Seed Storage Proteins in *Chenopodium Quinoa* Germplasm

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INTRODUCTION

- Quinoa (*Chenopodium quinoa* Willd.) is a pseudo-cereal from the Chenopodiaceae family originating in the Andean Mountains of the South America region [1].
- The production and consumption of quinoa seeds have increased recently. Cultivation has also spread to countries with temperate climates [2].
- Quinoa seeds are valued for their relatively high content of gluten-free storage protein with major storage protein fractions albumins and globulins [3].
- Quinoa grain also contains the essential amino acids lysine, methionine, and threonine, which are presented in limited amounts in other crops [4].
- The main goal of the study was to analyse the band spectra of seed storage proteins and characterize their polymorphism.

METHODOLOGY

- A total of 35 quinoa samples with various geographical origins were involved in the study.
- All varieties were cultivated under the climatic conditions of the Czech Republic at the Crop Research Institute, Prague in the years 2018–2020.
- Bulk samples of 0.25 mg of quinoa flour were extracted using Laemmli sample buffer [5].
- Isolated total protein was separated using SDS-PAGE with 12% (w/v) resolving gel and 4% (w/v) stacking gel [5].
- Resulting positions of protein bands were scored according to commercial Thermo Scientific™ PageRuler™ Unstained Broad Range Protein Ladder.

RESULTS

- A total of 20 allelic positions were detected in the molecular weight (MW) range from approximately 5 to 100 kDa.
- The majority of all the resulting bands can be classified as bands with medium or high intensity.
- The most abundant protein bands for all varieties were present at 5 to 35 kDa, followed by 48 to 60 kDa (Fig. 1), corresponding to the MW range of the major quinoa protein fractions albumins and globulins [4].
- The polymorphism of the samples was relatively low, but the samples can be distinguished from each other according to band positions and relative abundance (Fig. 2).
- The main variability in band position among varietis was found in the MW range around 30 to 38 kDa and 50 to 60 kDa (Fig. 2).

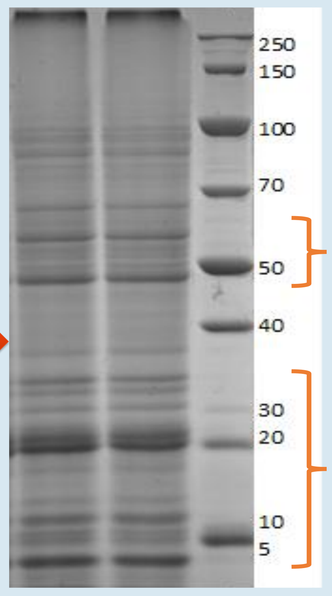

Figure 1. Example of quinoa total protein band profile.

