted to the *Cerasus* or *Prunus* branches. In effect, *FaSt* is not a single event but a long-running genomic process that leaves behind insertion fossils and active or recently active copies at the same time.

This pattern matters for marker development because lineage-specific insertions are ideal discriminators. They provide the presence/absence variation needed for phylogenetic inference and cultivar grouping. They also suggest that *FaSt* has been part of *Prunus* genome diversification over a substantial evolutionary timeframe.

4.4 *FaSt* insertion in the almond *PdCBF1* promoter

The promoter analysis identified a 358 bp *FaSt* insertion in the almond *PdCBF1* gene promoter in reverse orientation. The element shows strong similarity to the apricot *SFB*-associated *FaSt* insertion but is located in a different functional context. This makes it especially interesting because the same transposon family can participate in different biological processes depending on where it lands.

The promoter insertion is predicted to introduce additional transcription factor binding sites, including motifs associated with SBP, MADS-box, WRKY and related regulatory families. Such a change can influence stress responsiveness or developmental regulation. Even if the phenotypic effect is subtle, the insertion provides a concrete mechanism by which *FaSt* could modify gene expression.

The insertion *PdCBF1* discovery is significant because it moves the thesis beyond generic transposon mapping. It demonstrates that *FaSt* can be found directly in a promoter region with regulatory potential. That finding supports the view that *FaSt* is not only a marker of divergence but also a possible contributor to adaptive regulatory variation.

4.5 RNA-seq analysis in apricot reproductive tissues

The RNA-seq comparison between self-compatible and self-incompatible apricot tissues identified differentially expressed genes in anther and style samples, but the overall magnitude of the expression differences was limited. This result argues against a broad transcriptome-wide effect of the *FaSt* insertion in the conditions tested.

The data therefore support a localized model. *FaSt* may perturb the expression or function of specific loci without changing the general architecture of reproductive transcriptomes. Such a model is consistent with the way many TE insertions behave in perennial fruit crops: discrete, interpretable, and often trait-linked, but not necessarily system-wide.

The lack of strong broad-scale changes also suggests that the apricot *FaSt* insertion should be studied in a more targeted functional framework rather than through the expectation of large transcriptomic cascades. Future experiments could combine allele-specific assays, promoter testing, and tissue-specific expression studies to address this directly.

4.6 Development and evaluation of the SCoT-FaSt marker system

The marker system based on SCoT and *FaSt*-specific primers was the applied innovation of the dissertation. The guiding idea was simple: use a gene-targeted primer to reach coding-adjacent regions and a transposon-specific primer to anchor the assay to a known, biologically relevant insertion family. The combination should reduce non-target amplification and increase interpretability.

The gel profiles confirmed that the strategy worked. Relative to SCoT alone, the SCoT-FaSt combinations produced clearer banding, higher polymorphism, and stronger resolving power. This means that the transposon-specific primer is not merely an extra primer but a functional enrichment step that shapes the output of the assay.

Sequencing of amplicons showed that many fragments contained parts of protein-coding genes or RNA-coding genes and that *FaSt* copies were often located in UTRs or introns. This is an important result because it links the

marker output to the genomic regions where functional variation is most likely to occur.

The marker system also performed well in phylogenetic reconstruction. It grouped *Prunus* species according to their expected relationships and clustered European plum cultivars in ways consistent with pedigree and origin. In other words, the marker is informative enough to recover known history and specific enough to be used for germplasm characterization.

A further interesting observation is that the genomic landscape of *FaSt* appears to differ across taxa in a way that echoes their evolutionary divergence. Cherries show a stronger fragmentation pattern, whereas peaches and almonds retain a larger number of complete copies. This supports the view that *FaSt* has contributed to lineage-specific genome remodeling over time.

4.7 Functional and evolutionary interpretation

The overall functional interpretation of the results is that *FaSt* acts as a genome-shaping element rather than as a broad master regulator. It can be transcribed, can occupy regulatory contexts, and can create polymorphism without necessarily causing obvious phenotypic adverse effects. Such a profile is typical for successful transposon families that persist over long evolutionary periods.

