



# WP 5

## Buckwheat

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# WP 5 - Main Objectives

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- Identify genetic variation in agronomic and nutritional traits
- Identify genotypes with increased allelopathic activity
- Screen selected common buckwheat genotypes for P-mineralization capacity
- Perform crosses between and within common buckwheat (*Fagopyrum esculentum* Moench.) genotypes and self-compatible species of the genus *Fagopyrum* sp.



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# WP 5 – Important Information

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- Month 13 – 60
- Partners – KIS, SZG, CRI, RGA, UVIGO, UNEW, CAAS, WSU, PROBIO




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# *Task 5.1 Screening of genetic resources and breeding material*

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- Extensive phenotyping in field trials in 4 countries (CZ, SI, AT, and US and China)
  - Year 2  year 3 and 4
  - 100 genotypes in China year 3 and 4
- Morphological and phenological traits (e.g. growth, branch and shoot habit, plant height, number of days to flowering/maturity, etc.) according to the list of descriptors published as D5.1
- **Partners involved: KIS, CRI, SZG, WSU, CAAS**



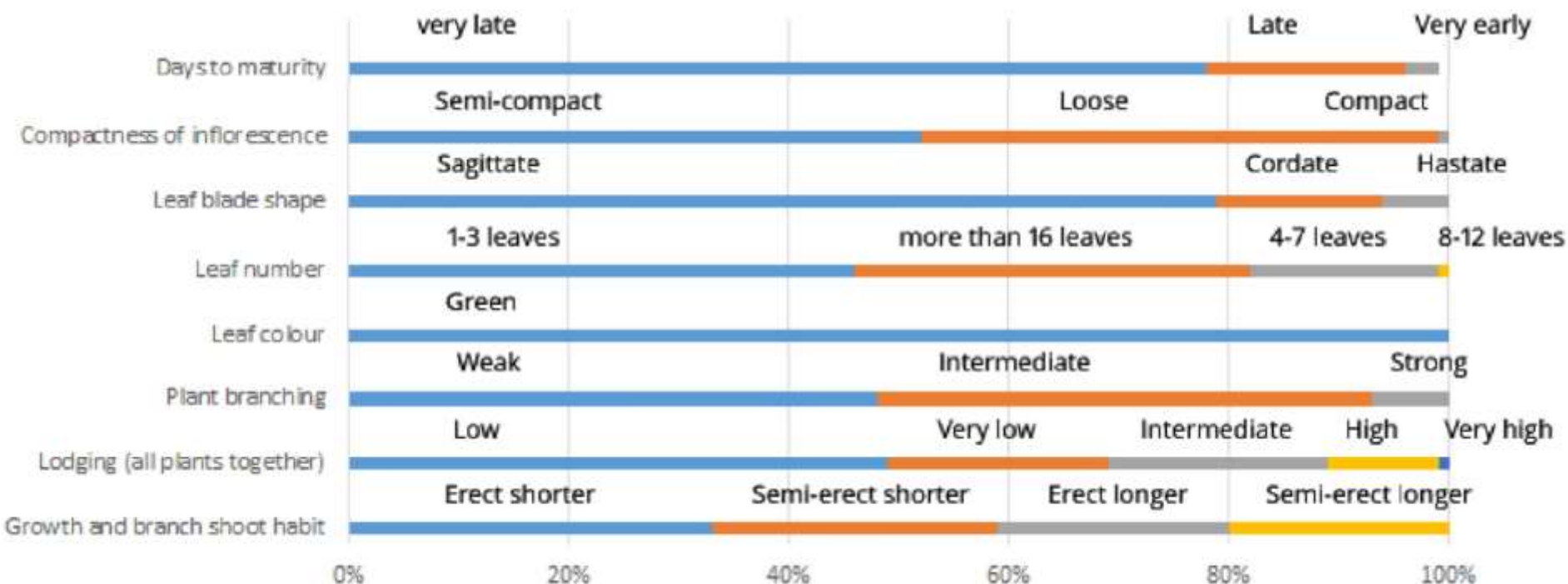
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## T5.1 Results achieved

