BRASSICA2017

VII International Symposium on Brassicas

Pontevedra 22-25 May

ABSTRACTS BOOK

CSIC
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ISHS
International Society for Horticultural Science

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Misión Biológica de Galicia

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VII International Symposium on Brassicas

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7th International Symposium on Brassicas

Abstract Book

Organized by

Misión Biológica de Galicia (MBG-CSIC)

International Society of Horticultural Science (ISHS)

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BRASSICA 2017

Welcome to the 7th International Symposium on Brassica

Dear colleagues

On behalf of the International Society of Horticultural Science (ISHS), the Group of Genetics, Breeding and Biochemistry of Brassicas (MBG-CSIC) is pleased to welcome you to Pontevedra (Galicia-Spain), to attend the 7th International Symposium on Brassica. We succeeded in attracting over 100 participants, from 24 countries in Europe, Asia, America and Africa.

During this conference we aim at bringing together scientists that are active in diverse areas of *Brassica* research in order to exchange scientific knowledge and ideas.

To stimulate exchange between the disciplines genetic diversity, agronomy, resistance to stresses, food technology, quality and ‘omics’ we chose seven plenary sessions and invited keynote speakers in the respective disciplines and poster session introduce by poster flash presentations.

We are grateful for the support and work of the International Scientific Committee for helping to ensure we have a high quality and varied scientific programme.

Thank you to the participants for their interest and contributions to the Symposium. We are also thankful to the sponsors of the Symposium.

We hope you will have a pleasant stay in Pontevedra and you take the opportunity to make new friends and contacts

On behalf of the Organising Committee

Elena Cartea

Elena Cartea
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Opening Lecture

VII International Symposium on Brassica

Russian *Brassicaceae* collection – from N.I. Vavilov and E.N. Sinskaya till nowadays

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The Russian worldwide *Brassicaceae* collection keeping in VIR consists of 10682 accessions of 26 species: vegetable, oilseed, spicy, ornamental crops. The collection includes wild species, landraces, old and advanced cultivars, hybrid populations, inbred and double haploid lines and mapping populations. The formation of VIR *Brassicaceae* collection had begun in 1923 after N.I. Vavilov visit West-European countries, USA and Canada (1921-1922), Russian resources were registered through All-Russian agricultural exhibitions, and the landraces were collected in the centers of origin and biodiversity determined by N.I. Vavilov and then E.N. Sinskaya. 1500 accessions of vegetable *brassicas* were collected by N.I. Vavilov himself and his colleagues till 1940; till nowadays VIR manages 2-4 collecting missions annually. In 1926 VIR scientists started to study the collection. As result of evaluation in different geographical zones and phylogenetic studies the subspecies, varieties, forms, cultivar groups distinguished on complex of biological traits were described (Sinskaya, 1928; Shebalina, 1974; Lizgunova, 1965, 1984; Shebalina, Sazonova, 1985; Artemyeva, 1999, 2001, 2004) and character and core collections reflecting diversity of all species were created. The VIR evaluation dates include 40-43 morphological characters for vegetable crops, 18-23 characters for oilseeds, immunological, physiological, and biochemical traits. For instance highest content of the nutritive and bioactive substances was found in pakchoi, tatsoi, leafy turnip in *Brassica rapa*. Every year 30-40 new brassicas genetic sources of investigated valuable traits VIR provides to breeders; some of sources have been DNA markered. The modern approaches – DNA fingerprinting, QTL and association mapping have been developed in VIR. Marker-phenotype associations have been found for many important traits (bolting and flowering time, growth related traits, morphological characters connected with quality, productivity, as well as biochemical and resistance features) using SSR and S-SAP molecular markers. SSR markers of characters of quality have been selected for screening collection and pre-breeding investigations.

Session 1. Genetic Resources and Agronomy

Keynote

Diversity and use of *Brassica oleracea* L. for the innovation of the agricultural systems and products

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Keywords: *Brassica oleracea*, germplasm, crop wild relative, food innovation, antioxidant compounds

Brassica crops have followed several evolutionary pathways leading to modern cultivars which are widely grown around the world. Broccoli, cauliflower and kale have their center of origin and diversity in the Mediterranean basin and their wide primary gene pool has been under evaluation since a few decades in South Italy and especially in Sicily. The high diversity of broccoli, cauliflower and kale, which belong to the *Brassica oleracea* L. species, seems to reflect the different steps of the same domestication process for these crops. In addition, the diversity within and between Sicilian landraces starts to be well known. This great diversity is exploited on the Island for different processing purposes, such as in the cases of the low curd density landraces of violet and green cauliflower and of the sprouting broccoli. The richness of types and forms diffused in Sicily, mainly in peri-urban farms and home gardens, is also paralleled by a wide range of wild *Brassica* species (n=9) which are widespread throughout the Mediterranean coasts and islands, and which in some areas seem to intercross easily with the widely cultivated *B. oleracea* crops. This wild material represents a broad source of diversity that could enhance the existing crop’s variability. During the last decades, several Authors have evidenced the contribution of wild and cultivated Sicilian *Brassica* germplasm to the improvement of agronomic and nutraceutical traits of *Brassica* crops, such as resistance to pests or the high content of health-related compounds like glucosinolates, anthocyanins, carotenoids, total polyphenols and ascorbic acid, as they are starting to be utilized as phytochemical indicators for the traceability of the products. We will discuss about the main results and perspectives devoted to the innovation of food and agriculture, thanks to the investigation and use of the Mediterranean gene pool of the *B. oleracea* species group (n=9).

A comprehensive perspective on *Brassica* vegetable crops grown in Turkey

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Keywords: *Brassica* vegetables, production potential, growing, yield, Turkey

Vegetable *Brassica* crops are an important and highly diverse group of crops grown world-wide that belong mainly to the species *Brassica oleracea* and *Brassica rapa.* Brassicas are widespread as wild, weedy and cultivated forms throughout Turkey. It has a significant place in world vegetable production. Turkey is fourth after China, India and the United States in the world in terms of vegetable production. *Brassicaceae* is one of the most important cultivated families in Turkey. The total production of *Brassica* vegetable species in Turkey is 995.294 tons in 2015. Cabbages are the most economically important members of the genus *Brassica.* Cabbages and kale are traditionally grown and consumed for many years in Turkey. They can be consumed in different ways. White cabbage is the most important cultivated *Brassicas* in Turkey; its production has the largest quantity (514.344 t). It is followed by cauliflower (182.266 t), red cabbage (178.679 t), kale (71.118 t), broccoli (46.353 t) and Brussels sprout (2.534 t). Broccoli, kohlrabi and Brussels sprouts have been cultivated in Turkey during the last 25-30 years. There are over four hundred different commercial cultivars of cabbage, cauliflower and broccoli in Turkey. Hybrid cultivars are commonly used in the cultivation of cabbage broccoli, cauliflower and Brussels sprout, whereas open pollinated cultivars are only used in kale growing. Farmers have maintained the local population of kale, which are mainly sold in local markets. The aim of this review is to present *Brassica* vegetable crops the last status in Turkey, the growing techniques and problems of the species, and the probable utilization of the presented species. This detailed overview will give an insight for agricultural scientists regarding the up to date situation with the *Brassica* vegetable species production potential in Turkey, and provide information about these species.

Potential usability of CMS rucola for the breeding process

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Keywords: *Eruca sativa*, *Diplotaxis tenuifolia*, CMS, Ogura, alloplasmic lines, male sterility, agronomical traits

The Ogura CMS is the most intensively analyzed source of alloplasmic CMS in *Brassicaceae* and broadly used in radish, cabbage and rapeseed breeding. Another crop from the *Brassicaceae* family with increasing demand is rucola. Under this name salad rocket (*Eruca sativa*) as well as the perennial wall rocket (*Diplotaxis tenuifolia*) are commercially distributed. So far, for both species no hybrid system is available. Therefore male sterile cauliflower cv. 'Korso', harbouring an 'Ogura' based cytoplasm, was crossed with *E. sativa* and *D. tenuifolia* as pollen parent. Intergeneric hybrid plants have been generated from these manual crosses. Allotetraploid F_1-hybrid plants obtained after colchicine treatment were backcrossed several times with the respective rucola parent. Elimination of *Brassica* genomic DNA was verified using molecular markers, GISH analysis, flow cytometry and chromosome analysis. All backcross plants from BC_2 up to the BC_6 generation of the *B. oleracea* x *E. sativa* (BE) cross showed male sterility and full seed set comparable to the *Eruca* parent. Agronomical traits such as plant vigour, biomass production, flowering and seed set were recorded for the different backcross generations. No further incompatibilities were noticed between the CMS inducing cytoplasm and the *E. sativa* genome. The developed alloplasmic lines are diploid with 2x = 22 chromosomes and could be introduced without any problems into the breeding process. Also BC_1 plants of the cross *B. oleracea* x *D. tenuifolia* (BD) had completely male sterile flowers. The phenotype was similar to that of the *D. tenuifolia* parent. Unlike the BE combination, BD needed embryo rescue to establish BC_2 plants. The flowers showed besides the male sterility a pronounced female sterility, expressed by the abort of ovaries and failed seed set. Hence, this combination seems to be not applicable for the breeding process. Reasons for this strikingly different behavior are under investigation.

Effect of the growing system in the leaf morphology of *Diplotaxis erucoides*

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Keywords: leaf colour, leafy vegetable, morphological traits, wall rocket

Worldwide there are around 7,000 edible plant species which are known to have been consumed by humans. Wall rocket (*Diplotaxis erucoides*) is an herbaceous plant widespread in the Mediterranean region. As a leafy vegetable, this plant can be used as a component of salads, providing a characteristic, mild pungent flavour. Due to the potential interest of this species, we are initiating a breeding program, of which the establishment of a correct growing system is an important part. In this study, two wild, pre-selected populations of wall rocket were analyzed and compared with a commercial variety. Material was grown in the late autumn-winter season under two different systems, greenhouse and open field, and leaf morphological traits were evaluated. Remarkable differences were found among the growing systems in the morphology of the leaves as well as in the leaf colour. Plants growing in greenhouse had larger total leaf area than those growing in the open field. The leaf length/width ratio was greater in greenhouse than in the open field for the wild populations, while it did not change significantly in the commercial variety. Leaf lobation was more marked in the open field in all populations assayed. The relative clorophyll content decreased in the greenhouse system, while both the hue angle and chroma increased compared to the open field system. Despite the larger size of the leaves in greenhouse, their lighter colour and few lobation makes them less attractive for the salads market. Therefore, cultivating this species in open field seems to offer a better potential for a ready-to-eat product.

Session 2. Genetic Diversity

Keynote

Morphotype diversification and convergent crop domestication in *Brassica rapa* and *Brassica oleracea*

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Keywords: *Brassica*, morphotypes, leafy heads, turnips, domestication, parallel selection

Brassica rapa and *Brassica oleracea* species have diversified into a large number of morphotypes due to domestication and further breeding. Surprisingly a similar range of morphotypes is present in both species although a common origin seems unlikely as the two species diverged long before they were domesticated for agriculture. As expected from this convergent domestication, many of the genes that were under selection in both species by showing a reduced DNA variation in the derived morphotype, were syntenic orthologs, proving convergent domestication at the molecular level. An additional finding was that for several loci evidence was provided for a parallel selection among the three subgenomes. A number of candidate genes that are responsible for the cabbage and the tuber forming morphotypes in both species were identified. Early events in leafy head formation in Chinese cabbages and tuber formation in turnips are identified and the function of some genes in these extreme phenotypes is presented.

Genome sequencing supports a multi-vertex model for *Brassiceae* species

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Keywords: *Brassica* crops, *Brassiceae* tribe, triangle of U, polyploidization

The economically important *Brassica* genus is a good system for studying the evolution of polyploids. *Brassica* genomes have undergone whole genome triplication (WGT). Subgenome dominance phenomena such as biased gene fractionation and dominant gene expression were observed in tripled genomes of *Brassica*. The genome of radish (*Raphanus sativus*), another important crop of tribe *Brassiceae,* was derived from the same WGT event and shows similar subgenome dominance. These findings and molecular dating indicate that radish occupies a similar evolutionary origin as that of *Brassica* species. Here, we extended the *Brassica* “triangle of U” to a multi-vertex model. This model describes the relationships or the potential of using more *Brassiceae* mesohexaploids in the creation of new allotetraploid oil or vegetable crop species.

