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BOOK OF ABSTRACTS

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How Genomics Can Contribute to Improve Herbicide Resistance Evolution Modelling Prediction in the Fields

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Abstract

Weed control is essential to guarantee crop yield and quality in modern agriculture. Integrated Weed Management (IWM) based on the right combinations of agronomic measures and herbicide uses is the major approach to insure a sustainable crop production at a reasonable costs for most of the farmers. The rare new herbicide modes of action found during the last decades and the intensive use of tolerant crops to few herbicides have contributed to resistance evolution with new unique resistant cases observed every year (Weedscience.org database). Herbicide resistance involved several resistance mechanisms which evolve independently and can be observed alone or in combinations in the weed resistant populations. Either the target can be modified by mutations (Target Site Resistance (TSR), a monogenic trait) or the herbicide cannot any more reach its target either because it is detoxified (enhanced metabolism), or its transport or its uptake can be inhibited, or it can be transported directly into the vacuole (sequestration). These non-target site resistance mechanisms (NTSR) are still poorly understood and in many cases are under the control of multiple genes (polygenic traits). Diagnostics of NTSR is still a challenge in term of time and costs. Models to predict resistance evolution in the fields can be a good alternative to discuss different weed control scenarios with farmers. They of two kinds. They can rely on mathematical equations mimicking the weed development cycle (mechanistic models) or on AI, like a random forest approach, based on field history. The number of genes involved in the resistance is one key parameter to improve the existing models, especially the mechanistic ones. Genomic can be of great help to find these genes and understand their activity and regulation. Examples will be presented using black-grass (Alopecurus myosuroides) and rye-grass (Lolium spp) resistant to post emergence ALS-inhibitor herbicides (HRAC Group 2) and pre-emergence herbicides inhibitors of the synthesis of Very Long Chain Fatty Acids (HRAC Group 15). Genomic analyses related to the characterization of cytochrome P450 and glutathione transferase gene families will be discussed. Finally it will be shown how to use this new knowledge to improve the modelling approaches aiming to choose the best strategies to mitigate the resistance evolution in the field in a cost efficiency way for the farmers.

Keywords: Genomics, Herbicide Resistance Evolution, Modelling, Farmers' Support.

Functional Genomic Approaches. Gene Function Analyses Involved in Metabolic Herbicide Resistance as an Example

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Abstract

Resistance to preemergence herbicides, e.g. inhibitors of the biosynthesis of very-long-chain fatty acids (VLCFAs, HRAC Group 15), is evolving in response to increased use of these compounds. Grass weeds such as rye-grass (Lolium spp.) and black-grass (Alopecurus myosuroides) have accumulated resistance to various herbicide modes of action. Here, an RNA-seq analysis was conducted using rye-grass and black-grass populations resistant to the VLCFA biosynthesis inhibitor flufenacet to investigate this phenomenon. Besides various transcripts, including putative long noncoding RNAs (lncRNAs), a single putatively functional tau class glutathione transferase (GST) was constitutively differentially expressed in rye-grass. It was further induced by herbicide application. This GST was expressed as a recombinant protein in Escherichia coli along with other GSTs and detoxified flufenacet rapidly in vitro. Detoxification rates of other herbicides tested in vitro were in accordance with cross-resistance patterns previously determined in vivo. A genome-wide GST analysis revealed that the candidate GST was located in a cluster of 3 intronless GSTs. Their intronless nature possibly results from the retroposition of cellular mRNAs followed by tandem duplication and may affect gene expression. The large number of GSTs (≥195) in the genome of rigid ryegrass (Lolium rigidum) compared with other plant organisms is likely a key factor in the ability of this weed to evolve resistance to different herbicide chemistries. However, in the case of flufenacet resistance, a single upregulated GST with high affinity for the substrate flufenacet possibly contributes over-proportionally to rapid herbicide detoxification in planta. The regulation of this gene and the role of differentially expressed transcripts, including various putative lncRNAs, require further investigation. In black-grass, several GSTs active on flufenacet and other herbicides were over-expressed. These genes were clustered in three major locations in the black-grass genomes. Genomic structures of GSTs were compared between rye-grass and black-grass. The steps to analyze gene families in different genomes and gene function will be discussed.

