

Identification and Characterization of High-Protein Oat Lines from a Mutagenized Oat Population

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Background

Oat (*Avena sativa* L) seeds contain the highest proportion of globular proteins of all cereals. An oat with protein content of 20% or higher would have great potential as an alternative, vegetative protein source and as ingredients in various food products.

Objectives

- * To identify high protein oat lines from a mutagenized oat population
- * To characterize proteins patterns in high protein lines using SDS-PAGE
- * To quantify macromolecules like total dietary fiber (TDF) and β -glucans in the lines with a high protein content
- * To investigate the stability of the high protein character in the field
- * To study inheritance, segregation patterns and stability of the high protein character by crossings

Methods

Total protein levels in seeds from 1050 lines from a mutagenized oat population were determined by an elemental particle analyzer. Total Dietary Fiber was calculated using a gravimetric method and β -glucans levels were determined by a modified Megazyme method.

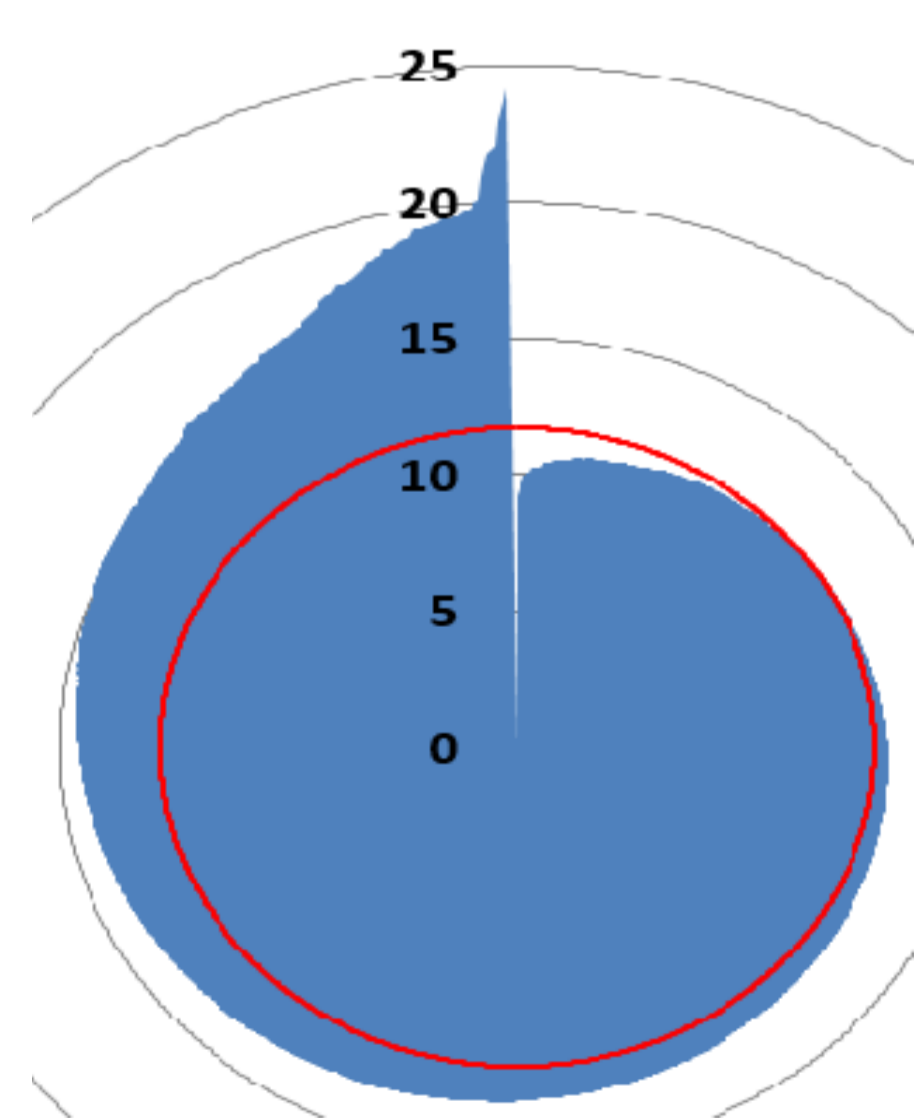


Fig. 1 screening of 1,050 randomly picked lines from the mutagenized oat population. The chart shows the total protein content in the assayed lines. The red circle indicates the protein level of the Belinda reference (11,7%). The data is ordered from the lowest to the highest values.