Weedy and wild *Brassica rapa* worldwide: origins, relationships, and a surprising pool of diversity

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Keywords: germplasm, ferality, weediness, *Brassica rapa*, dedomestication

Distinguishing truly wild crop relatives from feral escapes is important for germplasm conservation, weed control, and further research on local adaptation, domestication and dedomestication. In addition to its economically important crop derivatives (e.g. oilseeds, turnips, pak choi, Chinese cabbage), *Brassica rapa* includes one of the most invasive agricultural weeds of temperate regions: weedy field mustard. The relationship between the weedy populations and crop types is largely unresolved and as a result, some of the populations that appear to be weeds may be wild material instead. This means that instead of being conserved, the wild populations may be eradicated as undesirable weeds instead of conserved for genetic diversity which may be useful for breeding in *B. rapa*, *B. napus*, and *B. juncea*. To address this gap in knowledge, we analyzed GBS data for 192 individuals derived from 87 spontaneous *B. rapa* populations from 18 different countries. These were compared to a diverse panel of 333 *B. rapa* samples previously analyzed by Kevin Bird and collaborators. We found that the weedy *B. rapa* was similar to turnips and rapini and contained nearly as much nucleotide diversity as all of the crop types combined suggesting a potential exoferal origin. We also conducted a common garden greenhouse experiment comparing phenotypes of spontaneous *B. rapa* populations with the crop types found to be most similar by GBS analysis. We grew seeds from 31 global weedy populations and 8 populations of rapini. We measured 12 traits associated with domestication/dedomestication and found that weedy populations typically had earlier flowering and less edible aboveground biomass, but otherwise were phenotypically very close to rapini. Our results clarify the relationships of various spontaneous *B. rapa* populations to each other and to major cultivar groups. These findings lay the groundwork for germplasm collection, mechanistic studies of dedomestication, and local adaptation.

Genetic analysis of seed vigour in *Brassica napus*

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Keywords: *Brassica napus*, seed, germination, vigour

Seed vigour is a key to the success of an oilseed rape crop from sowing through to final yield. This infield trait describes the fast and uniform emergence of seedlings leading to strong seedling establishment. With early vigour comes an improved ability to withstand pest and disease damage, rapid canopy closure leads to weed suppression, with a resultant increased crop yield. Currently most seed germination quantification is manual, this is very time consuming, labour intensive and limiting in what can be achieved. To address this problem we developed a high-throughput phenotyping platform using *Raspberry Pi* computers to control and perform high resolution time-lapse imaging of seed germination. The resultant image datasets are analyzed using a machine learning based software application to quantify seed germination frequency. In order to identify the driving genetic components underlying seed vigour we screened a large, diverse, collection of 96 *Brassica napus* species (Diversity Fixed Foundation Set) for their seed germination qualities using our newly developed system described above. All seed germination data was put through Genome Wide Analysis mapping (GWAS) for the identification of causative genomic regions and associated candidate genes within these regions identified. Knockout mutants of these genes were grown and analyzed for their germination and seedling vigour. We found that both flowering time and oil breakdown rate can be linked to seed vigour.

Session 3. Biotic Stress Interaction

Keynote

Brassica beats back the bugs. Constitutive and induced defense responses to herbivores

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Keywords: hervibores, glucosinolates, induced defences, aboveground-belowground interactions, volatiles

Plants are attacked by herbivores and pathogens both above and below the ground. They defend themselves by producing a wide range of morphological and chemical defenses. Many of these defenses are inducible and their production increases upon attack. An intrinsic network of hormonal signaling pathways determines which defenses are induced upon feeding by a particular herbivore. Because these hormones do not only act locally, but are transported throughout the plant, root herbivores elicit systemic responses in the shoot, and vice versa. These systemically induced responses not only have profound effects on the interactions with herbivores in the other compartment, but also on the effectiveness of natural enemies that prey upon or oviposit in these herbivores. In order to fully understand the mechanisms as well as consequences of (induced) resistance in plants, the different organizational levels involved need to be studied from molecule to ecological effect in an integrative fashion. Here I present our research on induced and constitutive defenses induced by a wide variety of aboveground and belowground herbivores in various wild and cultivated *Brassica* species. The general picture that arises is that the interactions between *Brassica* plants and their herbivores is extremely diverse and (species) specific. Signaling interactions caused by multiple herbivores feeding on the same plant cannot easily be predicted by studying single interactions. The implications for applications in agroecosystems are discussed.

Detection of Pro1 gene sequence polymorphisms in *Plasmodiophora brassicae* for the identification of geographical isolates in China

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Keywords: *Plasmodiophora brassicae,* Pro1 gene, geographical isolates, nucleotide variation, cleaved amplified polymorphism

Clubroot, caused by *Plasmodiophora brassicae* (*P. brassicae*), is one of the most economically important diseases of cruciferous crops as it can cause severe yield losses. When infecting the same host materials, *P. brassicae* from different geographic areas showed difference in pathogenicity. Serine protease, the expression product of *Pro1* gene from *P. brassicae*, could trigger resting spore germination. To find pathogenicity-related genes in *P. brassicae,* 8 isolate samples were collected from 8 locations in 7 provinces in China. PCR amplification, sequencing and data analysis were conducted. Results showed that there were 85 nucleotide variations in *Pro1* gene sequence among these 8 samples. Based on these variations, 8 samples were divided into 3 categories, the first category included XY, HB, QD, SY, the second included SM, WL, CY, while YY belonged to the third category alone. The result provides a reference for the further understanding of the evolution and variation of *Pro1* gene, as well as contributes to the further development of *Pro1* gene specific molecular markers. At the same time, it lays a theoretical foundation for scientific classification of *P. brassicae* by molecular markers. One CAPS (Cleaved Amplified Polymorphism Sequences) marker was developed in this research to distinguish the geographical isolates into three groups.

Pathogen identification of clubroot disease in Chinese cabbage from Yuanyang county, Henan province

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Keywords: Yuanyang County; clubroot disease; Chinese cabbage; pathogen indentification

To clarify the causal agent of clubroot disease in Chinese cabbage from Yuanyang experimental base, the isolate YY was collected from the clubroot for further research. After morphological, cytological observation and pathogenicity identification, the pathogen was preliminary inferred as *Plasmodiophora brassicae*. In order to quickly detect the pathogen, specific primers were designed according to D85819 and *Pro1* gene, respectively, and used to amplify the expected fragment from the template DNA of target pathogen. After PCR and sequence analysis, they showed 99% and 93% identity with the D85819 and *Pro1* gene sequences of *P. brassicae* from NCBI respectively. These results indicated that the pathogen was finally confirmed as *P. brassicae*, which were coincident with preliminary speculation. Moreover, *Pro1*-specific marker developed in this study can be applied to quick and accurate detection of *P. brassicae* isolate, which appears a useful assay method for detecting *P. brassicae* resting spores and improves efforts to halt the dissemination and better control this pathogen.

Changes in glucosinolates content in *Brassica oleracea* modulate disease severity caused by *Xanthomonas campestris* pv. *campestris*

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Keywords: secondary metabolites, resistant genotype, black rot; Phytochemicals

The potential of phytochemicals in sustainable disease management is increasing. *Brassica* crops have bioactive compounds called glucosinolates (GSL), which in higher quantities may result in plant resistance against biotic stress. Due to the lack of material with the same genetic background there are not conclusive studies on the defensive role of GSL against phytopathogens *in vivo*. The interaction between six genotypes of *Brassica oleracea* (kale) and the pathogenic bacterium *Xanthomonas campestris* pv. c*ampestris* (*Xcc*) was studied. These genotypes had different GSL content: high and low sinigrin (SINH, SINH), glucoiberin (GIBH, GIBL) and glucobrassicin (GBSH, GBSL), which had been obtained by a divergent selection program. During two consecutive experiments carried out in controlled conditions (time 1 and time 2), thirty plants of each genotype were inoculated with *Xcc*. Lesions area, disease severity and concentration of GSLs were measured at the end of each experiment. In general, the quantity of GSLs was higher and disease traits were lower in samples from time 2. There was diverse response among high content GSLs genotypes against pathogen. In GBS genotypes, less diseases severity and lower lesion area were observed in GBSH. In GIB selection, there was not significant difference between genotypes for disease severity but the interaction between genotype and time was significant. The individual analysis by time revealed that GIBH had higher disease severity in time 1 than GIBL, whereas in time 2 the relationship was inverted. SINH and SINL performed similar in both times and there was not effect on disease development with increased SIN quantity. As conclusion, increasing the amount of GSL in the plant, does not always lead to an increase in the response of the plant to pathogen. There was a clear effect of the indolic GSL (GBS) but not of the aliphatic (SIN, GIB).

Session 4. Resilience to Abiotic Stress

Keynote

Signaling and interacting proteins of Leucine-Rich-Repeat Receptor-Like Kinases in *Brassica* species

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Keywords: Receptor-Like Kinases, auto-and transphosphorylation, *Brassica* species, post-translational modifications, brassinosteroids

Plant and animal cells use receptor kinases that span the plasma membrane and function to transfer extracellular signals to the interior of the cell. In plants, binding of the ligand to the receptor's extracellular domain induces interaction with a co-receptor kinase. Among several Receptor-Like Kinases (RLKs), Leucine-Rich-Repeat Receptor-Like-Kinases (LRR-RLKs) are the major group of genes that plays crucial roles related to growth, development and stress conditions in plant system. Since it is involved in several functional roles it seems to be very important to investigate their roles in the *Brassica* species. Juxtaposition of the cytoplasmic protein kinase domains then results in their activation via auto- and/or trans-phosphorylation, and a signal transduction cascade that alters gene expression in the nucleus. We are broadly interested in the abiotic stress mechanisms that regulate the formation and activity of the receptor kinase signaling complex, including post-translational modifications such as phosphorylation and interaction with binding proteins (14-3-3 proteins and calcium/calmodulin). We identified phosphorylation sites with phosphor-specific Abs in *Brassica* BAK1 receptor kinase, co-receptor of BRI1. As we know, brassinosteroids modulate biotic/abiotic stress responses in higher plants. The function of specific sites of autophosphorylation is usually studied by directed mutagenesis of the protein to substitute the Ser/Thr/Tyr with a nonphosphorylatable residue or with an acidic amino acid phosphomimetic. In addition to these approaches we are also exploring the impact of a more subtle change, namely substitution of a Thr residue for a known Ser autophosphorylation site. Furthermore, the results establish that serine-threonine substitutions at known phosphosites are worth exploring as the residues may not be functionally equivalent and therefore may provide a new general strategy to engineer receptor kinase function in *Brassica* species.

Root phenotyping and lodging resistance in canola

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Keywords: root morphology, root anatomy, abiotic stress, electrical capacitance

Lodging is a main cause of yield loss and quality reductions in canola/oilseed rape and other crops. However, there has been little research to date on the mechanisms of crop lodging resistance, especially how this might be affected by high temperature stress and agronomic practices. Both controlled experiment and field trials were conducted to (1) examine the root morphological and anatomical traits of canola genotypes in response to heat and drought stresses and field management alterations; (2) determine the sensitivity of the root capacitance method for assessing crop lodging; (3) the impact of agronomic practices and abiotic stress on lodging and (4) develop an electrical capacitance method for estimating canola root morphological traits under soil conditions. At maturity, canola stems underwent a three point bending test, while the roots underwent a root lodging test. The morphological traits and anatomical features of the roots were also analyzed. The results showed that genotypes differed significantly in their overall ability for lodging resistance, which implied that a wide intraspecific variability existed for genotype selection. Root capacitance method was able to delineating genotypes in response to abiotic stresses; and heat stress greatly increased the risk of root lodging. Lodging risk can be reduced by appropriate agronomic practices and variety selection. Electrical measurements as an appropriate methodology suitable for studying canola root traits. Root capacitance method appears to be a non–invasive technique for in situ assessment of lodging resistance.

Winter hardiness as breeding aim for oilseed rape cultivation under changing climatic conditions

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Keywords: oilseed rape, winter hardiness, abiotic stress, vernalization requirement, stem elongation, breeding, frost tolerance

Despite climate warming, in some years, extreme weather conditions may occur that dramatically affect seed yield of winter oilseed rape (*Brassica napus* L.). Abiotic stress tolerance, frost tolerance in particular, is currently an important breeding aim. Frost periods with temperatures below -15 °C as in 2012 and partly in 2016 led to winterkill. The aim of this study was to assess the genetic variation and inheritance for winter hardiness in a genetic diverse set of 312 winter oilseed rape genotypes. The plant material was phenotyped for frost damage in field experiments in Poland, Ukraine and Finland. It was characterized for stem elongation before and after winter as well as for vernalization requirement in spring sown field experiments and greenhouse experiments in Germany. Results showed significant differences in frost damage, stem elongation before winter, vernalization requirement, and stem elongation in spring sown experiments. Vernalization requirement was closely negatively correlated with stem elongation in spring sown experiments ($r_S = -0.75^{**}$) The remaining trait correlations were significant, but weak, ($r_S = -0.34^{**}$ to 0.38^{**}) indicating that genotypes with a low stem elongation before winter, a good frost tolerance, but nevertheless with a rapid shoot development in spring may be selected.