Key words: Functional Genomics, Herbicide metabolic Resistance, Gene function validation

Climate conditions reshape species-specific transcriptional responses to glyphosate

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Abstract

Climate change may alter weed competitiveness and herbicide performance, yet its effects on molecular responses to glyphosate remain poorly understood. We investigated how elevated carbon dioxide and temperature influence glyphosate efficacy and transcriptional responses in wild oat *(Avena fatua*), barnyard grass (*Echinochloa crus-galli*), and oilseed rape (*Brassica napus*). Two dose-response experiments compared ambient conditions (400 ppm carbon dioxide; 18/12 °C day/night) with future conditions (800 ppm; 20.5/14.5 °C). At the three- to four-leaf stage, plants were treated with 0, 8.75, 17.5, 35, 70, 140, 420, 1260, or 2520 g glyphosate active ingredient ha^{-1} in a spray cabinet using Hardi LD-02-100 hydraulic nozzles, 3 bar pressure, a spray volume of 150 L ha^{-1}, and a speed of 5 km h^{-1}. Photosynthetic efficiency was measured after 48 h, shoots were sampled after 72 h for RNA sequencing, and biomass was determined after 14 days. Dose-response models showed no environmental effect on ED_{50} or ED_{90} in either grass species. Oilseed rape, however, required significantly less glyphosate under future conditions: ED_{50} declined from 95 to 76 g ha^{-1} and ED_{90} from 220 to 109 g ha^{-1}. Transcriptome responses were species specific. Climate conditions explained variation in wild oat, whereas glyphosate dose dominated in oilseed rape. In glyphosate-treated oilseed rape, protein-biosynthesis pathways were enriched among upregulated genes, while photosynthesis, carbon metabolism, and secondary metabolism were downregulated. At high glyphosate exposure, barnyard grass showed weaker stress-associated transcriptional responses under future than ambient conditions, consistent with greater tolerance. These results demonstrate that climate conditions reshape glyphosate responses in a species-dependent manner and that transcriptomics can reveal mechanisms not evident from biomass responses alone, improving forecasts of weed control under changing climates.

Keywords: climate change; glyphosate efficacy; RNA sequencing; transcriptomics; weed management

Detection and characterization of the ALS Pro-119-His mutation in *Digitaria sanguinalis* populations from Spanish maize fields

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Abstract

ALS-inhibiting herbicides are widely used for grass weed control in Spanish maize production systems, where Digitaria sanguinalis (L.) Scop. is one of the most troublesome species. As part of a larger project investigating herbicide resistance in grass weeds in these systems, twenty-six D. sanguinalis(DIGSA) populations collected in 2024 from two major maize-producing regions, Castilla y León (14 populations) and the Ebro Valley (12), were screened for target-site resistance by next-generation sequencing (NGS) of the ALS gene, as described in Délye et al. (2019). Fifty plants per population were sequenced to detect resistance-associated mutations and estimate resistant allele frequencies.The ALS Pro-119-His substitution was detected in four populations from the Ebro Valley, where allele frequencies varied between 1.4% and 83.8%. Although this substitution has been proposed as a potential resistance mechanism to ALS-inhibiting herbicides based on crystallographic and molecular docking studies, its phenotypic effect remains uncharacterised. To assess whether this mutation contributes to resistance, populations carrying the mutation were screened in greenhouse experiments using nicosulfuron at the recommended field rate (45 g a.i. ha^{-1}). Herbicide response was evaluated four weeks after treatment (WAT) using aboveground dry biomass relative to untreated controls, and populations were classified according to the resistance rating system of Moss et al.(1999). Two populations were classified as developing resistance. The DIGSA P058 population, with the highest Pro-119-His allele frequency (83.8%), wasfurther evaluated for resistance to ALS-inhibiting herbicides. Plants were treated with nicosulfuron at 0, 22.5, and 45 g a.i. ha^{-1} or imazamox at 0, 25, and 50 g a.i. ha^{-1}, representing untreated, 0.5×, and 1× the recommended field rates, respectively. Each treatment comprised four replicates of 20 plants. Plants were maintained in a growth chamber and survival was assessed 3 WAT. Following nicosulfuron application, survivalwas 14.5% at the 1× rate and 34.2% at the 0.5× rate, suggesting reduced sensitivity to sulfonylurea herbicides. No lants urvived either imazamox treatment. These results reveal the presence of a poorly characterised ALS gene mutation in Spanish populations of D. sanguinalis. Additional functional studies and dose-response assays are required to determine whether the Pro-119-His substitution contributes to nicosulfuron resistance

Alternative pesticides for pre-emergence liverwort control in nursery container production