- 216 genotypes – 54 in common + 16 in SZG, 26 in KIS and 120 in CRI



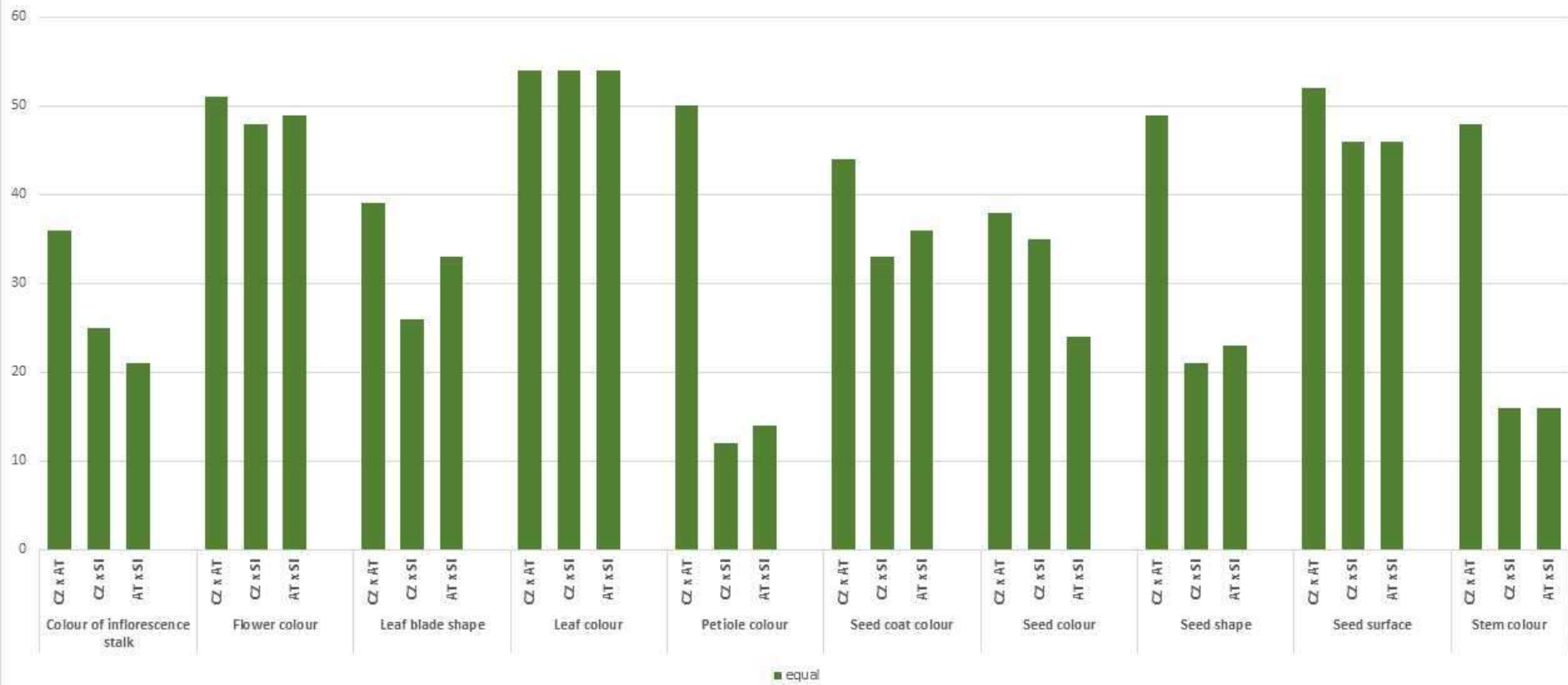
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Descriptors comparison between individual countries




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## *T5.1 Next steps*

- **Rearrangement of the list of descriptors**
  - 29  19,
  - added 4 traits
- **Sowing of all genotypes**
- **Analyses of nutritional quality of all genotypes**
- **Statistical analysis**
- **Phenotyping of Chinese collection of common and Tartary buckwheat**



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## ***TASK 5.2 Allelopathic activity screening***

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**A sub-set of 40 buckwheat genotypes will be assessed for:**

a) allelochemical root exudation/leaching *in vitro* including palmitic acid, squalene, epicatechin, vitexin, phenolic acids and flavonoids, and their phytotoxicity on a range of grass and broad-leaved weeds and other crops

**The 20 most promising cultivars**



b) where allelochemical release from adult plants in the soil will be assessed (soil solution extraction by means of micro-tubes)

c) study of the release of allelochemicals (mainly fagomine, 4-piperidone and 2-piperidinemethanol and several phenolics) from aerial parts induced by rain in a pot experiment in the greenhouse.

