WP 5 Buckwheat

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Who am I?

Crop Research Institute

- largest research institute devoted to crop production research under the auspices of the Ministry of Agriculture of the Czech Republic
- Genebank

HEALTHY MINORCEREALS.eu

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Why buckwheat?

Fagopyrum esculentum Moench.

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COVER CROP
Common Buckwheat
Fagopyrum esculentum

USDA ORGANIC

FULL SUN
30 - 40 DAYS
Sow in spring summer or fall

HEIRLOOM
In just a few weeks, grow your own green manure for healthier soil that is more productive. Great for controlling annual and perennial weeds. So easy to grow, and so good for the soil!

Botanical INTERESTS®

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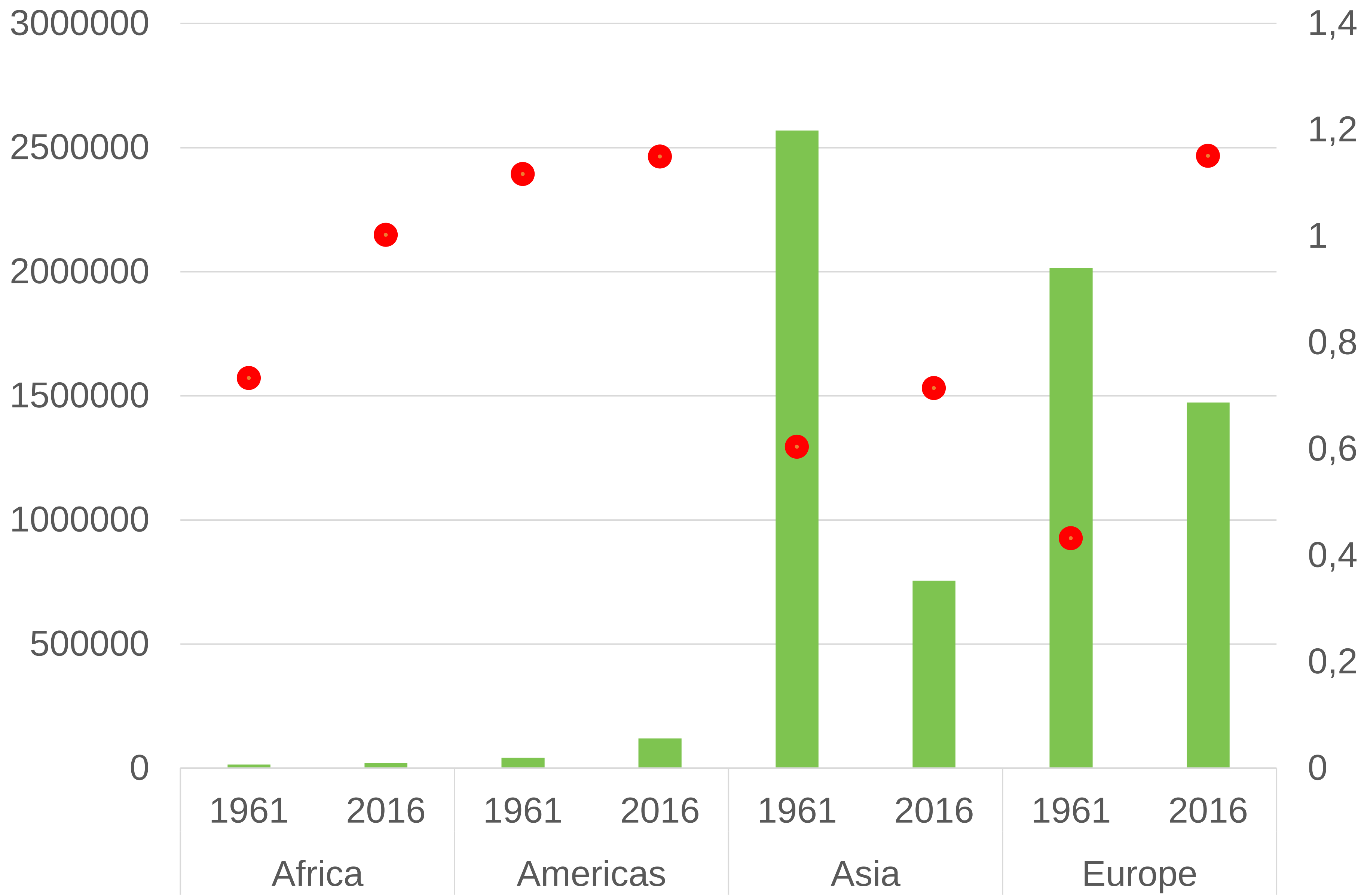