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Abstract

Common liverwort (*Marchantia polymorpha*) is a plant from bryophyte family growing in cool and damp areas, which makes it a persistent weed in greenhouse and nursery container production. Greenhouses being closed structures, hence conventional herbicide use is limited by crop sensitivity and production constraints. This study evaluated alternative pesticide formulations and a plant-derived extract for pre-emergence suppression of liverwort under greenhouse and controlled laboratory conditions. Two independent greenhouse runs tested Zerotol® (hydrogen peroxide + peroxyacetic acid), TetraCurb Max® (rosemary, clove, peppermint, and castor oils), and a 1× + 1× combination. Individual products were applied at 0.25×, 0.5×, 1×, 2×, and 4× using a carbon dioxide backpack sprayer equipped with an 8004 flat-fan nozzle calibrated to 252.6 L ha^{-1} at 206.8 kPa. Liverwort coverage was assessed weekly for 7 weeks, and fresh biomass was measured at 7 weeks after treatment. A complementary 20-day agar bioassay evaluated the same products and an additional botanical candidate maple leaf aqueous extract, including an untreated control for effects on gemma survival and germination. Greenhouse coverage was strongly influenced by assessment time ($P < 0.001$), with significant chemical × rate × time and run × chemical × rate interactions, indicating variable treatment performance between runs. By 7 weeks after treatment, liverwort coverage was high across all factorial treatments, demonstrating that a single pre-emergence application did not provide prolonged suppression under repeated inoculation pressure. Fresh biomass responses were also run dependent; in Run 1, Zerotol at 1× reduced biomass to 27.9 g compared with 44.5 g in the untreated control, whereas treatments did not differ significantly in Run 2. In contrast, laboratory responses were pronounced. Final gemma survival was 0% for all Zerotol rates, TetraCurb Max at 1× to 4×, and maple extract at 0.5× to 4×, while the untreated control maintained 100% survival and germination. These results demonstrate strong direct activity against liverwort propagules but limited greenhouse persistence. Alternative pesticides and plant-derived treatments may therefore contribute to integrated liverwort management, but application timing, persistence, repeat applications, and ornamental crop safety require further evaluation.

Keywords: Marchantia polymorpha, oils, maple extract

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Herbicide Resistance Mapping in the Czech Republic: From Field Reports to Molecular Characterisation

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Abstract

Herbicide resistance is an increasing challenge for sustainable weed management in the Czech Republic. Identifying and mapping resistant weed populations is essential for understanding the distribution of resistance, recognising emerging threats, and developing effective management strategies. This contribution presents an approach to herbicide resistance monitoring that combines reports of reduced herbicide efficacy from farmers and agronomists with systematic sampling, controlled pot experiments, and molecular analyses.

Seeds collected from suspected resistant populations are evaluated under controlled conditions using dose–response experiments to confirm resistance and quantify differences in herbicide sensitivity. Where appropriate, molecular analyses, including sequencing of target-site genes such as acetolactate synthase (ALS) and acetyl-CoA carboxylase (ACCase), are used to identify known resistance-associated mutations. Further investigations can help distinguish target-site resistance from potential non-target-site mechanisms.

Current monitoring efforts focus particularly on Apera spica-venti, Bromus sterilis, Tripleurospermum inodorum, Amaranthus retroflexus, and Chenopodium album, which represent important targets for resistance investigation in Czech cropping systems. The integration of field observations, phenotypic confirmation, and molecular characterisation provides a framework for documenting the occurrence and mechanisms of herbicide resistance in important Czech weed species. Linking these data with the geographical origin of sampled populations can support the development of a national resistance map, improve early detection of emerging resistance, and facilitate evidence-based decisions on herbicide use and integrated weed management. This approach also highlights the potential of weed genomics to strengthen resistance surveillance and support more sustainable crop production.

Keywords: herbicide resistance; resistance monitoring; dose–response experiments; molecular characterisation; weed mapping

Weed resistance research in Lithuania

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Abstract

Herbicide resistance is an emerging challenge in Lithuanian winter cereal production. Its development is promoted by cereal-dominated rotations, reduced or no-tillage systems, limited crop diversification, and repeated use of herbicides with the same mode of action, particularly acetolactate synthase (ALS) inhibitors. This review summarizes evidence on the occurrence, investigation, and management of herbicide-resistant weeds in Lithuania.