**Partners involved: UVIGO, UNEW**



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## *T5.2 Results achieved*

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- **54 genotypes – as in T5.1 sent for the assessment**
- **Optimization method for germination**



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## *T5.2 Next steps*

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- Application of optimized method on other genotypes
- Gas/mass chromatography to identify - fatty acids and the phenolic acids p-chlorobenzoic acid, p-hydroxybenzoic acid, vanillic acid, syringic acid, p-coumaric acid, ferulic acid, etc.



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# ***TASK 5.3 Screening for genetic variation in P-mineralisation***

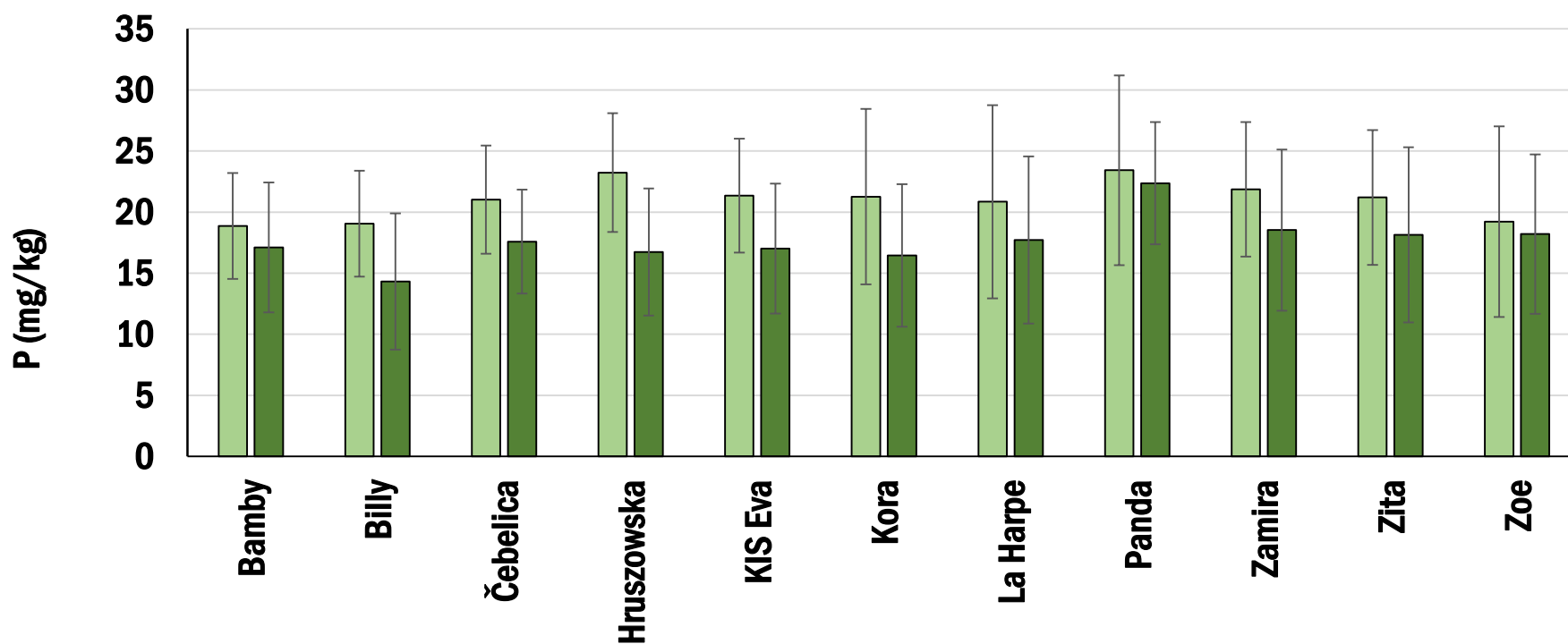
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- **At least two soils tests to determine total bioavailable P contents and readily available P fractions to enhance the real P availability and P mineralization capacity in soils.**
- **Soils of different soil types and management practices to evaluate and calibrate the appropriate method for determining of phosphorus in soils.**