Phenotyping of *Brassica napus* L. plantlets affected during in vitro growth by the presence of epoxiconazole

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Keywords: *Brassica napus* L., triazole fungicide, *in vitro* phenotyping

Epoxiconazole is a broad-spectrum triazole fungicide interfering with fungal cell membrane synthesis as inhibitor of ergosterol biosynthesis. Foliar application to the field (rates of 25-125 g of active substance per hectare) is mainly used for preventive and curative actions regarding cereals, sugar beet, apple, oilseed rape and ornamentals. Epoxiconazole like others triazole fungicides are known to be persistent into the soil. Several studies using foliar application experiments demonstrated the effect of its triazole metabolite as plant growth regulator through the anti-gibberellin activity and notably reduction of *Brassica napus L.* growth can be attributed to inhibition of gibberellin biosynthesis at the stage of conversion of *ent*-kaurene to *ent*-kaurenoic acid. We describe here an *in vitro* experiment studying the relation between epoxiconazole in culture medium (0 $mg.l^{-1}$; 0,120 $mg.l^{-1}$ and 0,200 $mg.l^{-1}$) and phenotyping (root and shoot growth) of three varieties of winter rapeseeds (*Brassica napus L.* var. *Es Astrid*, var. *toccata* and var. *catalina*). Shoots were micropropagated by axillary branching and explants were cultivated *in vitro* for 36 days in presence of epoxiconazole. Plantlets fungicide absorption was evaluated using QuEChERS® extraction method following by an automated UHPLC-MS/MS analysis (Waters® Acquity® TQD). Results showed that the shoots and roots growth of *Brassica napus L.* plantlets was significantly inhibited by epoxiconazole at 0,120 $mg.l^{-1}$ independently of the variety. The concentration of 0,200 $mg.l^{-1}$ leaded to necrosis and anthocyanosis symptoms and can be considered as lethal for *in vitro* growing explants. The huge epoxiconazole absorption by rapeseed plantlets clearly showed a dose-dependent relation and was closely similar for the three varieties. It will be interesting to confirm this behavior in the frame of multiple abiotic stress conditions regarding soil experiments and in relation with epoxiconazole soil residues.

Session 5. Quality

Keynote

Quality aspects in breeding *Brassica* species

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Keywords: oil, protein, tannin, glucosinolate, secondary metabolite, sinapine, phytosterol, tocopherol, flavour

The genus *Brassica* comprises a large number of species and subspecies that are consumed either as shoots, leaves, roots, turnip roots, etc. or in form of the seeds. Vegetative plant parts are merchandized mainly as raw product, whereas generative parts are marketed predominantly in a processed form either as oil, meal, powder, protein, condiment, etc. The glucosinolate content and composition of vegetative and generative *Brassica* plant parts have been for long subject of many scientific and sensory investigations. Plant breeding efforts have led to the development of canola seed quality cultivars in *Brassica napus* and in *Brassica juncea*, whereas this goal has not yet been achieved in *Brassica carinata*. Meanwhile, the scientific interest has shifted towards phytosterols, tocopherols, phenolic acids and proanthocyanidins (condensed tannins) and their effects on oil and protein content and quality. Furthermore, degradation products generated during processing of raw material that may positive or negatively affect quality and flavor of end products are getting into focus. The economic benefit of the *Brassica* oil crops is mainly due to their high oil content. The oil extracted meal is less valued and currently is used mainly in feed mixtures. However, with the ever increasing human demand for vegetable proteins, attempts are undertaken to improve the quality and the palatability of *Brassica* seed proteins in food products. Different 'omics' technologies are available allowing the identification of natural product components, their encoding genes and differences in their expression. Once critical components are identified, natural genetic variation for these components and genome editing techniques can be harnessed for an efficient and targeted quality improvement of *Brassica* crops. Recent developments in breeding for quality traits in *Brassica* species will be reviewed.

Variation in glucosinolate and mineral content in Galician germplasm of *Brassica rapa* L. cultivated under Mediterranean conditions

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Keywords: turnip tops, turnip greens, gluconapin, Calcium, Potassium, Zinc

In the North of Spain and Portugal, turnip greens and turnip tops (*Brassica rapa* L. var. *rapa*), are highly appreciated for human consumption. To spread its cultivation to other regions of the Iberian Peninsula, a set of Galician germplasm of *B. rapa* (19 accessions) have been cultivated under Mediterranean edaphoclimatic conditions (Córdoba, Andalusia), and evaluated for their agronomical performance and for the glucosinolate content of turnip greens and turnip tops harvested. The total glucosinolate content ranged from 10.29 to 44.97 µmol/g dw for turnip greens, and from 15.30 to 63.8 µmol/g dw for turnip tops, being gluconapin the most abundant glucosinolate (near 80% of the total amount) in all samples analyzed. Seven selected accessions were also evaluated for mineral composition. The range of minerals concentration in turnip greens and turnip tops, respectively, were: Ca (11.97-23.57; 4.63-32.25 mg/g), K (6.66-42.32; 5.73-13.37 mg/g), and Zn (21.08-44.63; 16.99-47.46 µg/g). Our results confirmed that *Brassica rapa* can be cultivated in Southern Spain to produce turnip greens and turnip tops having similar nutritive quality to those cropped in Galicia.

Phytochemical differences between white- and yellow-flowering rapeseed (*Brassica napus* L.) grown as sprouts and seedlings for human consumption

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Keywords: white flowers, rapeseed, glucosinolates, carotenoids

White flowers in rapeseed (*Brassica napus* L.) are an old trait, which has been bred into modern cultivars of yellow-flowering rapeseed resulting in new cultivars with white flowers. These new cultivars are suitable for human consumption when grown as sprouts and seedlings. Furthermore, they contain glucosinolates and carotenoids, which has been proposed to possess qualities towards inhibition of cancer and eye diseases. Previously carotenoids have been linked to flower color of rapeseed. Thus, the aim was to investigate if phytochemical content and composition could be ascribed to flower color and if these were affected by the ratio of blue/red light. Five white-flowering and two yellow-flowering cultivars were grown as sprouts or seedlings in climate chambers under blue/red light ratios of 32/68% (high blue) or 15/85% (low blue) provided by light emitting diodes (LEDs). Glucosinolate and total carotenoid contents were analyzed from freeze-dried material and evaluated by high-performance liquid chromatography and spectrophotometer, respectively. Results showed cultivar differences for the content of all individual glucosinolates besides the groups of aliphatic, indole and total glucosinolates but the differences were not related to flower color. The 4-hydroxy glucobrassicin content increased in sprouts whereas progoitrin decreased in seedlings under high blue light treatments. Total carotenoid content increased in a yellow-flowering cultivar but decreased in a white-flowering cultivar under high blue light treatments. Cultivar differences were ascribed to both sprouts and seedlings, and higher total carotenoid contents were found in yellow-flowering cultivars. In conclusion flower color could be linked to total carotenoid but not glucosinolate content and composition.

Effects of 3-butenyl isothiocyanate on phenotypically different prostate cancer cells

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Keywords: prostate cancer, isothiocyanates, docetaxel, chemoprevention, turnip greens

Isothiocyanates (ITCs) have gained growing attention since they have been attributed the merits for the beneficial potential of cruciferous vegetable dietary consumption on cancer. The aim of the present study is to determine the cytotoxic effects of 3-butenyl isothiocyanate (3BI) on prostate cancer cells under in vitro conditions. Two human prostate cancer cell lines, PC3 and DU-145 were assayed. Cells were cultured under the presence of growing concentrations of 3BI (5, 10, 30 and 50 μM) in absence or presence of the chemotherapeutic drug docetaxel (1, 2 nM). The cytotoxic effects of this compound were analyzed using the MTT (reduction of 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) colorimetric method at times 24, 48 and 72 h. Apoptosis and migration assays were also performed. Our results show that 3BI induced a dose-dependent cytotoxic effect on androgen-resistant PC3 cells at 24, 48 and 72 h. These effects were significantly higher than those found with docetaxel at 72 h of culture. Moreover, 3BI also potentiated the effects of docetaxel in a dose-dependent manner. Apoptosis were significantly higher in 3BI-docetaxel treated cells in comparison to docetaxel. Additionally, 3BI showed inhibition of migration of PC3. Nevertheless, 3BI was not effective on the androgen-insensitive DU145 prostate cancer cell line. Although the results of further studies (some of them are already being performed by our group) should be added, our results at present show a promising role of this compound as chemotherapeutic drug and/or co-adjuvant agent in docetaxel-based therapy in some types of prostate cancer.

Session 6. Omics

Keynote

Sipping from the firehose: *Brassica* biology in the era of omics and big data

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Keywords: omics, genomics, transcriptomics, metabolomics, systems biology, network, *Brassica*, domestication

There are now many “omes” beyond the original “genome” being used by Brassica biologists. An initial challenge is how to integrate genomics, transcriptomics, proteomics, metabolomics and other big data. However, given that there are many, large, and even streaming sources of data, a new grand challenge is determining how much data do we need to sip from the firehose to make inferences and decisions? And just as we make progress anchoring all the omics datasets for a few Brassica reference genomes, there is now a movement to develop pan-genomes that will exponentially increase not only the amount of data, but will also complicate (meta) data exploration. Here, we illustrate how to confront systems and network biology with examples from research where we are collecting several omics datasets for *Brassica rapa*, *Brassica oleracea*, *Brassica napus*, and relatives. Omics approaches enable qualitative and quantitative measurements of molecules in a high-throughput manner; which is relevant for modeling Brassica crop variation at different biological states from plant growth to food storage. We conclude with some community-minded thoughts on how to synergize our collective efforts.

`Omic´ profiling of Brassica oleracea challenged with Xanthomonas campestris pv. campestris

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Keywords: biotic stress, *Xanthomonas campestris* pv. *campestris*, Omics

‘Omic’ approaches have emerged as valuable technologies to monitoring the biological status of an organism. Among all their applications, the study of plant-pathogen interactions is on the cutting edge of plant research. Regarding to *Brassica* crops diseases, the causal agent of black rot (*Xanthomonas campestris* pv. *campestris*, *Xcc*) is one of the most devastating soil borne diseases worldwide. However, despite the black rot impact, few molecular and biochemical mechanisms of *Brassica* responses against *Xcc* have been elucidated. In this work, we investigate molecular changes produced on *Brassica oleracea* plants infected by *Xcc* using different ‘omic’ technologies. We carried out transcriptomic (MACE), proteomic (Maldi-TOF-TOF) and metabolomic (UHPLC-QTOF) analyses from leaves collected at 3 and 12 days post-infection. In all cases, infection causes deep changes on *Brassica* metabolism and these changes are different between the early and late response. Transcriptomics and proteomics results mainly showed an up-regulation of gene transcription and translation whereas metabolomic analysis indicated a down-regulation of most of the differentially expressed metabolites. In general, processes related with primary and energetic metabolism are repressed whereas those related with resistance and signaling are up-regulated. In conclusion, this study represents a step forward the understanding of *B. oleracea-Xcc* interaction and gives as pretty good imagen of the status of *B. oleracea* challenged with *Xcc*.

Volatile metabolomics indicates different glucosinolates metabolism in Norway grown cabbage

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Keywords: Volatiles, glucosinolates, metabolomics

Different cultivars of cabbage are common ingredients in Norwegian cuisine contributing their pleasant fragrance and flavor as well as their nutrimental value to the diet of Norwegians. We are mapping the chemical diversity of different cabbage cultivars grown in Norway as part of an integral project aiming to explain in detail the chemical basis of aroma and taste in the cabbage local production. We detect cabbage volatiles using GC-MS and apply multivariate statistics to highlight compounds displaying varying concentrations among different cabbage cultivars. Following this approach, we have identified cultivar specific volatile profiles. Furthermore, we have identified glucosinolate hydrolysis products as the most variable volatiles among cultivars. Interestingly, when we analyze extracts of the same cabbage cultivars using LC-MS we find that different glucosinolate combinations produce comparable volatile profiles. This observation prompts us to speculate that either: (i) different genetic make-ups or (ii) different catabolic pathways are present in different cabbage cultivars. This information will be incorporated into a nation-wide program designed to assist Norwegian consumers in the selection of cabbage varieties for cooking based on their chemical, and by extension, organoleptic properties and at the same time to assist Norwegian cabbage producers with their crop selection programs.

Integration of genotypic and phenotypic *Brassica* crop data with *Brassica* Information Portal

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Keywords: phenomics, brassica phenotyping data, data standards, crop ontology, community resource

In collaboration with the UK *Brassica* Research Community, we have built *Brassica* Information Portal (BIP), a tool that aims to assist global research on *Brassica* crops (https://bip.earlham.ac.uk). BIP facilitates crop improvement by filling the gap for standardized trait data and is already integrated with tools to perform on-the-fly phenotype-genotype association analysis online.

There are huge benefits from making organized trait data available and accessible and we hope that it becomes common practice to store brassica (and other crop data) trait data systematically and share it with the wider research community in a similar way as has become routine for sequence, transcript, metabolite and protein structure data. Users can store and publish their own study results in the Portal thanks to advanced data submission capabilities. Similarly, user-friendly interfaces and programmatic download mechanisms further facilitate work with the data. This makes the database content readily comparable and cross-linkable to that of other tools and resources for further downstream analysis. Integrated with the GWAS analysis tool GWASSER (CyVerse UK), it now enables the user to perform simple GWAS analysis with selected data on BIP. In addition we are working on integrating NGS data analysis through Galaxy and CyVerse platform to facilitate all steps of GBS, gene candidate selection and genotype - phenotype association studies. We will present the resource, status of analytical tool development and a GWAS use-case to demonstrate the value and utility of BIP, both for single research groups and global *Brassica* research and breeding community.