Herbicide resistance has been investigated most extensively in *Apera spica-venti*. Between 2014 and 2018, researchers at the Lithuanian Research Centre for Agriculture and Forestry collected seeds from fields where herbicides had failed to control this species. Greenhouse experiments conducted in 2016–2018 tested 159 populations against the ALS inhibitors iodosulfuron-methyl-sodium, sulfosulfuron, and pyroxsulam; the acetyl-CoA carboxylase inhibitors fenoxaprop-P-ethyl and pinoxaden; and the Photosystem II inhibitor isoproturon. Forty-three percent of the populations were resistant to ALS inhibitors. Resistance was most frequent to sulfosulfuron and least frequent to pyroxsulam. All pyroxsulam-resistant populations were also resistant to the other ALS inhibitors tested. In 2013, *A. spica-venti* was recorded in Lithuania as resistant to HRAC Group 2 herbicides.

Field observations and farmers' reports indicate reduced herbicide efficacy against other weeds, particularly *Alopecurus myosuroides*, and populations of *Poa annua*, *Lolium* spp., *Centaurea cyanus*, *Papaver* spp., *Stellaria media*, and *Chenopodium album*. However, dose-response and genetic studies remain limited for most of these species in Lithuania. Control failure should not automatically be regarded as evidence of resistance because it may result from inappropriate application timing, advanced weed growth stages, adverse weather, insufficient application rates, uneven spray coverage, or post-treatment emergence. Resistance should be confirmed through whole-plant bioassays, comparison with susceptible reference populations, and, where feasible, genetic analysis. Available evidence confirms the relevance of herbicide resistance but does not permit reliable estimation of its national prevalence because samples have originated from fields with documented control failures. Regional comparisons require standardized representative sampling, field-level herbicide-use histories, and repeated testing. National monitoring should integrate bioassays, rapid diagnostic techniques, and genetic characterization of resistance mechanisms. Management should combine diversified crop rotations and tillage systems, herbicides with different modes of action, non-chemical control methods, and prevention of seed production by surviving weeds.

Keywords: *Apera spica-venti*; ALS inhibitors; herbicide resistance; monitoring; winter cereals

Genomic Characterisation and High-Throughput Glasshouse Screening of Herbicide-Resistant Weeds to Drive Novel Solutions

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Abstract

Since the 1950s, a significant number of herbicide resistance cases have been documented as a result of repeated applications of a single mode-of-action, leading to substantial reductions in crop yields. The Resistance team at Syngenta Jealott's Hill International Research Centre has established pipelines for identifying, monitoring, and screening existing and novel resistance mechanisms. Our success hinges on our network of global contacts, who provide seed populations expressing unique characteristics, alongside field collections sourced from diverse cropping systems and selection pressures. These collections help us further understand resistance landscapes and best support local market needs. We use a combination of genomic methodologies (e.g. Sanger sequencing, Kompetitive Allele Specific PCR (KASP), next-generation sequencing) and glasshouse screens to characterise the resistance profiles of plants to identify any populations with significant interest for our assays. We also employ these methodologies to purify seed populations from inventoried parental lines for deployment within our herbicide screening portfolio, using the resulting data to inform product research and development. Our seed stocks supply high-throughput glasshouse screening platforms that utilise purified lines of both target-site and non-target-site resistance, allowing us to develop products such as VIRESTINATM technology (Metproxybicyclone), which is highly specialised in controlling acetyl-CoA carboxylase target-site mutations and non-target resistance. Supplying relevant, high-quality seed lines to purpose-built screening platforms empowers our research teams to better understand and tackle the growing challenge of herbicide resistance faced by growers worldwide.

Keywords: bulking, target-site resistance, non-target-site resistance, seed lines, Sanger Sequencing

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Mining the Angiosperms353 Probe Set for Biomonitoring:

A case study in Apera spica-venti

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Abstract

Apera spica-venti (loose silky-bent) is a widespread arable weed occurring in cereal-growing regions worldwide and representing an increasing challenge for sustainable crop production. Reliable species identification is essential for studying its distribution and can be useful for detecting the presence of the seeds in soil seed bank. Our research aims to design and validate species-specific primers for *A. spica-venti* using an integrative genomic and transcriptomic approach. The primary source for candidate marker development was the Angiosperms353 probe set, which provides nuclear sequence data from 353 conserved low-copy genes across angiosperms. Comparative analysis of these loci was combined with available transcriptomic reads and the genome sequence of *A. spica-venti* to identify regions that are both conserved within the species and sufficiently divergent from related taxa. Candidate sequences were screened for informative species-specific polymorphisms, and primer pairs designed to generate amplification products suitable for identification of the target species. Primer specificity was evaluated across 10 populations representing geographic range of *A. spica-venti* in Latvia, as well as in taxonomically related grass species, common weeds, and crops. The resulting primer set is expected to enable analysis of soil samples for presence/absence, as well as quantification of the seeds in soil seedbank. By integrating a standardized nuclear gene resource with species-level transcriptomic and genomic data, the project will establish a novel framework for developing diagnostic primers in non-model weed species. These tools may support monitoring of weed spread and development of evidence-based management strategies in cereal agroecosystems.

Keywords: *Apera spica-venti*, species-specific primers, Angiosperms353, arable weeds, biomonitoring

From Herbicide Response to Genomic Adaptation: Integrating Herbicide Resistance Phenotypes and Stress-Associated Variation in Parthenium hysterophorus and Other Weeds

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Abstract

Herbicide resistance is an increasingly important manifestation of rapid weed adaptation, yet the genetic and regulatory mechanisms underlying variable herbicide responses remain incompletely understood in many broadleaf weeds. Integrating weed genomics with phenotypic herbicide-response data offers an opportunity to move beyond descriptive resistance screening toward identification of genomic and molecular features associated with adaptive herbicide responses. We investigated this concept using *Parthenium hysterophorus* and other agriculturally important weeds as experimental systems within an ongoing programme on genomic variation and stress adaptation. In *P. hysterophorus*, molecular characterization of stress-associated genes revealed substantial polymorphism in key components of polyamine metabolism, including spermidine synthase (SPDS), spermine synthase (SPMS), arginine decarboxylase (ADC), and caffeic acid O-methyltransferase (COMT), with variation differing among phenological stages. These findings provide a molecular framework for examining how stress-responsive metabolic pathways may contribute to differential herbicide responses and weed resilience. Complementary investigations in *Alternanthera* spp. demonstrated stage-associated polymorphism in polyamine-metabolism genes, with *SPDS* showing consistent polymorphism across developmental stages and *ADC* and *COMT* displaying greater variation during reproductive development. The observed molecular variation was considered in relation to growth-stage-dependent weed management and herbicide efficacy. Building on these observations, our current work integrates phenotypic herbicide-response/resistance data with genomic and molecular variation to identify candidate mechanisms associated with differential herbicide sensitivity and adaptation. Particular attention is being given to distinguishing genomic variation potentially associated with target-site responses from broader stress-response and metabolic mechanisms that may contribute to non-target-site adaptation. This approach is especially relevant for weeds such as *Parthenium*, where strong ecological plasticity and environmental adaptability

complicate conventional management. Our working hypothesis is that herbicide adaptation is not determined solely by individual target-site mutations but may also involve combinations of genetic variation, stress-responsive metabolic pathways and developmental-stage-dependent regulation. Polyamine-associated pathways are therefore being investigated as potential components of a broader adaptive network rather than as isolated resistance determinants. The integration of phenotypic response data with genomic variation provides a framework for prioritizing candidate genes and pathways for subsequent functional validation. The study demonstrates how weed genomics can connect field-level herbicide-response phenotypes with molecular mechanisms of adaptation, providing a basis for more precise resistance diagnostics and sustainable weed-management strategies. Participation in the Prague Weed Genomics Training Course will further strengthen this work through practical approaches for genomic-data analysis, de novo annotation, RNA-seq interpretation, experimental design and identification of functionally relevant candidate genes. Ultimately, we aim to develop a genomics-informed framework for understanding herbicide adaptation in Indian weed populations and translating genomic information into improved resistance surveillance and integrated weed management.

Keywords: Genomic variation, stress adaptation, functional genomics, candidate genes, polyamine metabolism

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Enabling Nanopore duplex sequencing for cost-efficient and accurate haplotype-resolved gene analysis of pooled weed samples

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Abstract

Herbicide resistance in weeds threatens crop yields worldwide. Molecular techniques help to diagnose target-site resistance (TSR), one of the main mechanisms of herbicide resistance. As high-resolution diagnosis is becoming increasingly important, a cost-efficient, highly scalable method combining sample pooling with compact and affordable Nanopore sequencing was developed previously, and thousands of weed biotypes have since been screened for target-site mutations.