**Partners involved: KIS, CRI, WSU**

# T5.3 Results achieved

P - H<sub>2</sub>O - CZ



31.07.2019

15.10.2019



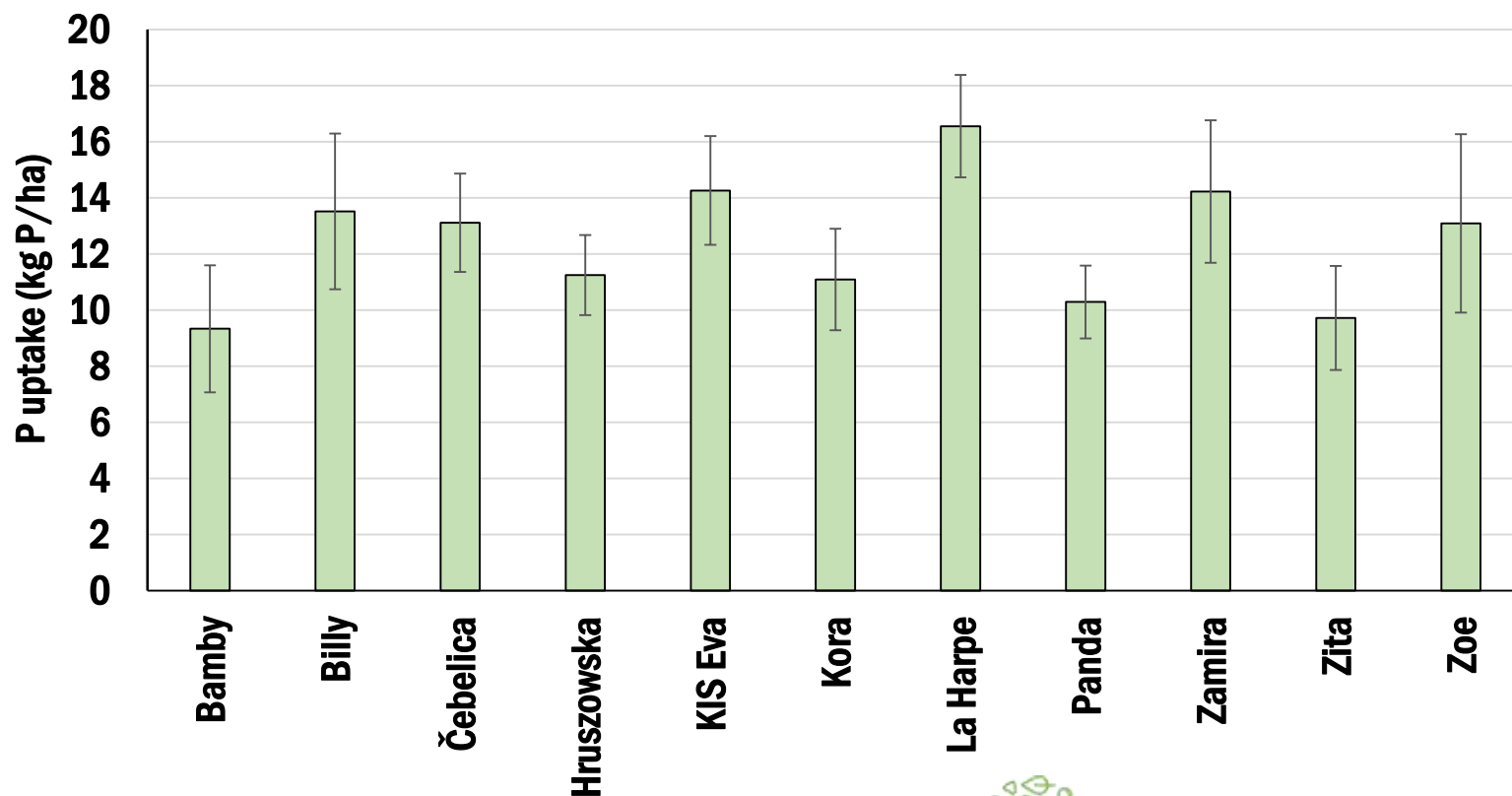
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## T5.3 Results achieved