Session 7. Food Technology

Keynote

Broccoli for food and health - research and challenges

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Keywords: *Brassicaceae*, glucoraphanin, functional food, inflammation, health

Nowadays, society accepts the direct relationship between foods and health. In this sense, fruits and vegetables are the major components in balanced diets, particularly for their implications in the prevention of certain conditions and types of cancer and chronic diseases. Broccoli (*Brassica oleracea* L. var. *italica*), is a cruciferous food very rich in glucosinolates (GLS) and their bioactive hydrolysis products, the isothiocyanates (ITC), which may exert beneficial biological activities against different conditions through protection against inflammation and oxidative stress in the cells, slowing or preventing a number of cancers and other diseases, such as cardiovascular or neurodegenerative. Broccoli inflorescences and sprouts are the main dietary sources of glucoraphanin (GR), precursor glucosinolate of sulphoraphane (SFN), widely studied in different pathological conditions. Current research includes multidisciplinary work integrating the food chain, such as the evaluation of the pre- and post-harvest factors affecting the phytochemical composition of foods, adding value to agro-waste by elaboration of new ingredients for culinary applications, and enriching natural foods in bioactive phytochemicals using sustainable practices. The evaluation of the bioavailability and metabolism of GLS/ITC is one of several challenges in the design of clinical studies to assess the potential health-benefits of crucifers related to their antioxidant, anti-inflammatory and chemoprotective effects. The anti-inflammatory effects of broccoli sprouts are related to their ability to decrease levels of cytokines as IL-6 and TNF-α, as well as C-reactive protein, implicated in the etiology of chronic and degenerative diseases. Human intervention studies are necessary for the assessment of these effects in the context of daily eating habits, to reach reliable conclusions for dietary advices beyond mechanistic animal models. Facing these challenges will be necessary to let consumers know that *Brassica* vegetables likely provide excellent health effects.

Probiotic aspects in the traditionally fermented cabbage from Wallachian Plain

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Keywords: sour cabbage, traditionally fermented cabbage, sour cabbage microbiota

The area that we studied in the present research, a small part of the Wallachian Plain that concentrates the production of cabbage (*Brassica oleracea* var. *capitata* f. *alba* – hybrid Buzaiana) and its processing into sour cabbage, namely the Titu Plain. The production of sour cabbage of the area can be estimated for 2016-1017 to around 10.000 t, of which 4.000 tons are estimated to be processed in modern processing plants and 6.000 tons in small private workshops. The workshops are using for the fermentation stage large wooden barrels of 200-2000 liters of volume or large pools dug into the ground, isolated with plastic foil and wood. The processing plants adapted the traditional barrel and are using big capacity (5.000 – 10.000 l of volume) plastic fiber vats, buried into the ground. If the small workshops production is mainly sold in marketplaces around Romania, the production of the processing plants is sold primarily through retail chains in Romania and through traditional Romanian stores across Europe. During the research, the microbiota of the product was analyzed in each of the four fermentation stages. The fermentation is made traditionally, without the use of any starter culture or any additives. The first fermentation stage (day 3) is characterized by the decrease of the Total Count value, due to the respiration of the plant material and the consumption of oxygen by facultative anaerobic enterobacteria. In the second stage of fermentation, the characteristic microorganism can be considered *Leuconostoc mesenteroides* which was found, in day 6 at 106 CFU/ml in the brine. The third fermentation stage was a homofermentation. Both in this this stage and the fourth and final stage colonies of *Lactabacillus plantarum* and *Lactobacillus brevis* were identified (using API 50CH strips), at a total maximum number (day 24) of Lactobacilli of 5x105 CFU/ml. Further studies are to be made for the precise specie identification of presumptive probiotic lactobacilli and their viability in the product throughout shelf life.

Comparison study about processing methods (postharvest treatments) and their effects of the nutritional quality of different *Brassica* vegetables

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Keywords: Processing methods, antioxidant capacity, total phenolics, anthocianin, vitamin C, *Brassica* foods, *Brassicaceae*, nutritional value, freeze drying, air drying, raw.

An increasing number of medical studies are focusing the attention on the correlation between a higher intake of *Brassica* vegetables and the decrease of the onset of several human chronic pathologies; this healthy activity of *Brassicaceae* is mainly due to the presence of healthy compounds that characterize the nutritional quality of this genus. The high nutritional quality of these vegetables, together with the consumer attention to the consumption of healthier foods, led to an increase in the production and consumption of Brassica foods in Europe during the last years. The aim of this study is to investigate the differences in the nutritional quality of different *Brassica* species subjected to many processing methods applied during the post-harvest period; in particular, the variation of nutritional quality in raw, freeze-dried, and air-dried samples were analyzed. The different *Brassica* species analyzed were broccolini (*Brassica oleracea* L. var. italica), broccoli rabe (*Brassica rapa* L. subsp. *sylvestris* L. Janch. var. *esculenta* Hort), black cabbage, red curly kale, green curly kale (*Brassica oleracea* L. var. *acephala sabellica*), and other Brassica vegetables, like jets and leaves, spigarello broccoli. For the assessment of the nutritional quality of the different species of *Brassicaceae* family, the total antioxidant capacity (through FRAP method), the total anthocyanin content (through the pH-shift method), and the total phenolics contents (through Folin –Ciocalteau assay) were analyzed. The vitamin C content was also measured, through the determination by HPLC analysis. The results confirm the high nutritional quality of the species belonging to the *Brassicaceae* family, pointing out that both the genotype and the post-harvest treatment significantly influenced the bioactive compounds concentration of the different materials tested. In particular, the air-drying processing seems to strongly influence the nutritional quality, in particular regarding the antioxidant activity.

Agronomic performance of two oilseed crops of *Brassica* genus for energetic purposes and the economic analysis of a pilot combined heat and power plant operating on pure vegetable oil in Sicily (Italy)

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Keywords: *Brassica napus*, *Brassica carinata*, PVO, renewable energy, cash/flow analysis, CHP

Brassica napus L. (var. *oleifera*) and *Brassica carinata* A. Braun are two oilseed crops that are commonly used for biodiesel production. In the inland areas of Sicily (Italy), these species can be introduced into a well-planned crop-rotation with durum wheat for the production of pure vegetable oil. The introduction of these species can produce significant economic benefits for farmers both in terms of yield and energy. The aims of this study were to evaluate the agronomic performance of rapeseed and Ethiopian mustard varieties and to carry out an economic analysis of a pilot combined heat and power (CHP) plant operating on pure vegetable oil. The research was carried out in Sicily (Italy) on a traditional cereal livestock farm. The two species were cultivated under conventional farming systems. The main biometric and yield parameters were determined following harvesting and pure vegetable oil (PVO) was obtained through cold-press extraction. The PVO was then filtered, decanted and stored. Chemical characterization was carried out on PVO and protein meals for each species using specific protocols. Glucosinolates and fatty acid content of the seeds and protein meal were also determined. During the second stage of the research, the cogeneration of renewable energy (electricity and heat) was carried out using a CHP system powered by FPT with a nominal power of 75kVA. The final stage focused on the economic viability analysis of the CHP system based on an average yearly operating time of 7400 hours and discounted cash flow analysis. Oil seed yield of rapeseed (7.6 q ha^{-1}) was found on average to be higher than that of Ethiopian mustard (4.1 q ha^{-1}) and this influenced the total surface area required to operate the system over the course of a year. Considering the lifecycle of the CHP system (20 years), cash-flow trend analysis showed good economic benefit to farmers. These results make *Brassica napus* and *Brassica carinata* promising energy crops for cultivation in semi-arid areas of the Mediterranean region and highlight the need to adopt these crops in the traditional crop rotation systems as proposed by multifunctional agriculture.

POSTER PRESENTATION ABSTRACTS

P1. All brassicas are beautiful, but some are more beautiful than others

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Keywords: brassicas, rapeseed, camelina, flower

The wealth of the family *Brassicaceae* is not only reflected by the number of the species, but also by the decorativeness of flowers and leaves of some species and the importance of planting green areas. A small number of species are annual and biennial, while the rest are perennial flowers. Composite flowers are generally small and can be white, yellow, orange, pink and purple. Beside basic green, the leaves of some species can be white, yellow or pink in colour. IFVCNS collection of vegetable brassicas (*Brassica oleracea*) holds cabbage intended for human food with light-green and light-red head leaves and kohlrabi with light-green leaves and red thickened stem. Rapeseed (*Brassica napus* L.) is the most important of the brassicas which are cultivated for seed from which oil of excellent quality is extracted. The remaining meal has high protein content excellent for feed. Worldwide growing areas of 35 million hectares stand out from the landscape when rapeseed flowers with beautiful warm yellow colour. Besides its basic use, brassicas are also honey producing crops that are very attractive to the pollinators due to high pollen and nectar production in flowers. In the rapeseed collection the number of flowers per branch was observed on 33 plants for 4 genotypes. The number depended on the genotype and ranged from 498 to 1382, while the highest number was on the central branch and ranged from 63 to 223. The flowers were mostly intensive yellow in colour, apart from the genotype L 52 with distinctly orange flowers. In contrast to rapeseed, camelina (*Camelina sativa* (L.) Crtz.) is a half-forgotten, sleeping beauty: Although cultivated as a food plant since the Iron-age, it has never been a dominant crop. It is presently revived because of its unique oil quality useful both for food and fuel. Camelina has tiny yellow flowers and lime-green, arrow-shaped leaves, fruits are pear-shaped siliques containing about 10 seeds of a golden colour.

P2. Antioxidant profiles of the wild and cultivated *Brassica* (n=9) collection of the ECPGR "COCHEVA BRAS" project

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Keywords: *Brassica oleracea*, crop wild relatives, glucosinolates, phenols, DPPH

The COCHEVA BRAS *Brassica* collection was grown in Catania, at the experimental fields of Di3A-UNICT, and it was represented by twenty-nine landraces and four hybrids F1 of *B. oleracea* vegetable crops, and six wild *Brassica* species (n=9). The collection was transplanted July and at the beginning of the flowering stage leaf samples were collected randomly from three single plants per accession and then immediately freeze-dried and sent to CREA-IAA for the analysis. The biochemical data showed a specific and well identified pattern in terms of glucosinolates (GLS), polyphenol (PHP) profiles and antioxidant capacity (DPPH) detected in the leaf samples of the accessions characterized. The profiles of the studied accessions showed a variation mainly in relation to their geographical origin. The profile of GLS in leaf samples is featured by the presence of glucoiberin, progoitrin, sinigrin, glucoraphanin, glucosinalbin, gluconapin, glucoiberverin, 4-hydroxyglucobrassicin, glucobrassicanapin, glucobrassicin and neoglucobrassicin. The amount of total GLS varied from 3 to more than 50 µg/g dw. The Portuguese accessions are characterized by the presence of glucoiberin, sinigrin and glucobrassicin, whilst in the Italian accessions glucoraphanin, glucobrassicin and neoglucobrassicin are the major GLS. The F1 hybrids showed different GLS profiles in comparison to both Italian and Portuguese landraces and wild species studied. The same trend was observed for the polyphenol and ascorbic acid content and for the antioxidant capacity as for GLS. The level of total phenols ranged from 784.6 to 2991.1 mg/100 g dw, with a total mean value of 1911.1 mg/100 g dw (Fig. 4). The level of total phenols ranged from 165.1 to 2283.0 mg/100 g dw. The total mean values were similar, being equal to 900.4 and 880.1 mg/100 g dw, for Portuguese and Italian dried samples, respectively. The plant-to-plant variability was similar between Portugal and Italy, with an average CV of 30%. The DPPH scavenging indexes were higher for the Italian accessions than for the Portuguese. The profiles of the polyphenols varied mainly in relation to the geographic origin; the Italian accessions were characterized by the presence of kaempferol and sinapoyl derivatives whilst in the Portuguese it was detected caffeic acid esters. According to great diversity within accessions it is possible to consider the major of them as most appropriate accessions for AEGIS.