Going forward, not only SNP allele information but also gene haplotype information should be assessed. This would make it possible to study e.g. the number and distribution of haplotypes carrying resistance alleles in weed populations. However, obtaining this information by sequencing single plants individually is costly and time-consuming. We therefore saw the need for a method that generates accurate sequences from pooled plants. PacBio HiFi sequencing is one option, but it is inflexible, slow, and expensive to set up and run. Another option is duplex sequencing by Oxford Nanopore Technologies (ONT), in which the template and complement strands of a single DNA molecule pass through the same pore in succession, achieving a per-base accuracy above Q30 (>99.9%). However, ONT's duplex method is not compatible with low-complexity amplicon libraries. We have therefore developed an extension of ONT's method that generates duplex reads even from highly similar amplicons.

Building on the approach of Karst et al. (2021), which uses unique molecular identifiers (UMIs) to identify reads derived from the template and complement strands of the same molecule, we further optimized library preparation to increase the duplex rate. After sequencing, a pipeline that we developed specifically for this application extracts candidate duplex read pairs based on a high similarity of their UMIs, the sequencing pore and the time of sequencing. The reads are then demultiplexed by their barcodes, and duplex reads are called with the Dorado duplex basecaller.

We will describe the principle of the method, present preliminary results and outline useful applications for herbicide resistance research and for practical resistance management, such as gene analysis at haplotype resolution, detection of complex variants and variant combinations, detection of rare variants, monitoring of gene amplification events and comparison of resistance haplotypes between neighboring fields

Can Provisia® Solve Herbicide Resistance Problems in Rice Fields? Lessons from the First Experience in Turkey

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Abstract

Herbicide-resistant in grass weeds have become one of the greatest constraints to sustainable rice production in Turkey. For more than two decades, intensive use of acetolactate synthase (ALS)- and acetyl-CoA carboxylase (ACCase)-inhibiting herbicides has selected resistant populations of *Echinochloa crus-galli*, *E. oryzoides*, E. oryzicola and *Leptochloa fusca* become increasingly difficult to control. To overcome resistance to these herbicide, the Provisia® rice production system, based on cycloxydim-resistant rice cultivars, was recently introduced in Turkey. The system was expected to provide an effective alternative for managing resistant grass weeds. However, its long-term sustainability under field conditions remains uncertain. Field surveys were conducted during the 2025 and 2026 growing seasons in the major rice producing regions of Turkey where the Provisia® production system had been adopted. Commercial rice fields with a history of ALS- and ACCase-resistant weeds were inspected approximately two years after the introduction of cycloxydim-resistant rice. Weed control efficacy following cycloxydim application was visually assessed, surviving plants were recorded, and seed samples of *Echinochloa oryzoides* and *Leptochloa fusca* were collected from fields where control failures occurred. Preliminary greenhouse screening was performed by treating collected populations with the recommended field rate of cycloxydim to verify resistance under controlled conditions. The surveys revealed that although the Provisia® system initially provided excellent control of resistant grass weeds, its effectiveness rapidly declined in several commercial fields. Surviving populations of *E. oryzoides* and *L. fusca* were observed despite applications at the recommended cycloxydim dose. Greenhouse evaluations confirmed that these populations survived cycloxydim treatment, indicating the evolution or rapid selection of cycloxydim-resistant biotypes within only two years of Provisia® adoption. These findings suggest that the widespread presence of pre-existing ACCase resistance mechanisms and the repeated use of a single herbicide mode of action have accelerated resistance development. The first experience with the Provisia® system in Turkey demonstrates that introducing a herbicide-resistant crop alone cannot provide a sustainable solution to herbicide resistance in rice production. Reliance on cycloxydim as the sole post-emergence grass herbicide has already resulted in control failures of *E. oryzoides* and *L. fusca*. To preserve the usefulness of the Provisia® technology, integrated weed management strategies must be implemented immediately. Future studies should characterize the resistance mechanisms responsible for cycloxydim resistance and evaluate integrated management strategies to delay further resistance evolution. The Turkish experience highlights the importance of stewardship programs and demonstrates that herbicide-resistant crop

technologies must be integrated with diversified weed management practices to remain effective over the long term.