P-uptake - 31.7. 2019, CZ



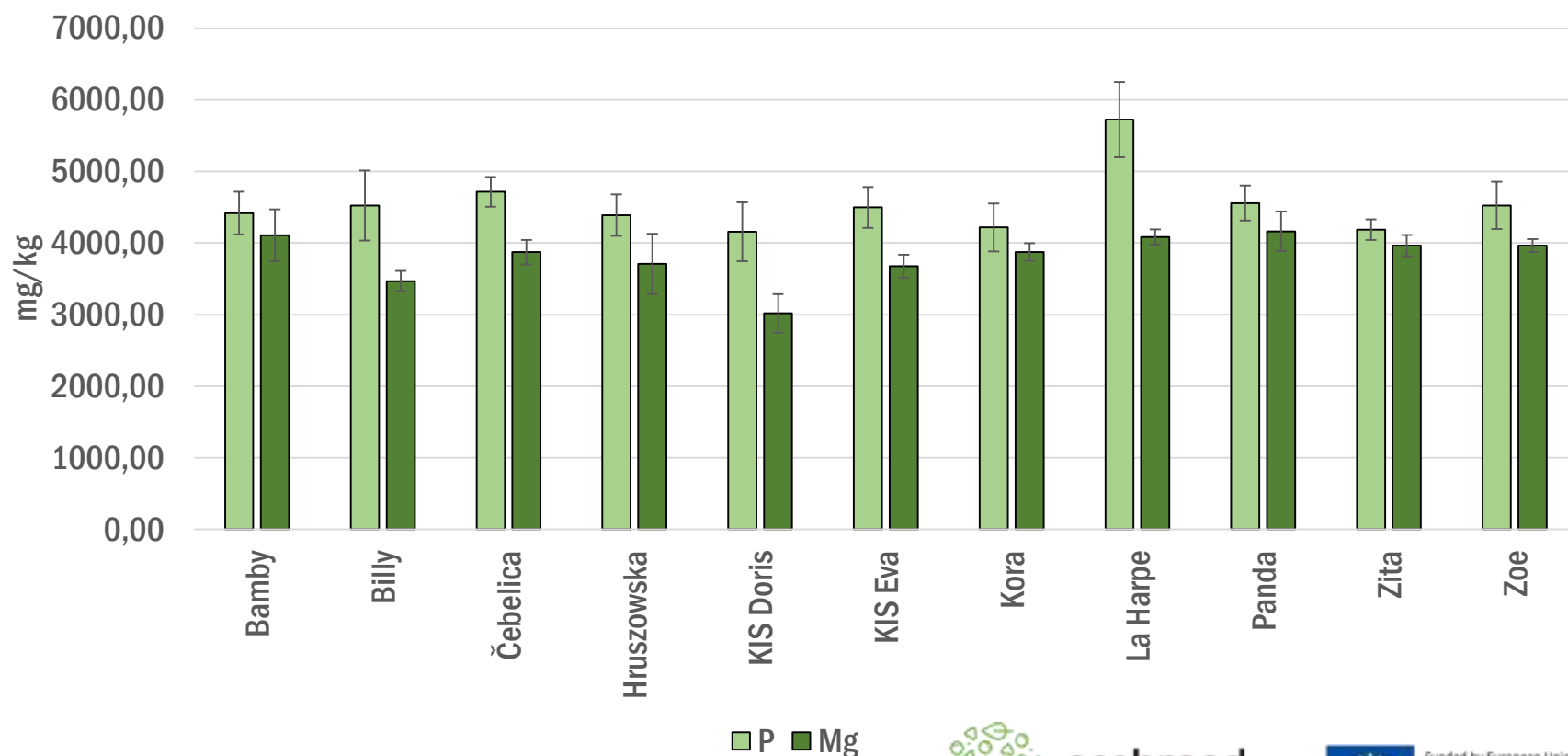
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# T5.3 Results achieved