P3. Bio-morphological characterization of Mediterranean wild and cultivated *Brassica* species

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Keywords: *Brassica oleracea*, wild relatives, characterization, most appropriate accessions, AEGIS

The activities carried out by the *Brassica* Working Group (BWG) in the recent years allowed to achieve interesting results on the diversity expressed in *Brassica oleracea* and its wild relatives. Following these results, the granted "COllection, CHaracterization and EVAluation of wild and cultivated BRASsicas (COCHEVA BRAS)" project aimed at characterizing *Brassica* landraces, commercial cultivars and wild relatives grown in Italy and Portugal, and to identify sources of resistance to downy mildew. The identification of eligible accessions, well characterized and diverse, to be proposed as Most Appropriate Accessions (MAAs) for registration as AEGIS (A European Genebank Integrated System) accessions was among the objectives of the project. At UNICT we characterized 6 accessions of *B. incana*, *B. rupestris* and *B. villosa* and 33 accessions of *B. oleracea* var. *achephala*, *botrytis*, *capitata*, *costata*, *italica*, *gongylodes* and *sabauda*. The bio-morphological characterization was performed according to the IBPGR and UPOV descriptors. Data were processed using SPSS by applying the hierarchical cluster analysis with the method of the complex linkage furthest neighbor. The cluster allowed us to classify the accessions in nine main groups with different characteristics. On this basis 9 accessions were proposed as MAAs for AEGIS. For groups with numerous accessions, those showing higher variability among them were chosen. Bio-morphological data were acquired on landraces of broccoli, cabbage, cauliflower, kale, kohlrabi and savoy cabbage grown in Italy and Portugal, and on *Brassica* wild relatives widespread in Sicily. In general Portuguese accessions were similar among them for several traits, as they belong all to *Brassica oleracea* var. *acephala* (var. *costata*), while Italian ones showed higher diversity for several descriptors among and within the crops, especially broccoli and cauliflower, and compared to the F1 hybrid used The great diversity detected among the accessions will allow to consider the major of them as MAAs for AEGIS.

P4. Effects of healing conditions on the growth of grafted cabbage seedlings

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Keywords: cabbage, grafting, healing condition

Cabbage (*Brassica oleracea* L. var. capitate), which belongs to *Brassicaceae* family, is an important and common vegetable in the world. Grafting technique is widely used in commercial production of cucurbits and solanaceous vegetables, but seldom applied to the members of the *Brassicaceae* family. This research aims to set up a grafting method for cabbage along with optimal healing conditions for grafted cabbage seedlings. The tested healing conditions include temperature (15°C, 20°C or 25°C), relative humidity (RH) (75%, 85% or 95%), light intensity (high light intensity, low light intensity or full darkness) and duration of healing (3, 4 or 5 days). With tube grafting, the highest survival rate of the grafted cabbage seedlings was found after treated with the healing conditions of 15°C, RH 85%, or full darkness or high light intensity (79~107 $\mu mol \cdot m^{-2} \cdot s^{-1}$). On day 35 after grafting, the highest seedling index of the grafted cabbage seedlings was shown after treated with the healing conditions of 20°C, RH 75% or 95%, or high light intensity. The survival rate and the seedling index appeared not to be affected by the tested healing durations. Upon comparing all the healing conditions, it was found that the condition of 20°C, RH85% and high light intensity resulted in a high survival rate up to 93% and the highest seedling index. The grafting along with the optimal healing conditions developed in this research could be employed in the future for diverse grafting purposes, e.g., to improve resistance to soil-borne diseases, increase tolerance to abiotic stresses, promote plant vigor and/or increase yield.

P5. Effects of irrigation regime, leaf biostimulant application and nitrogen rate on gas exchange parameters of Wild Rocket

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Keywords: *Diplotaxis tenuifolia* f. *integrifolia*, photosynthesis, transpiration, WUE, bio-stimulant

Biological stimulants (biostimulants) can have physiological effects on plants that improve yield, quality, and nutrients use efficiency. The mechanisms activated by these compounds are unknown and are difficult to identify, because the most part of these substances are mainly composed by plant and algae extracts, amino acids, vitamins and mineral nutrients. Therefore, their effect is a result of many components that may work synergistically. In the recent years, the biostimulants are gaining importance for their possible use in organic and sustainable agriculture. The results of a study conducted to assess the interactive effects of irrigation regime (IR), leaf application of a biostimulant and nitrogen rate on leaf net photosynthesis (Pn), transpiration (Tr), stomatal conductance (gs), and instantaneous water use efficiency (WUE), are reported. The research was carried out during November-February 2016-2017, into an unheated greenhouse located in southern Italy. Two irrigation regimes (restoration of 100 and 50% of crop evapotraspiration-ETc, respectively named I_{100} and I_{50}), two leaf biostimulant application (Bioproject SM23-BioKimia® International S.r.l., and a control without biostimulant, respectively named B and C) and three nitrogen rates (0, 70 and 140 kg ha^{-1} N, respectively named N_0, N_1 and N_2) on wild rocket (*Diplotaxis tenuifolia* f.*integrifolia* (Koch) De Langhe) grown in pots, were compared. A split plot experimental design was utilized. All treatments compared affected gas exchange parameters. I_{50} in respect to I_{100} reduced Pn, Tr and gs, but improved WUE, and the differences were raised with increasing soil water content gap between treatments. N rate increase improved Pn but, in condition of high water stress, the higher N rate was detrimental. Biostimulant improved Pn by about 9% on average, and the positive effect was greater with lowest N input. Positive effects of Bioproject SM23 on net photosynthesis, suggest its use for the cultivation of wild rocket with low N inputs.

P6. Genotypic variation and medium pH affect embryo yield and quality in the microspore culture of *Brassica oleracea* L. var. *capitata*

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Keywords: doubled haploid, microspore culture, medium pH, genotype, MES, arabic gum

The doubled haploid (DH) technology may accelerate breeding for white cabbage (*Brassica oleracea* L. var. *capitata*) up to 3 times compared to the conventional inbreeding technique and it has been used worldwide in both applied and fundamental research. The genotypic variation of donor plants, however, is still one of the main factors affecting microspore embryogenesis and plant regeneration. In this study, the effect of the genotypic variation and pH of NLN-13 liquid medium (pH 5.8, 6.1 and 6.4) on embryo yield and embryo quality in the microspore culture was evaluated using four white cabbage genotypes (Ag, Gr, Ti, AkBu). The relatively high pH 6.1 caused a significant increase in embryo yield and embryo quality of the responsive genotypes Ag, Gr and Ti. The high pH 6.4 induced microspore embryogenesis in the nonresponsive line AkBu. A two-way ANOVA analysis revealed a high genotype-depended variance (49%) of microspore embryogenesis, 9% of the variance was determined by the medium pH and 22% by the genotype-pH interaction. Additionally, the effect of MES (2-(N-Morpholino) ethanesulfonic acid) and arabic gum on the medium pH stability was studied using seven genotypes (Et4ge, MCC, CEM, Et3Fr28, Cyg2, Frg28, Et4). It was found that MES and arabic gum could reduce the variation in the medium pH, although their efficiency also appeared to be genotype dependent.

P7. Review of cultivated and spontaneous *Brasicaceae* species for use as medicinal in NE part of Romania

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Keywords: local population, varieties, yield, benefits

The main objective of this study was to save precious resources that are endangered, by collecting local native populations, old, primitive varieties, which are under risk in order to reduce genetic erosion and save entire material obtained by breeding, in order to exploit its medicinal potential. We accomplish the screening of entire range of *Brasicaceae* species from cultivated and spontaneous flora in North East part of Romania, in order to detect and highlight an important plant genetic resource. Among investigated species: cabbage and relatives (genus *Brassica*), horseradish (*Armoracia rusticana*), arugula (*Eruca sativa*), peppergrass (genus *Lepidium*), radish (*Raphanus sativus*) wild radish (*Raphanus raphanistrum*), wallflower (genus *Erysimum*), white mustard (*Sinapis alba*), shepherd's purse (*Capsella bursa-pastoris*). Despite the fact that *Brasicaceae* species are an important source of vitamin C, β-carotene, folic acids, potassium, fiber, in our country only a few species are used especially for culinary purposes. Romania has a valuable tradition in use of these species as medicinal. The paper presents data related to yields, surfaces, Romanian varieties and medicinal use of investigated species.

P8. The adaptation of celery cabbage [pak choi (*Brassica campestris* ssp. *chinensis*)] varieties from Samsun, Turkey

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Keywords: pak choi, adaptation, variety, sowing time, yield, Turkey

This study was carried out to investigate the possibilities of celery cabbage growing and to determine the suitable varieties of celery cabbage under Samsun ecological conditions between the autumn and spring growing season in 2010-2011. In this study, intervals 15 days and three sowing dates (1 August, 15 August, 1 September) at the end of autumn period in 2010, two sowing dates (1 April, 15 April) in spring season in 2011 and three sowing dates (15 June, 1 August, 15 August) at the end of 2011 autumn season and four celery cabbage varieties (Dwarf canton white, Pak choi green, Green fortune, Tai sai) were used. At the end of this research, it was found that celery cabbage vegetable could be successfully grown in autumn under Samsun ecological conditions. In the spring season, all of the varieties were flowered due to the bolting. In this study, according to the year and growing season, for Dwarf canton white variety averagely leaf number found 14.55-18.33 units, leaf weight changed 375.06-381.65 g and stem weight found 23.18-24.05 g. For pak choi green variety, leaf number found 16.0-20.33 units, leaf weight changed 252.80-327.95 g, and 23.58-29.10 g. Dwarf canton white and Pak choi green were determined as the promising varieties. According to the years, the highest yield was determined 4.11-4.33 tonnes/da for Dwarf canton white, and 3.13-3.45 tonnes/da for Pak choi green varieties. These results showed that the best suitable sowing date for the Pak choi cultivation was 15 July period for the autumn growing season.

P9. Development of molecular markers for low progoitrin cabbage breeding

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Keywords: cabbage, glucosinolate, progoitrin, molecular marker

Glucosinolates constitute a natural class of organic compounds that contain sulfur and nitrogen and are derived from glucose and an amino acid which are abundant in Brasssica species. *Brassica oleracea* contains various nutrients such as minerals, vitamines, anti-oxidants and phyto-chemicals. Glucosinolates (GSLs) is the most important nutrient in the brassica species due to its strong anti-cancer functions. Nevertheless, progoitrin is known to induce the goiter and thyroid cancer which is considered as the only undesirable GSLs in the Brassica species. To develop the molecular makers related to the progoitrin content, we analyzed GSL contents and key enzyme expression patterns using TBDH population. A total of 12 GSLs were detected from the population, and nine of the GSL synthesis genes (BoMAM1, BoCYP97F1, BoCYP83A1, BoSUR1, BoGSL-OH, BoCYP83B1, BoGSTF9, BoCYP81F2, and BoSOT16) were selected to be correlated with the progoitrin content. By the incorporated analysis with the genome wide SNP and gene expression data, 5 SNPs were selected as the key molecular markers for the low progoitrin content.

P10. Genetic diversity and cultivation technique of 'norabona': *Brassica napus* L. leafy vegetable landrace in western suburban Tokyo

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Keywords: cultivation method, dendrogram, genetic resources, genotyping, traditional cultivar

‘Norabona’ (*B. napus* landrace) is widely grown in the western suburban area of Tokyo where the flower stalks of the main stem or lateral shoots are consumed as a traditional early spring leafy vegetable. It has a pleasant taste and high nutritive value, and it can be used in many kinds of dishes. Therefore, ‘norabona’ has potential to become a more widely produced leafy vegetable crop. However, its genetic diversity and quality among local producers is unknown and it is necessary to comprehend its germplasm. Furthermore, there has not been any research into suitable cultivation methods to obtain good yields. In this study, we first investigated the genetic relationships between 22 samples of ‘norabona’ and other *B. napus* landraces collected from local markets and producers, based on 24 microsatellite (SSR) markers. And the composition of flower stalks among the 22 samples was also measured by a reflectometer (RQflex; Merck, Germany). The 22 samples could be categorized into 4 groups in the SSR analysis. The ‘norabona’ samples from the Kawasaki area were genetically distinct from the other groups and also had higher ascorbic acid and calcium contents. Then we studied the effect of altering the timing of pinching the main stem, a common practice in ‘norabona’ cultivation, on the yield of the major cultivar in the Kawasaki area, which is an early maturing type. Pinching at the beginning of the bolting stage increased yield compared with pinching at the pre-bolting or visible bud stage.

P11. Genome-wide identification, structural analysis and expressional validation of the *Brassica rapa* F-Box gene family

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Keywords: *Brassica rapa*, BrFBX genes, structural characteristics, expression, stress

The F-box genes form one of the largest functionally important, rapidly evolving plant gene families. The F-box proteins regulate diverse functions, including embryogenesis, organ development, floral organ identity, self-incompatibility, senescence, homeostasis, signaling, and responses to biotic and abiotic stresses. Due to functional importance of these gene family in plant species, we identified 571 *Brassica rapa* F-box genes (*BrFBX*), and mapped approximately 560 genes onto 10 chromosomes and classified the duplicated genes. A phylogenetic tree consisting of the *B. rapa* F-box genes and an analysis of conserved motif enabled us to categorize them into 11 subgroups based on node support. Additionally, we determined the intron–exon structural characteristics, which helped detect differences among the *BrFBX* genes. The 69 genes differentially expressed under abiotic stress conditions (i.e., cold, drought, and salt stresses) exhibited various spatio-temporal expression and quantitative reverse transcription polymerase chain reaction (qRT-PCR) analysis of 30 *BrFBX* genes showed tissue specific expressional difference among eight tissues during *B. rapa* (Chiifu) growth. The genome-wide study results reveal the relationships among the *BrFBX* genes regarding evolution, structural variability, potential functions and these data can be further used as a resource for the gene characterization in relation to growth, development and during different stress conditions for the development of *Brassica* rapa.