Keywords: acetolactate synthase (ALS) inhibiting herbicide, acetyl-CoA carboxylase (ACCase)-inhibiting herbicide, *Echinochloa crus-galli*, *Leptochloa fusca*

Amplicon Sequencing and Seed Biopriming Insights into Cover Crop Weed Suppression in a Med vineyard

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Abstract

Weeds are major competitors for resources in vineyard systems, and their management increasingly relies on non-chemical strategies to reduce herbicide dependency and resistance selection pressure. Winter cover crops can suppress weeds through resource competition, and this ability may be enhanced by seed priming technologies that improve early crop vigour. This study evaluated the effect of seed priming (hydropriming combined with Bacillus spp. spores) on the weed-suppressive performance of five winter cover crop treatments in a Mediterranean vineyard and explored associated changes in soil active carbon and bacterial communities. A field trial was conducted over two growing seasons (2023 and 2024) in a non-irrigated vineyard in Askri, Boeotia (Central Greece), using a randomized complete block design. Lathyrus sativus, Pisum sativum, Hordeum vulgare, Trifolium subterraneum and a H. vulgare–Vicia sativa mixture were sown as unprimed or hydro-bioprimed seed, alongside a weedy control without cover crops. Above-ground weed biomass, soil active carbon (POXC) and bacterial community composition (16S rRNA metabarcoding, Illumina MiSeq) were assessed. All cover crop treatments reduced weed biomass compared with the weedy control, with the strongest suppression under H. vulgare and the H. vulgare–V. sativa mixture. Seed priming on cover crops resulted in reduced weed biomass in most cover crop reatments. POXC was generally higher under cover crops than in the weedy control in the first season. In the second season, POXC declined in all treatments, including the control, most likely due to inter-annual variability, with P. sativum showing the smallest decline. Preliminary microbiome analysis revealed differences in bacterial diversity. Between full flowering (T0) and one month after residue incorporation (T1), most bacterial genera increased in abundance, particularly the decomposer genera Massilia, Olivibacter and Sphingobacterium, whereas decreases were few and mainly observed under L. sativus, involving the genera Rhodoplanes, Nitrospira and MND1. Seed priming improved the weed-suppressive ability of most winter cover crops, with cereal-based treatments providing the strongest

suppression. These results support seed priming as a practical, non-chemical tool for integrated weed management in Mediterranean vineyards. The soil carbon and microbiome data suggest that these changes indicate cover crops influence short-term soil functioning, which needs long-term validation.

Keywords: weed suppression , cover crops , seed priming , integrated weed management , soil microbiome

Preliminary Screening of Amaranthus Populations Collected from Potato-Growing Areas in Türkiye for Resistance to Metribuzin

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Abstract

The intensive and repeated use of herbicides for weed management in agricultural production is one of the major factors promoting the evolution of herbicide resistance in weed populations. *Amaranthus* species, which are commonly found in potato-growing areas, can cause significant yield losses by competing with crops for essential resources. Metribuzin, a photosystem II (PSII) inhibitor, is an important herbicide widely used for weed control in potato production. This study aimed to evaluate the responses of *Amaranthus* populations collected from different potato-growing regions of Türkiye to the registered field rate of metribuzin and to identify populations with suspected herbicide resistance.

A total of 367 populations belonging to *Amaranthus retroflexus* L., *Amaranthus hybridus* L., and *Amaranthus albus* L., collected from potato-growing areas in Afyonkarahisar, Aksaray, Ankara, Bolu, Düzce, Eskişehir, Konya, and Sakarya provinces, were evaluated using a herbicide bioassay. Metribuzin was applied post-emergence to all populations at the registered field rate of 75 g/da, using a spray volume of 30 L/da. Plant responses to the herbicide treatment were assessed at 7, 14, and 28 days after application (DAA) using a 0–5 rating scale.

At 28 DAA, surviving plants were observed in 31 of the 367 populations (8.45%). Of these populations, 18 were identified as *A. retroflexus*, 12 as *A. hybridus*, and one as *A. albus*. These findings indicate that some *Amaranthus* populations were able to survive the registered field rate of metribuzin, suggesting that further investigations are required to evaluate their potential resistance. In the subsequent stages of the research, dose–response experiments are planned to assess the suspected populations and confirm their resistance status to metribuzin. This preliminary screening study provides baseline data for identifying *Amaranthus* populations with suspected resistance to metribuzin in major potato-growing areas of Türkiye and contributes to guiding further herbicide resistance investigations.

Keywords: *Amaranthus retroflexus*, *Amaranthus hybridus*, *Amaranthus albus*, metribuzin, herbicide resistance, potato.