The evolutionary interpretation is equally clear. The distribution of complete and fragmented copies suggests a mixture of ancient and recent activity, differential retention, and lineage-specific degradation. This makes *FaSt* a useful proxy not only for local marker work but also for understanding how *Prunus* genomes have diversified.

In practical terms, the element is valuable precisely because it is both biologically real and methodologically exploitable. It gives the breeder a marker and gives the genome biologist a window into regulatory evolution.

5. Conclusions and recommendations

FaSt should be regarded as an active and biologically relevant *Prunus* MITE rather than as a passive repeat. The evidence is multi-layered: transcripts were detected, copy number and genomic location were non-random, and a promoter insertion with potential regulatory consequences was identified in almond.

The work also clarifies the scale of *FaSt*'s effect. In the tested apricot reproductive tissues, the element did not generate broad transcriptomic reprogramming. This result is a useful biological constraint, that suggests that *FaSt* acts mainly at the locus level and that its effects are likely to be context dependent, tissue dependent, and insertion specific.

The SCoT-*FaSt* marker system is the most immediately applicable outcome. It improves polymorphism detection and maintains biological interpretability because its fragments are linked to a known transposon family and frequently to gene-adjacent regions. This makes it attractive for cultivar identification, diversity analysis, and pedigree reconstruction.

Further work should prioritize three directions. First, the *PdCBF1* promoter insertion should be tested functionally, for example by expression assays or stress-response phenotyping. Second, the marker system should be validated in broader germplasm collections and across additional *Prunus* species. Third, the most informative loci should be converted into higher-throughput genotyping formats if they are to be used routinely in breeding programmes.

6. New scientific results

I. The *Falling Stones* (*FaSt*) transposon is ubiquitously transcribed in all examined tissues (leaf, flower bud, calyx, petal, anther, and pistil) of diploid (*P. armeniaca* and *P. avium*), tetraploid (*P. cerasus*), and hexaploid (*P. domestica*) *Prunus* species.

II. Quantitative RT-PCR confirmed that *FaSt* expression was higher in the anther tissue of the SC apricot cultivar ‘Pannónia’ than in the anther of the SI European plum (*Prunus domestica* L.) cultivar ‘Hanita’.

III. A novel 358 bp *FaSt* insertion was discovered in the promoter region of the almond (*Prunus dulcis*) *PdCBF1* gene (in reverse orientation), sharing 84.2% identity with the previously described apricot *SFB FaSt* insertion, this *FaSt* element introduces new transcription factor binding sites (SBP/MADS-box, WRKY, SRS) not present in the homologous *PdCBF2* promoter.

IV. A new molecular marker was developed for *Prunus* analysis by the combination of SCoT primers and a newly designed, *Falling Stones* transposon-specific primer. The marker significantly enhanced PCR polymorphism, band clarity, and resolving power compared to SCoT analyses.

V. Partial sequences of a total of 17 protein-coding genes and one RNA-coding gene were identified in SCoT-*FaSt* amplicons where *FaSt* copies were located in the 5’ and 3’ UTRs, and the introns of genes critical for physiological processes, supporting a role for *FaSt* in diversifying gene regulation.

VI. The SCoT-*FaSt* marker analysis is a reliable tool for elucidating phylogenetic relationships. It accurately reconstructed the evolutionary relationships of six *Prunus* species (peach, almond, European plum, apricot,

sweet and sour cherries) with 95–100% bootstrap support, and grouped 28 European plum cultivars into five clusters consistent with their breeding origins.

VII. Differential expression analysis on the RNA-Seq data from anther and style tissues of SC versus SI apricot cultivars revealed no statistically significant gene expression changes attributable to the presence of the *FaSt* transposon, confirming that *FaSt* insertion did not markedly alter transcript levels under the tested conditions.

7. Publications related to the dissertation

7.1 Papers related to the thesis:

Ivanovska, Beti, Thanyarat Onlamun, Júlia Halász, and Attila Hegedűs. (2025).