## P and Mg content in buckwheat plants, SI summer trials



■ P ■ Mg



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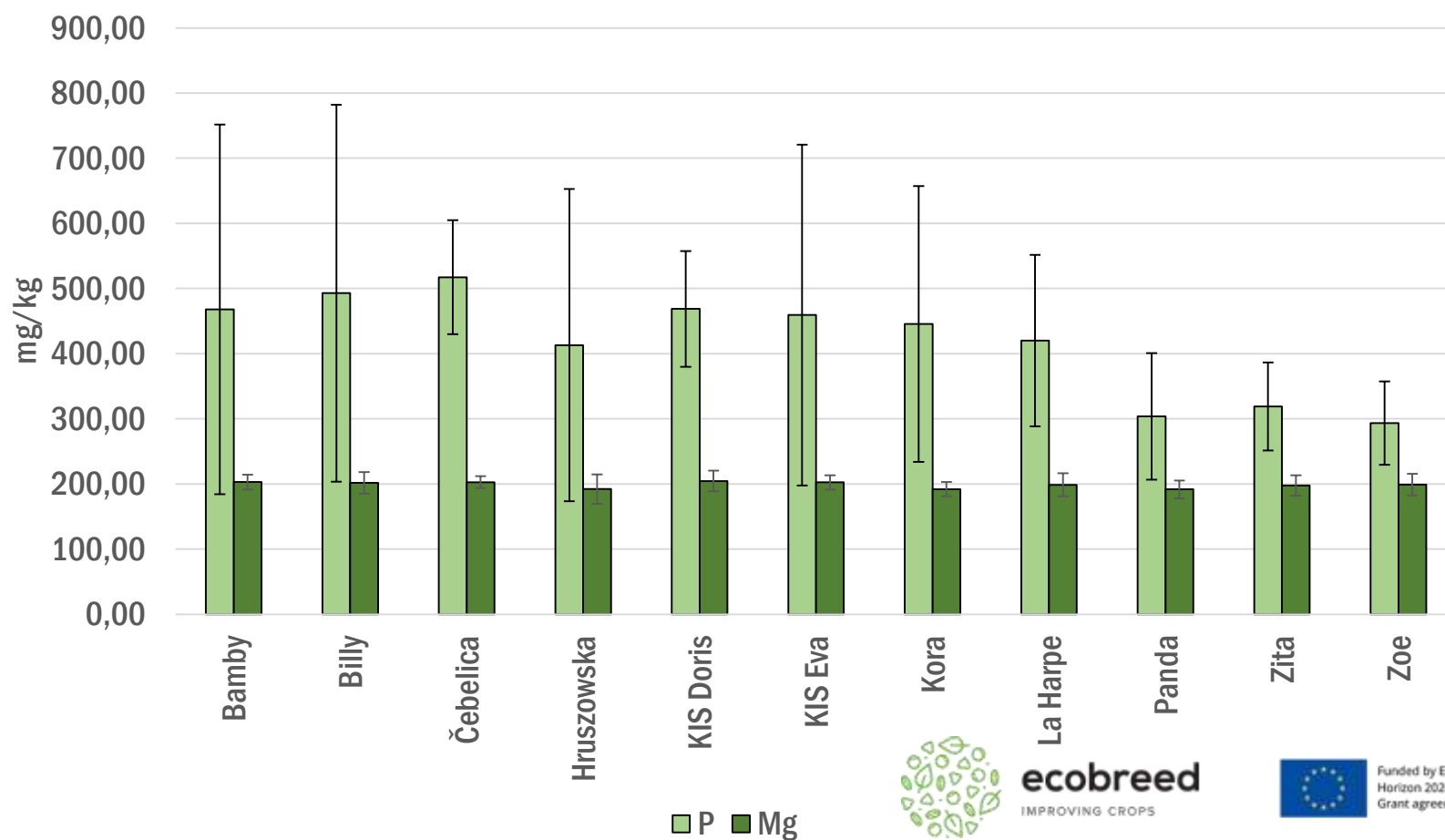


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# T5.3 Results achieved

## P and Mg content, soil, SI summer field trials



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## *T5.3 Next steps*

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- Assessment of grain quality - ongoing
- Spring field trials sown – SI, US and CZ (twice)
- Summer sowing planned



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# ***TASK 5.4 Genotyping***

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- Genotyping-by-sequencing (GBS) marker system RNA-seq and RACE-Clone to identify underlying genetic response to abiotic (cold, drought, salinity) and biotic stresses together with quality traits (e.g. rutin content)
- KIS and CAAS → optimization of method prior to the genome-wide association study (GWAS) of the European and Chinese core collections → KIS / template DNA for up to 100 accessions selected within T.5.1 to assess genetic diversity performed by CAAS applying GBS and available SNP markers by the end of Year 2
- Data obtained will be used for the production of improved varieties in TASK 5.5.