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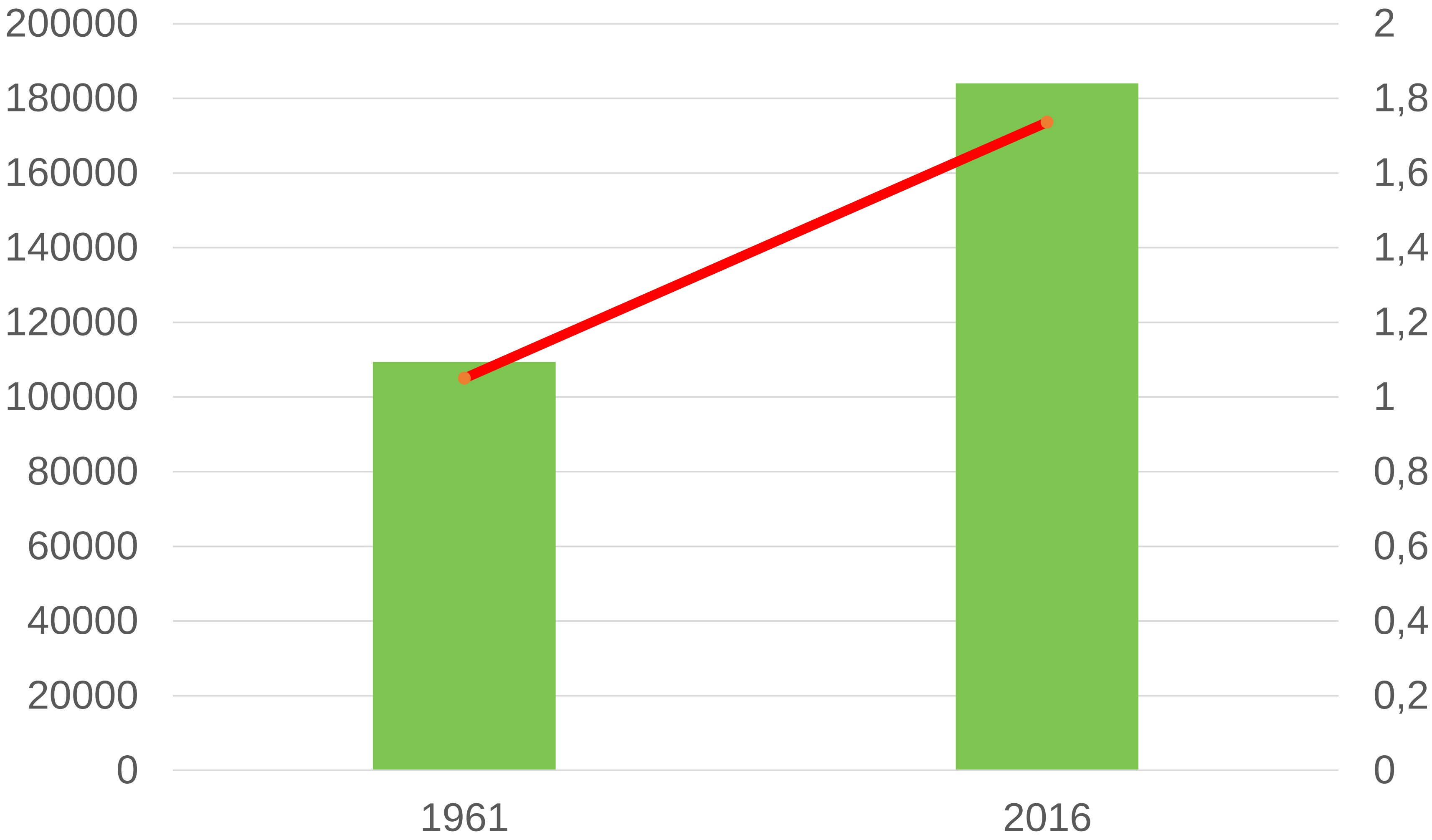

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The main objectives of WP5

- 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 common buckwheat (*Fagopyrum esculentum* Moench.) and Tartary buckwheat (*Fagopyrum tataricum* ssp. *potanini*) and self-compatible genotypes to identify fertile progenies

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Task 5.1 Screening of genetic resources and breeding material

- 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.)