P12. Inheritance of major gene plus polygene underlying bolting and flowering traits in pak-choi

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Keywords: pak-choi, bolting trait, flowering trait, major gene plus polygene, genetic model

Naturally, bolting and flowering are interrelated greatly with the yield and quality of pak-choi cultivated in spring. It is of importance to study the inheritance of bolting and flowering tolerance for pak-choi. The mixed major gene plus polygene inheritance model was used to analyze the inheritance of bolting and flowering traits in pak-choi with six generations of early bolting variety M10-1(P1), bolting variety M10-2(P2) and their F1, B1, B2 and F2 generations. The results showed that the bolting trait was fitted the genetic model of two pairs of additive-dominant-epistatic major gene plus additive-dominant polygene model. It confirms that bolting trait was mainly controlled by two major genes expressing in the mode of additive-dominant-epistatic effects, and that additive effects of the two major genes were similar. In addition, there were main of the second major gene in the dominant effect. There were additive × additive interaction effect and dominant × dominant interaction effect of major gene and negative additive effects of polygene. Heritability of major genes in B1, B2, and F2 generations were 83.83%, 87.82% and 88.31%, respectively, while those of polygene in B1, B2, and F2 generations were all 0%, with an average of 86.65%. The rate of environmental variation was 13.35% in the total phenotypic variance. The bolting trait in pak-choi was dominated by major genes, and that environmental factors played a key role in inheritance. Thus, the selection of bolting trait in pak-choi was effective in early generations. The flowering trait was similar to the bolting trait inheritance. Heritability of major genes was 9.57% on an average, and the variance with an average of 90.43% was affected by environmental factors. These findings revealed that the flowering trait in pak-choi was greatly affected by environmental factors and that the flowering trait should not be considered as an identification indicator of bolting resistance in pak-choi.

P13. Mapping and expression profiling reveal an inserted fragment from purple mustard involved anthocyanin accumulation in Chinese cabbage

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Keywords: mapping, expression analysis, HPLC-MS, purple mustard fragment, Chinese cabbage

Anthocyanins are the major pigments responsible for purple coloration in flowers, fruits and leaves, and the genes involved in their biosynthetic pathway have been identified in many plants. A purple-leaf Chinese cabbage was bred by interspecies crossing between Chinese cabbage and purple-leaf mustard. In this study, high-performance liquid chromatographic analysis indicated purple coloration in Chinese cabbage is due to the accumulation of the same kind of cyaninin as in purple mustard. To elucidate the genetic factors controlling anthocyanin accumulation in this purple- leaf Chinese cabbage, we mapped the anthocyanin gene from the mustard (Anm) locus in an F2 population and performed expression profiling of anthocyanin- related genes. A genetic analysis revealed that the purple-leaf phenotype is a qualitative trait and that its inheritance is unstable in purple-leaf Chinese cabbage. Mapping insertion/deletion markers from 288 individuals of the F2 population located the Anm locus within a 2.5-cM interval on *Brassica rapa* chromosome A02. The sequencing and alignment of the amplified fragments demonstrated that purple Chinese cabbage contains fragments of purple mustard on chromosome A02. We evaluated the expression profiles of 12 anthocyanin-related genes on A02 by reverse-transcription and quantitative real-time PCR methods, which revealed that the expression levels of five genes were higher in purple Chinese cabbage than in the non- purple variety. These results offer insights into the molecular mechanism of anthocyanin biosynthesis and improve the knowledge on molecular breeding of purple-type Chinese cabbage.

P14. QTLs of resistance to race 1 of Xanthomonas campestris pv. campestris in Brassica oleracea

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Keywords: black rot, bacteria, plant disease

Black rot caused by *Xanthomonas campestris* pv. *campestris* (Xcc) is one of the most devastating diseases in *Brassica oleracea* crops. Bacteria enter through hydathodes and wounds in the leaves, colonizing mesophyll and the vascular system. As a consequence plant may wilt and die. There are 9 races of the pathogen, being race 1 the most damaging in *B. oleracea* crops. Breeding for resistance to *Xcc* race 1 is complicated because there are only partial sources of resistance. A genetic dissection of the resistance and its location in a genetic map would help in obtaining linked molecular markers to do a MAS breeding program. Mapping the resistance would be also the first step in localizing genes underlying this trait. Leaves of individuals of the BolTBDH mapping population were inoculated two consecutive times in order to study constitutive and inducted resistance. This experiment was carried out under controlled conditions. Subjective score (scale from 1 to 9, where 1 is a healthy leaf), percentage of lesioned area per leaf and percentage of inoculated points with symptoms were measured. A QTL approach was chosen to analyze the data. Sixteen QTLs related to disease traits and to leaf size were found spread on six linkage groups. Resistance is related to area of the leaf, since QTLs for score and percentage of lesioned area co-located with QTLs for leaf size. Three QTLs for resistance were found during the second inoculation but no in the first one indicating that plants acquired some kind of induced resistance after being in contact with *Xcc* for the first time.

P15. Screening of endophytic fungi in *Brassica oleracea* roots

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Keywords: Brassica, endophytic, fungus, mutualism

Endophytes are fungi that infect plants without causing symptoms of diseases. There is a large biological diversity among endophytes, and it is not rare for some plant species to be hosts of more than one hundred different endophytic species. Endophytes are gaining attention as a subject for research and applications in Plant Pathology. This is because in some cases, plants associated to endophytes have shown increased resistance to plant pathogens. In this experiment, we have screened the presence of endophytes in the roots of five *Brassica oleracea* local populations. The isolated fungal endophytes were identified based on the morphological traits and fungal ITS1-5.8S-ITS4 region sequence analysis. From all the roots analyzed, we found 24 different genera. *Acrocalymma vagum, Setophoma terrestris* and *Fusarium oxysporum* were the most abundant species, with a percentage of 24%, 22% and 13% of the total samples analyzed, respectively. Other endophytes, recognized by its beneficial effects on plants like *Trichoderma hamatum* or *Penicillium janthinellum*, were also found in *B. oleracea* roots.

P16. Variation in floral organs in wild populations of *Brassica rapa* L

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Keywords: floral traits, pollination efficiency, reproductive system, spontaneous accessions, *Brassica rapa*.

In the hermaphroditic plants, floral morphological traits can significantly affect reproductive system by favoring the deposit of self or cross pollen. In the *Brassica* species, the self-incompatibility mechanism is undoubtedly the main cause of the allogamy; however, floral organs variation can modulate or reinforce the cross pollination level of the plants. In this study, we investigated floral variation among wild populations of *B. rapa* L. from Algeria. We estimated 20 floral traits, including sepals, petals, pistil, stamens and nectaries as well as ovules production. Floral parameters were measured using stereomicroscope. Each flower’s ovule number and stigma-anther separation were also quantified under dissecting microscope. We found that the flower size, the sepals, the petals and the stamen traits did not vary much among populations or among individuals. However; a great variation was observed between individuals and between populations for the three parameters: stigma surface, nectary surface and stigma-anther separation. Moreover, the individual variation is different according to the populations. These results suggest that floral morphology may affect pollination efficiency and as a consequence seed production in *Brassica rapa* wild populations but with different contributions according to the floral traits.

P17. Study on distance hybridization compatibility between pak-choi and watercress

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Keywords: pak-choi, watercress, distance hybridization, compatibility, seed pod length

To breed new pak-choi cultivars with waterlogging-resistant, we investigated the effects of distance hybridization compatibility and the variation of seed pod length between pak-choi and watercress by observing pollination time and different pollination methods and seed pod length. The results showed that there was poor hybridization compatibility between pak-choi and watercress. 4 in 19 hybridization combinations set seeds, but these were identified as false hybrids. The embryos were aborted in other hybridization combinations. It was incompatibility after fertilization. The hybridization compatibility was closely related to the genotype of pak-choi and was not significant effects by repeat-pollination and cut-style-pollination. The seed pod length of hybrid combinations increased gradually with time. But it was slightly significant difference of the different hybridization combinations. It was a key period for the growth and development of seed pods in 5-15 days after fertilization. This was an important basis for time selection of culturing immature embryo.

P18. Aboveground-belowground plant-insect interactions: from genes to compounds

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Keywords: root herbivory, herbivore-induced defenses, plant-insect interactions, glucosinolates, defense signaling

Root and shoot insect herbivores feeding from the same plant can affect each other via induced plant defenses. Plant-mediated interactions between root and shoot herbivores have received increasing interest recently; nevertheless, the molecular mechanisms underlying these interactions are not fully clear yet. Herbivore-induced plant responses are complex and comprise different levels, including phytohormonal signaling, gene expression and production of defensive compounds, each with their own temporal dynamics. Jointly they shape the response that will be expressed, though they are seldom measured in the same experiment. We investigated changes at different response levels of *Brassica rapa* plants exposed first to root herbivory by *Delia radicum* and subsequently to shoot herbivory by either one of the specialists *Pieris brassicae* or *Plutella xylostella,* or one of the generalists *Spodoptera exigua* or *Mamestra brassicae.* Changes in phytohormone levels, defense-related gene expression and the levels of glucosinolates (GLS), the most typical defensive compounds of *Brassicaceae* plants, were measured in damaged leaves. Glucosinolate levels and the expression of the JA-marker gene *VSP2* were suppressed in plants exposed to both root and shoot herbivores, compared to plants exposed only to shoot herbivory in case of the specialist *P. brassicae* and *P. xylostella,* but also for the generalist *Mamestra brassicae*. Enhanced expression of *VSP2*, the SA- marker gene *PR1* and JA-Ile levels were found in plants exposed to *D. radicum* and the generalist *S. exigua* compared to plants with shoot herbivory alone. These results show that *D. radicum* feeding prior to shoot herbivory may not only enhance but also suppress inducible defenses in the shoots, depending on the aboveground herbivore species. Our study also shows that interactions between root and shoot herbivores do not depend on the specialization level of the shoot herbivores.

P19. New sources of resistance to downy mildew in a collection of wild and cultivated Brassicas

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Keywords: *Brassica* sp., cotyledon resistance, germplasm collection, *Hyaloperonospora brassicae*

Brassica downy mildew (DM) is a foliar disease caused by the oomycete *Hyaloperonospora brassicae* (syn. *Hyaloperonospora parasitica* subs. *brassica*) that can affect plants at all stages including the nurseries and can limit the production of vegetable *Brassica* especially in temperate climates. Twenty-eight landraces and wild genotypes from different *Brassica* species, coming from Portuguese and Italian germplasm collections, were screened for DM resistance. Genotypes of *B. oleracea* (23 acc.), *B. rupestris* (3 acc.), *B. incana* (1 acc.), and *B. villosa* (1 acc.) were tested with four *H. brassicae* pathotypes from different geographical origin at the seedling stage. DM evaluation showed no differential responses to the four *H. brassicae* pathotypes but great differences in resistance were observed between accessions. Seven accessions including one *B. villosa* (UNICT3944), two *B. oleracea* var. *acephala* (BPGV4533 and UNICT4448), three *B. oleracea* var. *costata* (BPGV1773, BPGV1726, and BPGV1747), and one *B. oleracea* var. *sabauda* (UNICT4633) were resistant to DM infection at cotyledon stage. These accessions are potential sources of DM resistance to be genetically characterized and further exploited in breeding programs.

P20. Rb gene introgression from *Brassica carinata* to *Brassica oleracea*

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Keywords: interspecific hybrids, white cabbage, *B. carinata*, *B. oleracea*, race, resistance, black rot, *X. campestris*

Black rot caused by bacterium *Xanthomonas campestris* pv. *campestris* (Pammel) Dowson (*Xcc*) is one of the most devastating diseases to *Brassica* crops. Breeding and utilization of resistant cultivars is the efficient way to control black rot. However, for now there is no one available white cabbage (*Brassica oleracea* var. *capitata*) variety resistant to three and more *Xcc* races on Russian seed market. The aim of this study is to transfer race specific black rot resistance to white cabbage by interspecific hybridization. Ethiopian mustard (*B. carinata*) line PI199947 - donor of a single dominant black rot resistance gene (*Rb*, resistance to 1, 3, 4 and 5 races) was crossed to susceptible tetraploid (4n = 36) white cabbage (*B. oleracea*) line Bu1. Ovules/embryo culture was used to rescue embryos and to develop two reciprocal interspecific hybrids *B. oleracea-carinata* (OC) and *B. carinata-oleracea* (CO). Both OC and CO were resistant to *Xcc* races 1, 3 and 4 (race 5 was not used for inoculation) that confirmed a dominant mode of *Rb*-gene inheritance and no cytoplasmic effects on black rot resistance. OC and CO had 3n = 4x = 35 chromosomes and partially fertile pollen. OC and CO were reciprocally backcrossed by di- and tetraploid white cabbage lines. A BC1 progeny chromosome numbers varied from 18 to 29 and from 34 to 36 when crossed to *2n* and *4n* lines, respectively. Resistance/susceptibility segregation to particular *Xcc* races was observed. Out of 92 total number of BC1 plants 16 were resistant to all three *Xcc* races, 3 of them had 18 chromosomes and white cabbage phenotype. Genetic control of resistance of selected plants will be examined for following introgression.