"The Combination of Start-Codon-Targeted (SCoT) and *Falling Stone* (*FaSt*) Transposon-Specific Primers Provides an Efficient Marker Strategy for *Prunus* Species" *International Journal of Molecular Sciences* 26, no. 9: 3972. <https://doi.org/10.3390/ijms26093972>

Hegedűs, Attila, Pamulaklakin Eusebio Geronima, **Ivanovska Beti**, and Júlia Halász. (2023). "Molecular Characterization of the Eukaryotic Translation Initiation Factor 4E Isoform, eIF(iso)4E, in Traditional Cultivars of *Prunus domestica*." *TURKISH JOURNAL OF AGRICULTURE AND FORESTRY* 47 (6): 1155–1164. doi:10.55730/1300-011X.3154.

Júlia, Halász, Szendy Gergő, **Ivanovska Beti**, György Tóth Endre, and Hegedűs Attila. (2023). "The Self-Incompatibility Locus and Chloroplast DNA Regions of *Prunus Domestica* Reflect the Origin and Genetic Diversity of Traditional Cultivars." *JOURNAL OF THE AMERICAN SOCIETY FOR HORTICULTURAL SCIENCE* 148 (5):230–239. doi:10.21273/JASHS05330-23.

Peona, Valentina & Martelossi, Jacopo & Almojil, Dareen & Bocharkina, Julia & Brännström, Ioana & Brown, Max & Cang, Alice & Carrasco-Valenzuela, Tomas & DeVries, Jon & Doellman, Meredith & Elsner, Daniel & Espíndola-Hernández, Pamela & Friis, Guillermo & Gaspar, Bence & Zagorski, Danijela & Hałakuc, Paweł & **Ivanovska, Beti** & Laumer, Christopher & Lehmann, Robert & Suh, Alexander. (2023). Teaching transposon classification as a means to crowd source the curation of repeat annotation – a tardigrade perspective. *BioRxiv*; doi: <https://doi.org/10.1101/2023.11.06.565293>.

7.2 Oral presentations and conference abstracts:

- Beti Ivanovska**, Júlia Halász, and Attila Hegedűs. (2023). “Application of SCoT and MITE Insertion-Based Polymorphism Markers for Assessing the Genetic Diversity of *Prunus* Species.” In Abstract Book of XVI Eucarpia Symposium on Fruit Breeding and Genetics,
- Beti Ivanovska**, Onlamun Thanyarat, Júlia Halász, and Attila Hegedűs. (2023). “Assessment of Genetic Diversity of European Plum Cultivars Using Transposon-Based Markers.” In XXIX. Növénynevelési Tudományos Napok, 127.
- Halász, J., **B. Ivanovska**, T. Onlamun, G. Szendy, E.Gy. Tóth, and A. Hegedűs. (2023). “Application and Development of Molecular Marker Systems for the Analysis of Polyploid *Prunus* Species.” In Abstract Book of Plant Biology 2023 Annual Meeting of the American Society of Plant Biologists.
- Hegedűs, A., **B. Ivanovska**, T. Nagy, and J. Halász. (2023). “Steps toward Unraveling the Secrets of a Mysterious Transposon: The *Falling Stones* in Stone Fruits.” In Abstract Book of Plant Biology 2023 Annual Meeting of the American Society of Plant Biologists.
- Ivanovska Beti**, Attila Hegedűs, and Júlia Halász. (2022). “In Silico Analysis of *Falling Stones* (*FaSt*) Transposable Element Inserted in the Promoter Region of an Almond *CBF* Gene.” In A Lippay János – Ormos Imre – Vas Károly (LOV) Tudományos Ülésszak Tanulmányai [Proceedings of János Lippay – Imre Ormos – Károly Vas (LOV) Scientific Meeting], 365–369.
- Ivanovska, B**, J Halász, and A Hegedűs. (2020). “The Presence of *FaSt* Transposon in *Prunus* Transcriptome.” In SZIEntific Meeting for Young Researchers 2020, 204–208.