**Partners involved: CAAS, KIS, WSU**



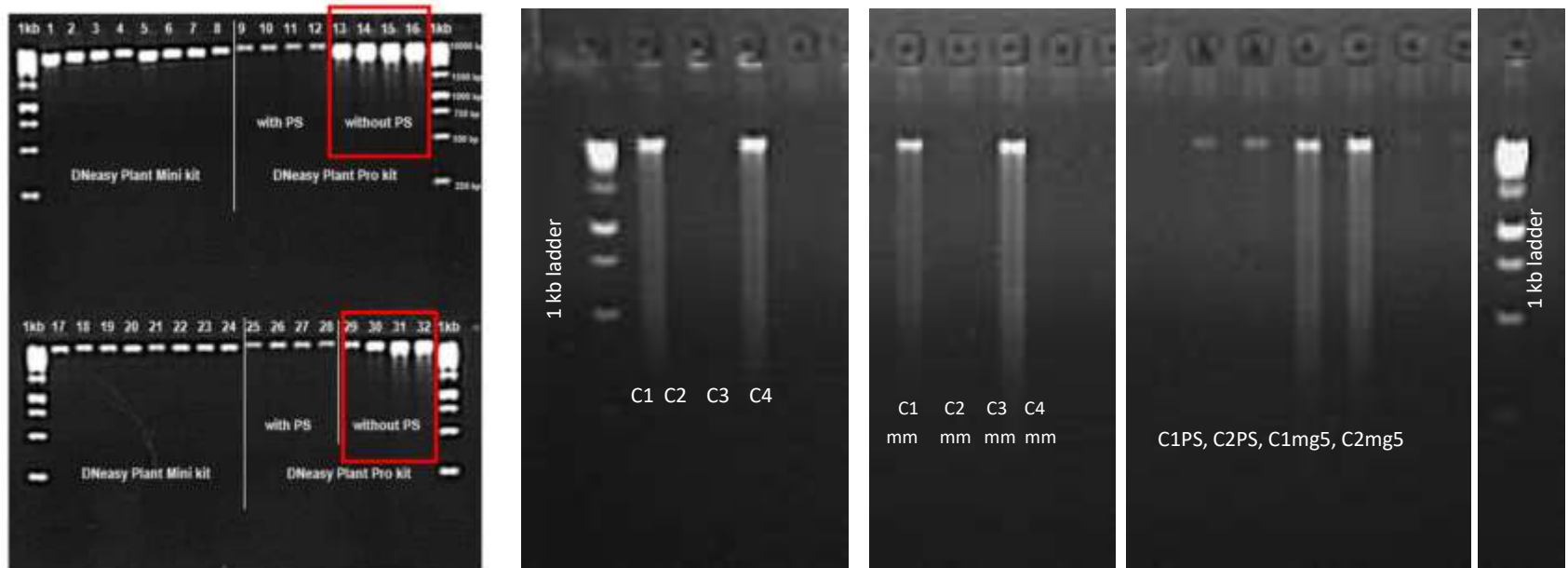
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# T5.4 Results achieved

- Optimisation of the DNA extraction method for GWAS and testing the shipment procedures from the EU (KIS) to China (CAAS)



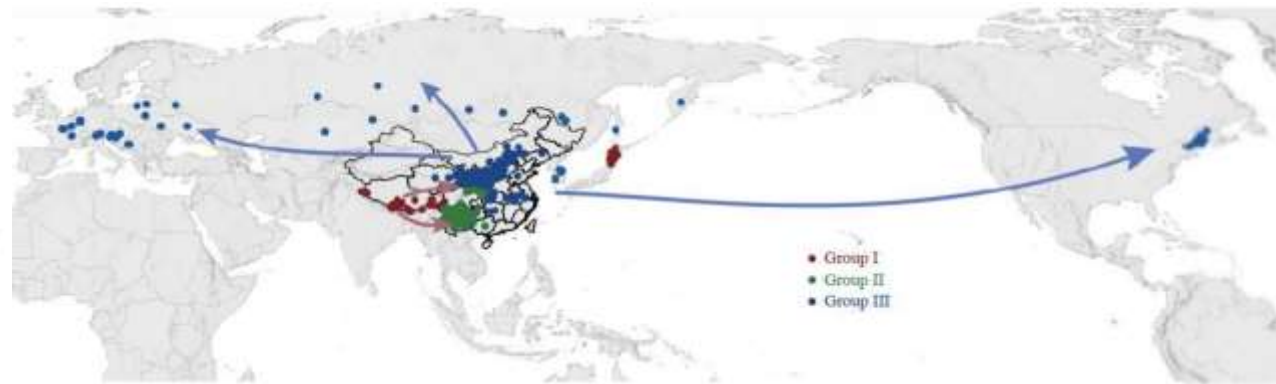
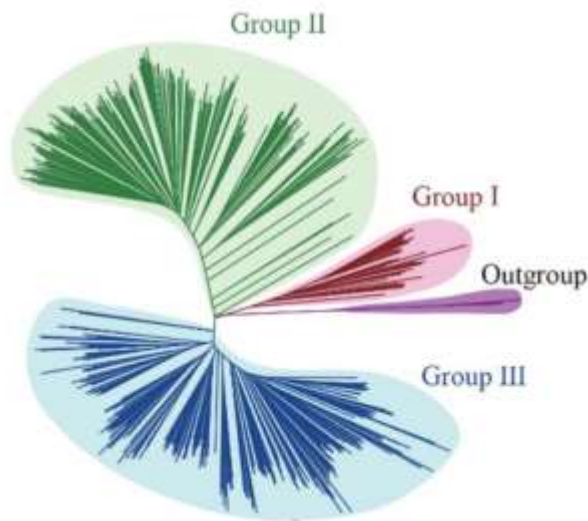
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## *T5.4 Results achieved*