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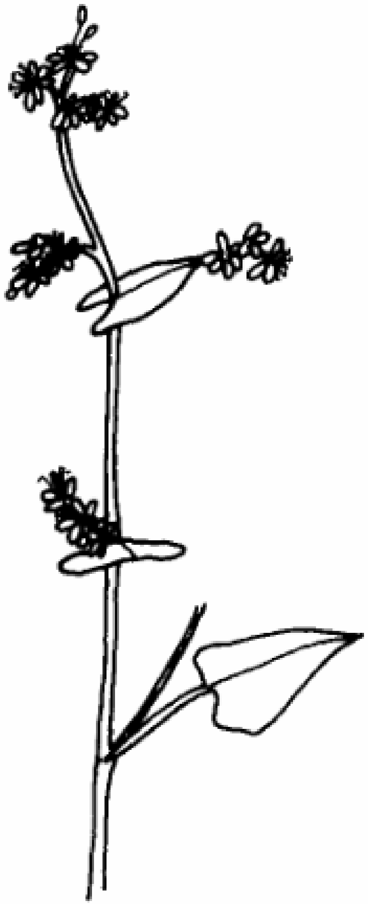

3 Cyme loose

5 Cyme semi-compact

7 Cyme compact

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Task 5.1 Screening of genetic resources and breeding material

- Tolerance/resistance to naturally occurring biotic/abiotic stresses (e.g. susceptibility to fungi regarding locality/geographic position such as *Peronospora*, *Fusarium*, etc.),
- Achene yield and yield components
- Protein content/fractions, starch, starch digestibility (according to Englyst), total and dietary fibre, total phenolics, antioxidant activity (ABTS, DPPH), rutin content

Responsible: CRI; involved: KIS, WSU, SZG, CAAS

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TASK 5.2 Allelopathic activity screening

- 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.

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TASK 5.2 Allelopathic activity screening

d) in greenhouse experiments, isolating different competitive factors (light, space, water, nutrients and phytotoxicity) to evaluate weed control capacity attributable to the allelopathic capacity of the cultivars

e) a study of the release of allelochemicals and their effects from plant residues in pots in the greenhouse.

Responsible: UViGO; involved: UNEW

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TASK 5.3 Screening for genetic variation in P-mineralisation

- 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 (e.g. conventional vs zero tillage) to evaluate and calibrate the appropriate method for determining of phosphorus in soils.
  - Field experiments in three different countries (US, SI, CZ) using a minimum of 10 varieties/genotypes of common buckwheat.
  - Soil samples for the assessment of pH and P availability with repeat analyses prior sowing and after harvest.
  - Characterisation of phenology, biotic and abiotic stress levels/occurrence, lodging, yield, etc.

Responsible: CRI; involved: KIS, WSU

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TASK 5.4 Genotyping

- 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.

Responsible: CAAS; involved: WSU, KIS

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TASK 5.5 Production of elite varieties and advanced breeding lines

- Crosses between common buckwheat (*Fagopyrum esculentum*), Tartary buckwheat (*Fagopyrum tataricum* ssp *potanini*) and self-compatible genotypes
- Use of hand emasculation, hot-water emasculation and environment sensitive male sterility of some buckwheat accessions (photo or thermo, photo-thermo or thermo-photo male sterility systems).
- Production of common and Tartary buckwheat crosses (F1, F2, BC1 and BC2 generations) → the production of buckwheat cultivars suitable for organic farming → the creation of synthetic varieties evaluated under different agronomic → practices/environments to optimise performance

Responsible: RGA; involved: WSU, KIS, SZG

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Deliverables

- 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)

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Thank you very much for your attention

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