P21. Resistance comparison of cauliflower and kohlrabi to clubroot

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Keywords: disease index, tolerance, *Plasmodiophora brassicae*, *Brassica oleracea* L. var. botrytis L., *Brassica oleracea* L. var. *gongylodes* L.

Obligate biotroph soil borne pathogen *Plasmodiophora brassicae* Wor. causes clubroot disease and is one of the most serious disease of cruciferous crops worldwide. Cauliflower and kohlrabi are important and favorite *Brassica* vegetables. Their growing in a soil infested by *P. brassicae* leads to economically significant loses in yield. The most effective is to grow resistant cultivars. Thus, in total 7,079 plants of 50 cultivars of cauliflower (*Brassica oleracea* L. var. *botrytis* L.) and 4,486 plants of 30 cultivars of kohlrabi (*Brassica oleracea* L. var. *gongylodes* L.) from germplasm collection maintained by Crop Research Institute in Olomouc, Czech Republic were tested for resistance to clubroot disease under controlled conditions of plant growth chamber. Tolerance of these two crops was compared and statistically evaluated by PCA and parallel coordinate plot. Kohlrabi showed higher tolerance by average disease index (DI) 73.07. Average DI of cauliflower was 77.21. Higher average percentage of resistant plants with no visible swelling or very light swelling showed kohlrabi (22.86) then cauliflower (16.33). Obtained results can be used by breeders as initial resources for resistant breeding to clubroot.

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P22. Screening for resistance to stem canker (*Leptosphaeria* spp.) in selected rapeseed cultivars and *Brassica* genotypes

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Keywords: resistance gene, *Leptosphaeria* spp., Loop-mediated Isothermal Amplification

Stem canker of brassicas (blackleg), caused by the fungal complex *Leptosphaeria maculans*-L. biglobosa, is one of the most destructive diseases of *Brassicaceae* worldwide. In numerous countries, including Poland both pathogen populations co-exist and they can jointly lead to severe disease symptoms as well as yield losses. The aim of this study was to look for the genetic resistance to stem canker in selected *Brassica* genotypes in field conditions and to detect or even discriminate the population of the pathogens by LAMP technique. Screening of plant susceptibility/resistance was done twice in 2016. The field experiment was done in a randomized complete block design with two replicates in two locations in the Wielkopolska region (Greater Poland), situated 80 km apart. Disease incidence was assessed in summer and autumn, on 50 plants per replicate, according to the scale 0-4. The experiment was composed of 44 cultivars of winter oilseed rape, officially registered in Poland by the Central Station for Variety Testing (COBORU) and two candidate cultivars with Rlm7 resistance gene. Moreover, other Brassica genotypes were also assessed. The population of *Leptosphaeria* was studied using Loop-mediated DNA amplification (LAMP) method. For this purpose leaf or stem samples were collected from three individual plants per variety. The genotypes differed with their reaction to the pathogen. In both seasons, the cultivars with Rlm7 resistance gene showed significantly less symptoms, as compared to cultivars with no Rlm7. The analysis of leaf symptoms performed using a LAMP technique showed a higher proportion of *L. maculans* compared to *L. biglobosa*, what reflects changes in the composition of pathogen population of fungi causing blackleg on Brassica plants in Poland.

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P23. SWEET-mediated sugar transport is important for the *Plasmodiophora brassicae*-induced formation of clubroot

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Keywords: *Plasmodiophora brassicae,* SWEETs, clubroot, Chinese cabbage

Plasmodiophora brassicae is a soil borne pathogen of cruciferous plants and the causal agent of clubroot, a devastating disease of *Brassica* crops. The pathogen lives inside roots, and hijacks nutrients from the host plants. Root as one of the sink tissue, obtains main carbon source sugar from distant leaf tissues via the symplastic route. It is suggested that clubroot galls created an additional nutrient sink in infected root tissues. However, the molecular mechanism underlying *P. brassicae* infection and sugar transport is unclear. Here, we analyzed sugar contents in leaves and roots before and after *P. brassicae* infection using a pair of Chinese cabbage (*Brassica rapa*) near-isogenic lines (NILs), carrying either a clubroot resistant (CR) or clubroot susceptible (CS) allele at the CRb locus. *P. brassicae* infection caused significant increase of glucose and fructose contents in the root of CS NIL compared to CR NIL, but reduction in the leaves of CS NIL after 1.5 days, suggesting that sugar translocation and *P. brassicae* growth are tightly connected. Therefore, the global expression of SWEET (Sugar Will be Eventually Exported Transporters) genes were investigated in leaves, hypocotyls, and roots of CR and CS NILs in response to *P. brassicae* infection. Among 32 SWEET homologs (hereafter BrSWEETs) identified in the *B. rapa* genome, a few SWEETs (1a, 2a, 11a) is highly induced, especially in CS NIL upon *P. brassicae* infection. To determine the role of SWEETs in clubroot disease development, we performed pathogenicity test on Arabidopsis sweet11;12 double mutants, in which sucrose phloem loading was impaired. Significantly, the sweet11;12 mutants exhibited a delay of gall formation and a lower disease index when compared to the wild-type plants. Taken together, our analyses suggest that *P. brassicae* infection triggers active sugar translocation between the sugar producing tissues and the clubed tissues, and that the SWEET family genes are involved in this process.

P24. Inheritance of vernalization requirement and freezing tolerance in oilseed rape

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Keywords: *Brassica napus*, frost tolerance, cold acclimation, hardening, winter survival

Freezing tolerance is an important factor determining the winter hardiness in oilseed rape (*Brassica napus* L.). For winter oilseed rape genotypes, considerable differences in vernalization requirement have been reported and a positive correlation between the degree of vernalization requirement and frost tolerance has been discussed in the literature. Furthermore, stem elongation before winter is known as a critical factor affecting winter survival in oilseed rape. The main objective of the present project is to study the relationship between vernalization requirement and frost tolerance, respectively winter survival. Therefore a segregating doubled haploid population derived from a cross between spring-type variety Topas (DH4079) and winter-type oilseed rape Express 617 is phenotypically characterized for (a) its vernalization requirement under greenhouse conditions, (b) its frost tolerance as determined after subjecting hardened plants to sub-zero temperatures in a frost chamber, and (c) its segregation for stem elongation before winter and winter survival in field experiments sown in August. QTL analysis will show if QTL for frost tolerance, stem elongation before winter, winter survival and vernalization requirement obtained under different environmental conditions will collocate or differ in their positions. A complementary high resolution transcriptomic analysis (MACE; "Massive Analysis of cDNA Ends") will be performed to identify genes that are differentially expressed in contrasting bulks of early vs. late flowering and in frost sensitive vs. frost tolerant genotypes. Preliminary results regarding freezing tolerance of the DH population and the correlation with vernalization requirement will be presented.

P25. Role of glucosinolates on resilience to low temperatures in *Brassica oleracea*

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Keywords: Stress temperature; glucosinolates; *Brassica oleracea*

The literature demonstrating the role of glucosinolates in plant defense against herbivores is extensive. However, little information is available about the role of these secondary metabolites on the plant response to abiotic stresses. We took advantage of four recently developed divergent selected populations (with high glucobrassicin (HGBS) and low glucobrassicin (LGBS) and high sinigrin (HSIN), and with low sinigrin (LSIN) content) to evaluate the influence of different glucosinolate content on the plant resilience to low temperatures. Plants were grown in a growth chamber at constant 12 and 20 °C in a 14 h light/12 h dark photoperiod regime. Differences in GBS and SIN content were confirmed also at low temperatures with marginal effects in other glucosinolates. Plants from populations with high glucosinolate content show significantly higher fresh weight under low temperature than those showed by the population with low glucosinolate content, whereas not differences were observed at control temperature. To identify the metabolic changes in these populations due to exposure to low temperatures we performed a LC-qTOF metabolomics analysis. Performance of HSIN vs LSIN and HGBS vs LGBS were compared using multivariant analysis (PLSDA) at both temperatures. Metabolites with a common response under both temperatures were removed to identify those ions specifically involved in low temperature response. In addition, the performance of both divergent selections was compared at 12 °C to identify the metabolites specifically responding to SIN or GBS selection. We found 12 and 6 metabolites specifically involved in the response to low temperature in the SIN and GBS selections, respectively. Some of these metabolites were putatively identified using public available databases.

P26. Circadian variation of glucosinolate accumulation in *Brassica* crops

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Keywords: glucosinolates, *Brassica*, circadian clock

Environmental light signals entrain the endogenous circadian clock or timing system in plants to a period of 24 h, precisely corresponding to the exogenous period of the earth's rotation. It has been shown that the diurnal cycle strongly influences many physiological processes in plants. However, rather less attention has been paid to circadian clock effect on daily accumulation of plant secondary metabolites. Since glucosinolates play a major role as plant defensive compounds and could impact the palatability and health value of edible crops, we studied the daily cycling of glucosinolate content in five crops belonging to three Brassica species (cabbage and broccoli from *Brassica oleracea*; Chinese cabbage and turnip greens from *B. rapa*; and rapeseed from *B. napus*). To accomplish that, we entrain the plants to cycles of 16 h/ light and 8 h/ dark at 22°C for five weeks prior to release them into continuous light. In this way, any rhythmic fluctuation on glucosinolate accumulation when the plants are transferred to constant light can be an indicative of a truly endogenous plant circadian rhythm. Three replicate samples per genotype were collected at four intervals of the day during four days. Results showed that for all the evaluated genotypes, the glucosinolate content fluctuated strongly in a daily period. Interestingly, under constant light regime, the aliphatic glucosinolates content maintained rhythmic fluctuations, although these variations exhibited less visible amplitude compared with circadian oscillations under light-dark regime and were genotype dependent. On the contrary, cyclical indolic glucosinolate accumulation was largely lost at constant light conditions. These findings provide new support on how the circadian clock acts as a central regulator of glucosinolates metabolism and further highlight the potential of applying circadian clock coordination with the external environment for enhanced resistance to insects and pathogens in *Brassica* crops.

P27. Development of protein-related traits in *Brassica napus*

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Keywords: *Brassica napus*, canola, protein

Developing canola with enhanced protein and nutritional qualities could revolutionize canola meal utilization and functionality. Canola meal has historically been a by-product and utilized only for animal feed, even though it has very similar available energy compared to soybean meal. This provides an immense opportunity to expand the utilization of canola in Canada. The Canadian canola industry contributes $26.7 billion to the economy annually; only about $525 million of this is composed from meal production and utilization. This value could grow several fold if high-quality protein products were developed for use in human food products. Protein-related traits may include protein, amino acid, cruciferin and napin contents. Cruciferin and napin are the two main seed storage proteins found in canola meal. Each of these have specific functional properties with cruciferin acting as an excellent emulsifying, gelling and binding agent. Napin provides strong solubility, the ability to form transparent solutions, foaming properties and excellent nutritional value. If the genes controlling seed storage protein type were known, genotypes high in cruciferin and/or high in napin could be developed and utilized in specialty food products. Collaborators and the *Brassica* Breeding Program at the University of Manitoba are working to determine the variation and the regions controlling these protein-related traits. Genetic insight into these traits will provide the resources necessary to tailor canola genotypes for use in specialty, high-value protein products.

P28. Effects of phenethyl isothiocyanate on prostate cancer in vitro

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Keywords: prostate cancer cells, isothiocyanates, docetaxel, growth, apoptosis, migration

Isothiocyanates (ITCs) have gained growing attention since they have been attributed the merits for the beneficial potential of cruciferous vegetable dietary consumption on cancer. The aim of the present study is to determine the cytotoxic effects of phenethyl isothiocyanate (PEITC) on prostate cancer cells under in vitro conditions. Two human prostate cancer cell lines, PC3 and DU-145 were assayed. Cells were cultured under the presence of growing concentrations of PEITC (1, 2 y 4 μM) in absence or presence of the chemotherapeutic drug docetaxel (1, 2 nM). The cytotoxic effects of this compound were analyzed using the MTT (reduction of 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) colorimetric method at times 24, 48 and 72 h. Apoptosis and migration assays were also performed. Our results show that PEITC induced a dose-dependent cytotoxic effect on both PC3 and DU-145 cells at 24, 48 and 72 h. These effects were significantly higher than those found with docetaxel at the same time periods. Moreover, PEITC also potentiated the effects of docetaxel in a dose-dependent manner. Apoptosis were significantly higher in PEITC-docetaxel treated cells in comparison to docetaxel, PEITC or control groups at 72 h. Additionally, PEITC showed inhibition of migration of PC3 and D145 cells. Although the results of further studies (some of them are already being performed by our group) should be added, our results at present show a promising role of this compound as prostate cancer chemotherapeutic drug and/or co-adjuvant agent in docetaxel-based therapy.