- a whole-genome re-sequencing of 517 buckwheat accessions (510 accessions of Tartary buckwheat – including 30 varieties, 448 landraces and 32 in wild-collected accessions representing 14 countries)
- the independent domestication and geographical differentiation of Tartary buckwheat were for the first time discovered.
- GWAS has identified key loci associated with agriculturally important traits, especially genes controlling the weight of 1000 seeds, pericarp colour and accumulation of kaempferol-3-O-rutinoside



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## *T5.4 Next steps*

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- Shipment of extracted DNA of all genotypes (more than 200 genotypes)
- Assessment of DNA for GBS
- Comparison of data from genotyping enhanced by data from phenotyping



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# ***TASK 5.5 Production of elite varieties and advanced breeding lines***

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- Crosses between genotypes chosen on the basis of results from T5.1 and T5.4
- Other *Fagopyrum* species are involved (*F.tataricum*, *F.homotropicum*)
- All crosses according to the recommendations of IFOAM International

**Partners involved: RGA, KIS, SZG, WSU**



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## ***T5.5 Results achieved***

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- **First crosses**
- **256 genotypes, 3 different male genotypes**
- **Harvested 5,911 seeds from 166 combinations**





## *T5.5 Next steps*

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- Crosses of other genotypes in RGA and SZG
- US samples to SI
- Crosses with other *Fagopyrum* species



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# Deliverables

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- **D5.1 Phenotypic data management system produced for partners (M 12)**
- **D5.2 Characterisation of allelopathic activity of selected genotypes (M 48)**
- **D5.3 Characterisation of P-mineralisation capacity of selected genotypes (M 48)**
- **D5.4 Genetic diversity analyses of common buckwheat genetic resources (M 48)**
- **D5.5 Phenotypic characterisation of common buckwheat genotypes (M 54)**
- **D5.6 Buckwheat crosses (F1, F2, BC1 and BC2 generations), providing a starting point for the production of buckwheat cultivars suitable for organic farming (M 60)**
- **D5.7 Final publishable report on WP5 (M 60)**

# Milestones

M7	Multiplication of seed for phenotyping	NPPC	12
M8	Multiplication of seed for FPT and breeding activities	NPPC	36
M9	Phenotyping data management system sent to partners	UNEW	12
M11	Selection of sub-set from core collection for allelopathic screening	UVIGO	13
M12	Selection of suitable markers for screening, sharing of protocols between partners, allocation of traits between partners	IFVCNS	13
M13	Establishment of segregating populations for specified traits	IFVCNS	36
M14	Sharing molecular data and bioinformatic protocols for joint analysis	BOKU	48
M15	Delivery of DNA samples to CAAS for genotyping	CAAS	12
M16	Selection of sub-set of core collection for P mineralisation study in buckwheat and delivery of seed to partners	CRI	13
M17	Advanced breeding lines available for further selection and varietal development	IHAR	48
M22	Selection of varieties to use in FPT and start of seed multiplication	BOKU	24
M24	Formation and distribution of CCP to farmers	NATURLAND	36
M28	Genotyping of buckwheat core collection completed	CAAS	36



# Problems, Deviation and Solution

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- **T5.1: no data from WSU**
  - Trials established in 2020 and will be repeated in 2021
- **T5.2: delay due to COVID-19**
- **T5.3: spring trials in North-East Slovenia collapsed due to weeds**
  - spring field trials will be repeated in 2020 and 2021 in SI and CZ
- **T5.3: missing trials in the WSU**
  - spring field trials established in 2020, will be repeated 2021



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**Thank to my  
colleagues in WP5 and  
to all of you for your  
attention**