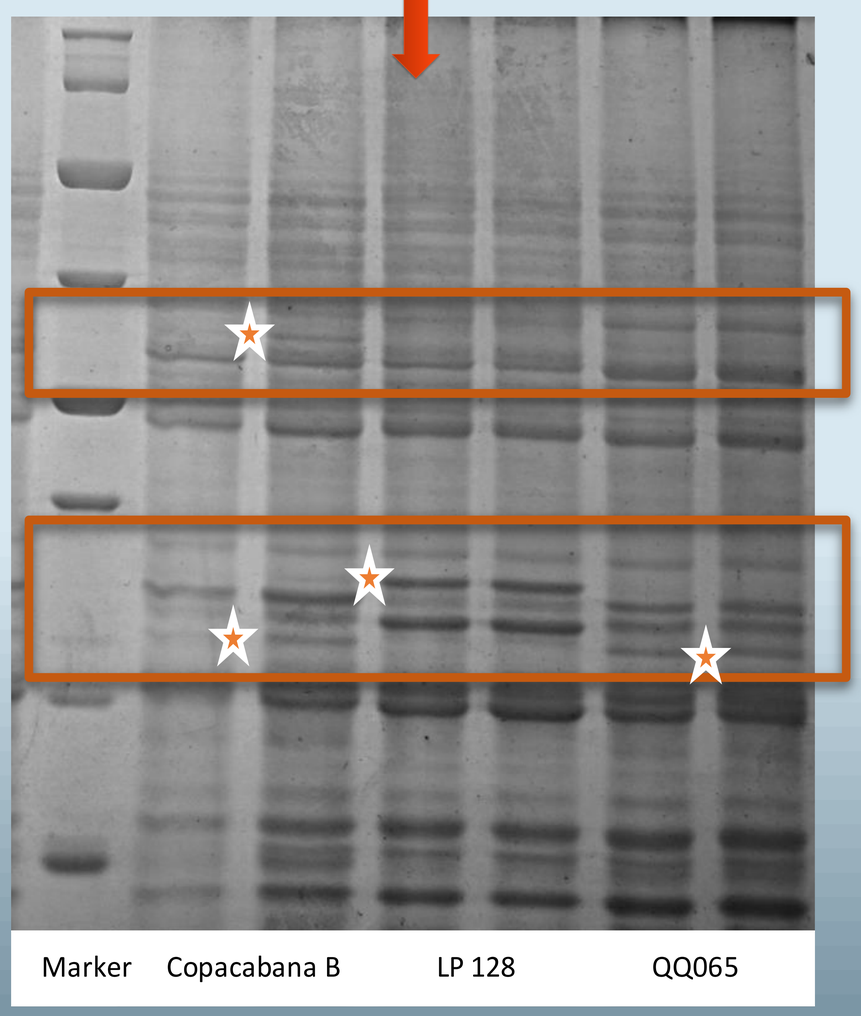

Figure 2. Three quinoa sampless with various band patterns (marked by star). Region of band pattern variability is marked by brown rectangle.

RESULTS

- The influence of crop year on total protein profile was not detected, however, the relative intensities of the bands differed across the crop years.
- Various phenotypes within the same variety (e.g. different leaf/inflorescence/seed colour) resulted in the same protein band pattern (Fig 3).

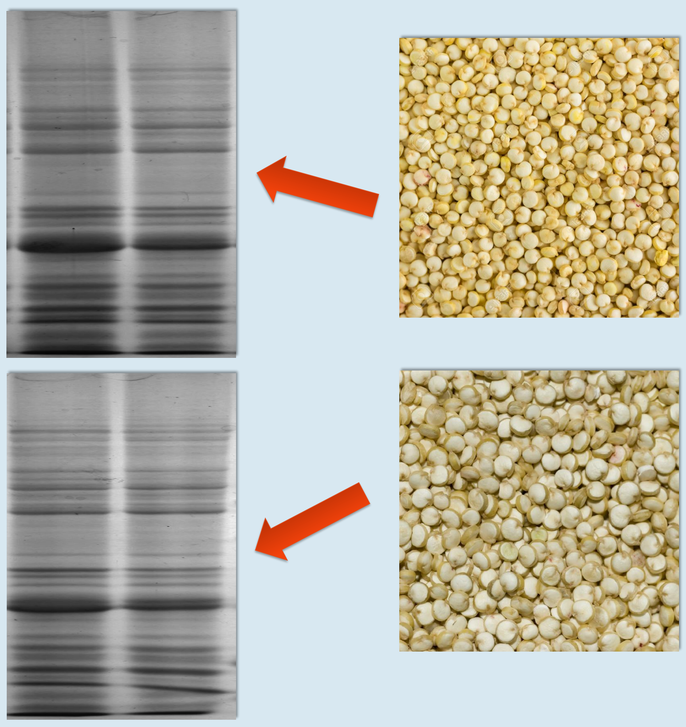

Figure 3. Variable seed colours of variety Baer with idential band pattern..

CONCLUSION

- The evaluated samples showed some degree of heterogeneity at the level of overall seed protein polymorphism.
- The most abundant protein bands were present at the MW range corresponding to the MW range of albumins and globulins.
- Banding patterns of quinoa obtained from seed bulks are reproducible and not affected by crop year, however, SDS-PAGE is not sensitive enough to distinguish phenotypically different genotypes.
- Electrophoretic analysis of seed storage is a helpful tool to discriminate quinoa varieties as a first step in evaluating quinoa genetic resources.

ACKNOWLEDGEMENT

This work was financed by project by the Ministry of Agriculture of the Czech Republic (No. RO0418) and by the Internal Grant Agency of Faculty of Tropical AgriSciences, Czech University of Life Sciences Prague IGA (Project No. 20213114) Partially funded Subsidy Programme – the National Programme for the Conservation and Use of Plant Genetic Resources and Agrobiodiversity (No. 6.2.5/51834/2017-MZE-17253).

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