P29. Evaluation of a Sicilian black broccoli extract on in vitro cell models

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Keywords: broccoli, glucosinolate, cancer, MTT assay, myrosinase

Vegetable crops of *Brassica oleracea* contain significant quantities of antioxidant compounds, such as glucosinolates (GLSs) which, upon disruption of the tissue, are broken down by the endogenous enzyme myrosinase, resulting in production of isothiocyanates, thiocyanates, nitriles, goitrin and epithionitriles. In particular, isothiocyanates are known to exert beneficial effects for human health. Several studies describe isothiocyanates as inhibitors of mitosis and stimulators of apoptosis in human tumor cells. The Sicilian black broccoli is a neglected crop of Mt. Etna S-W towns showing a particular GLS profile mainly represented by GRA and NGBS and its derivatives. We investigated the effects of different concentrations (0-25mM) of various GLS: gluconasturtiin (GNT), glucoraphanin (GRA), progoitrin (PRO), sinigrin monohydrate (SIN), glucoiberin (GIB), gluconapin (GNA), sinalbin K salt (GSI), glucobrassicin (GBS), glucobrassicanapin (GBN) and glucoerucin (GER) on the growth of HT29 (colon cancer cells), and A2058 (melanoma cancer cells), after 24h of treatment, in presence or not of MYR (0.018U) (*in situ* method). The same cell lines were also exposed to the Sicilian black broccoli juice extract (from leaves and stems) at different amount (0.05%, 0.1%, 0.5%, 1%, 5%), with and without myrosinase (0.018U). Cellular viability was evaluated by MTT assay. GLSs, alone and/or in presence of myrosinase, elicited different grades of toxicity in both cell lines models; while GRA and GNT showed less toxicity then their breakdown products, opposite results were obtained with GBS and GBSN. Black broccoli juice showed to be less toxic in presence of MYR; this effect is particular evident at higher juice percentages (1%; 5%), corresponding to 5mM; 25mM (respectively) of GRA and NGBS**.** Certainly, juice extract activity on in vitro cell lines cannot be explained by the peculiar GLS profile; probably the interaction of others compounds, such as polyphenols, have to be taken in consideration. In conclusion, not all breakdown glucosinolates products show more toxicity than their precursors, at least in our in vitro models.

P30. Evaluation of individual glucosinolates, phytochemicals, and antioxidant activities in three *Brassica* sprouts under different far-red light ratios

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Keywords: antioxidant activity, flavonoid, far-red light, glucosinolate, sprout, vitamin C

The aim of this study was to evaluate the individual glucosinolate (GSL) profile and concentration, total phenol, total flavonoid, vitamin C content, and antioxidant activities under various monochromatic light quality conditions in three *Brassica* sprouts (radish, Chinese cabbage, and broccoli). Five days old sprouts grown under dark conditions were exposed to three different red (R, 660 nm) to far-red (FR, 730 nm) light ratios for 2 days and their phytochemical contents were compared with three control treatments; fluorescent, red: blue (8:2) and dark treatments. Total GSL content in broccoli significantly increased with increasing the R/FR ratio, but no significant result was observed in radish and Chinese cabbage sprouts. The major individual GSLs in radish sprouts were identified as glucoraphanin and glucoerucin, and the content change by FR light quality treatment was not significant to both GSLs. The progoitrin content in Chinese cabbage and broccoli decreased by 38.0 % and 54.4 % with the decreasing the R/FR ratios, compared to the control light quality of red: blue (8:2), respectively. The increase of R/FR ratio in broccoli sprouts increased the gluconasturtiin content by 23.3 times compared to dark condition. The content of total phenol, total flavonoid, and vitamin C in radish was highest at 0.6 R/FR by 11.2 %, 12.0 %, and 6.0 %, respectively. The total phenol content of Chinese cabbage sprout was also the highest at 0.6 (R/FR) (7.4 $mg \cdot g^{-1}$ DW), and the vitamin C content of broccoli was the highest at 0.6 (R/FR) (8.5 $mg \cdot g^{-1}$ DW) compared to the control conditions. Antioxidant activities were not significantly affected by different light quality treatments. All these results confirmed that the increase of far-red light ratio could increase the phytochemicals in *Brassica* sprouts, while the responses were highly dependent on crop species.

P31. Selection of F1 hybrid candidates by comparative analysis of phytochemical contents and antioxidant activity in broccoli

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Keywords: broccoli, F1 hybrid candidates, glucoraphanin, glucosinolates, kaempferol, phenolics

The aim of this study was to select the superior broccoli F_1 hybrid candidates on the basis of their phytochemical contents and antioxidant activity. Twenty one broccoli genotypes (19 F_1 hybrid candidates for regional adaptation tests, and 2 commercial cultivars) were grown in open field, and their glucosinolates (GSLs), flavonoids, total phenolics, and antioxidant activity were evaluated. Ten GSLs were identified in that four GSLs; glucoraphanin (2.5-12.0 $\mu mol \cdot g^{-1}$), glucobrassicin (0.8-5.2 $\mu mol \cdot g^{-1}$), gluconapin (0.1-1.8 $\mu mol \cdot g^{-1}$), and gluconasturtiin (0.1-0.4 $\mu mol \cdot g^{-1}$) were major GSLs present in all the genotypes. Glucoraphanin, the most dominant GSL, was significantly higher in 14 F_1 hybrid candidates (R-6 to R-19) (4.3-12.0 $\mu mol \cdot g^{-1}$) compared to commercial cultivars (3.4 $\mu mol \cdot g^{-1}$), while glucobrassicin and gluconapin showed reverse accumulation pattern with the higher value in commercial cultivars. Total GSL contents were significantly higher in four F_1 hybrid candidates (R-10, R-14, R-15, and R-18) than in commercial cultivars. Among the flavonoids analyzed, kaempferol was the most abundant (2.0-8.8 $mg \cdot 100\ g^{-1}$) throughout the genotypes followed by quercetin and apigenin. Total flavonoid content ranged from 3.1 to 11.7 $mg \cdot 100\ g^{-1}$, and only ten F_1 hybrid candidates (R-03, R-04, R-06, R-07, R-11, R-12 R-13, R-16, R-17, and R-19) showed significantly higher flavonoid content (>4.7 $mg \cdot 100\ g^{-1}$) than in the commercial cultivars. Furthermore, higher total phenol content (>350 $mg\ GAE \cdot 100\ g^{-1}$) and antioxidant activity (>75.0%) were found in seven F_1 hybrid candidates (R-11, R-12, R-13, R-16, R-17, R-18, and R-19). In conclusion, six F_1 hybrids candidates (R-11, R-12, R-13, R-16, R-17, and R-19) showed higher glucoraphanin, total phenol, and flavonoid contents with higher antioxidant activity, suggesting their higher nutritional value, and can be considered for the commercialization.

P32. A high density genetic map of *Barbarea vulgaris*

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Keywords: *Barbarea vulgaris*, RAD-seq, genetic linkage map

Barbarea vulgaris is a wild cruciferous plant, including G- and P-type which are different in insect resistance and secondary metabolite profiles. It can be used as model plant for studying saponin and glucosinolate biosynthesis, insect resistance and plant-insect co-evolution. But up to recently, rare high density linkage map has been constructed in *B. vulgaris*, which hinders its molecular research. In this study, the RAD sequencing was conducted to the G-, P- type and their generated 255 F_2 individuals. A total of 134.5 G paired-end (150 bp) high-quality clean data was obtained on Illumina HiSeq 2500. The data size was 3.3 and 3.5 Gb for G- and P-type plant and ranged from 385.5 to 886.6 Mb for the 255 F_2 individuals. Between the G- and P-type *B. vulgari*s, a total of 80,928 polymorphic sites were identified. Amongst, 60,287 codominant “aa × bb” type markers were identified. Subsequently, the polymorphic markers were detected in the F_2 populations, resulted in 8,448 markers present in at least 216 plants (85% of the population). After segregation distortion filtered at P value < 0.001, the remaining 2,052 markers were used for linkage maps construction. Finally, 1,545 markers were mapped onto eight linkage groups (LGs) with total length of 567.996 cM and an average distance of 0.381 cM between adjacent markers. LG7 (110.97 cM including 219 markers) and LG2 (33.804 cM including 168 markers) achieved the longest and shortest genetic distance, respectively. LG5 (257 makers spanning 61.482 cM) and LG1 (146 markers spanning 62.723 cM) have the higher and lower number of markers. The average gaps between adjacent markers of individual LGs vary from 0.202 to 0.582 cM. This is the most high density linkage map for *B. vulgaris*. It will be useful for QTLs mapping, comparative genomics, and improve the assembling of the genome of *B. vulgaris*.

P33. Transcriptomics and metabolomics: stress responses in broccoli flower buds during postharvest storage treatments

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Keywords: omics, UV-B irradiation, postharvest, plant secondary metabolism

Broccoli (*Brassica oleracea* L. var. italica) is one of the most popular *Brassica* vegetables. The green flowering heads are rich in potentially health-promoting phytochemicals such as ascorbic acid, glucosinolates, carotenoids and polyphenols. Phytochemicals play important roles in plant defense, and their content can be greatly influenced by various forms of stress. The aim of this study was to explore stress responses, in terms of gene expression and phytochemical content, in broccoli flower buds during postharvest storage treatments. Freshly harvested broccoli heads (cv. Ironman) were acclimated for four days at 4 °C in total darkness before the storage treatments. The broccoli heads were then stored for six days with the following treatments: a) 4 °C in darkness, b) 10 °C in darkness, c) 10 °C under visible light, and d) 10 °C under visible light and UV-B radiation. The radiation treatments were conducted for 12 h per day. Stress responses were explored by comparative transcriptomics and metabolomics before and after storage treatments. Gene expression profiles were obtained by microarray analyses, and metabolomics fingerprinting was performed using LC-MS. Selected phytochemicals were also measured by targeted chemical analyses. The results demonstrate that the postharvest storage treatments had large effects on the transcriptome, metabolome and phytochemical content of broccoli flower buds.

P34. Mapping sensory quality and plant compounds to improve consumer choice of *Brassica oleracea* vegetables

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Keywords: Brassica, taste, flavour, sensory maps, sensory quality, LC-MS metabolomics, headspace GC-MS

Increased vegetable consumption is a goal in the nutritional guidelines issued by the Norwegian health authorities. *Brassica* vegetables are important parts of a Nordic diet and excellent sources of essential nutrients and a range of health-promoting phytochemicals. However, the bitter and sulfurous taste and variable sensory quality of these vegetables are often hinders for consumers to increase their *Brassica* consumption. To date little is known about how sensory attributes vary among *Brassica* varieties and their cultivars, or how they are affected by climate and crop production factors. Hence, delivering *Brassica* vegetables with a stable sensory quality and distributing knowledge about their sensory attributes to the consumer is challenging for both growers and traders. The aim of the “Cabbage Taste” project is to generate and disseminate knowledge about the sensory attributes of *Brassica* vegetables, their content of flavour- and health-associated plant compounds and the relationship between these parameters. The work includes generation of sensory descriptive maps as well as mapping of the content and variation of plant compounds in 30 cultivars of head cabbage (*capitata* group) in different seasons, 11 cultivars of cauliflower (*botrytis* group) and 12 cultivars of leafy cabbage (*acephala* group), and *Brassica* grown under varied nutrient (N and S) and water regimes. Improved knowledge on how genetic and environmental factors influence the sensory and nutritional quality will give producers a potential tool to influence the quality already during the growing season. It will also provide traders a potential for product differentiation, and give consumers information about the expected sensory attributes of products. Results of the project so far have highlighted that the sensory profiles of 30 cultivars of head cabbage cultivars with 25 attributes/characteristics present a great diversity of flavours with diverse potential culinary applications. The presentation will discuss some of the results and their implications. The project includes Norwegian seed companies, producer organization, trading company and growers.

P35. Turnip tops derived by-products: a promising source of bioactive compounds

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Keywords: agro-waste, agro-food industry, *Brassica rapa*, by-products, nutrients, phytochemicals

Brassica rapa crops are consumed by using the leaves (turnip greens) and the young sprouting shoots (turnip tops) in different culinary preparations. Many by-products of the agri-food industry may be useful as sources of nutrients and potentially functional compounds, giving the opportunity to obtain added-value products. In this work we are interested in adding value to turnip tops by-products (old and damaged leaves and stems) that represent a real problem in the production sites because no intended use for this material has been envisaged. Therefore, the aim of this study was to add value to the turnip tops-derived by-products, since recycling all this agro-waste to obtain bioactive compounds for industry can boost profits and reduce costs and environmental problems. The content on the bioactive compounds (glucosinolates, phenolic compounds), nutrients (vitamin C and minerals) and the antioxidant capacity was analyzed and simultaneously determined. In addition, the level of retention of each individual compound after industrial steaming was evaluated in the edible organs and also in the cooking water, in order to compare their composition to a fresh uncooked control. The bioactive compounds and nutrient contents varied according to the organ analyzed (leaves or by-products), growth seasons and sites. The content of phytochemicals and nutrients of the by-products of turnip tops fell within the range of health-promoting levels of edible commercial parts (leaves and shoots). High retention of health-promoting compounds in the cooking water should be considered for increasing the intake properties of *B. rapa*. Therefore, adding value to turnip tops agro-waste by obtaining bioactive compounds and nutrients could benefit economically the agro-food industry.

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