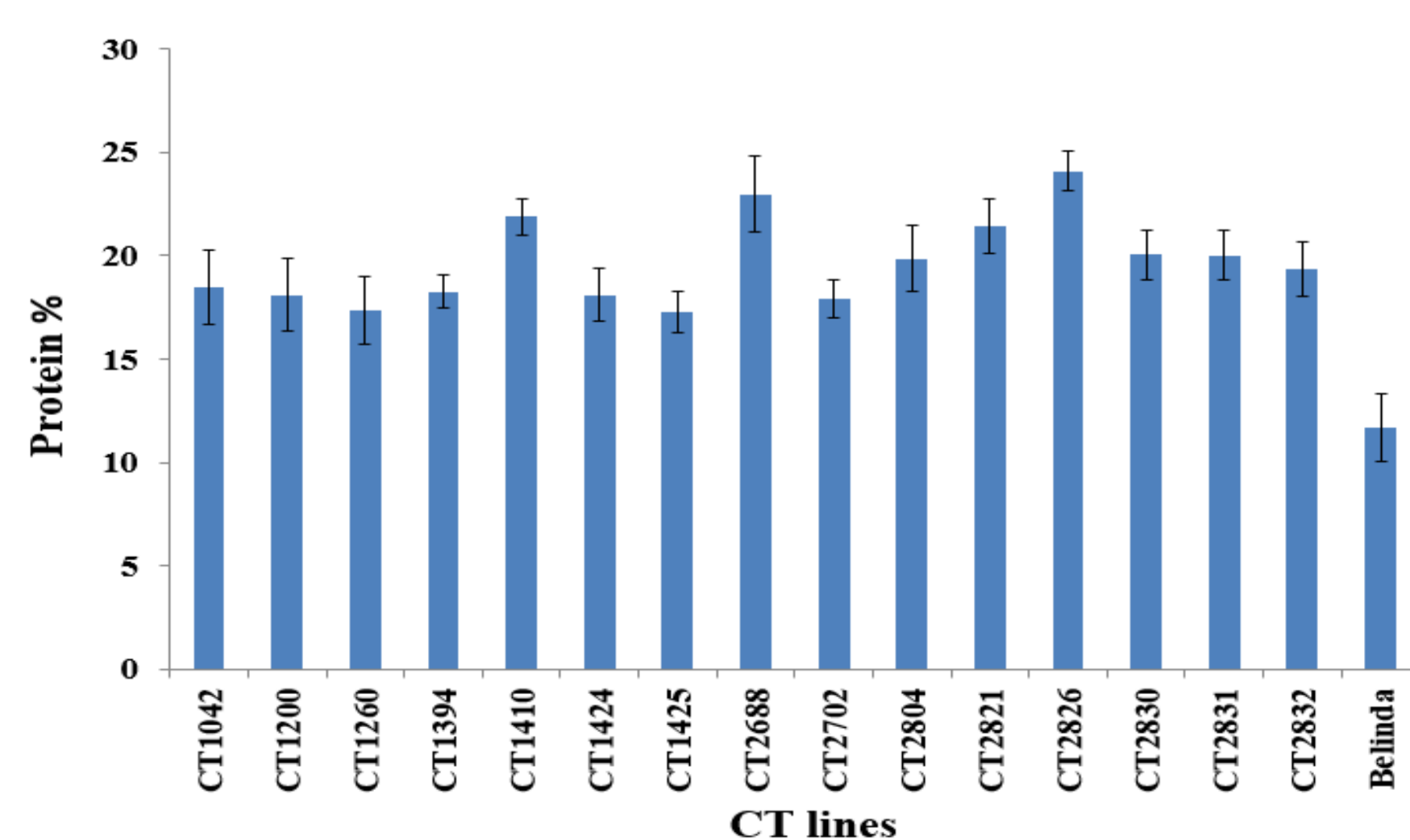


Fig. 2. Average protein content in the highest 15 lines. Each blue column represents the average protein content in 10 individual seeds from the indicated CT-line and the control variety Belinda. The error bars represent standard deviation values between the different seeds from the same CT-line (n=10).

Results

The protein levels in the investigated lines varied from ca 2-24% (Fig 1) and 15 lines had 18% or higher (Fig. 2). As a comparison, the original Belinda variety from which the mutagenized population was derived has ca 12% protein. SDS-PAGE showed that the distribution of albumins, globulins and prolamins were different in the different lines (Fig. 3). After crossing to Belinda, protein levels in ten individual F2 seeds from each of the 15 high protein lines were determined. This confirmed the high protein level but also showed that in some lines the high protein trait was segregating (Fig.4)

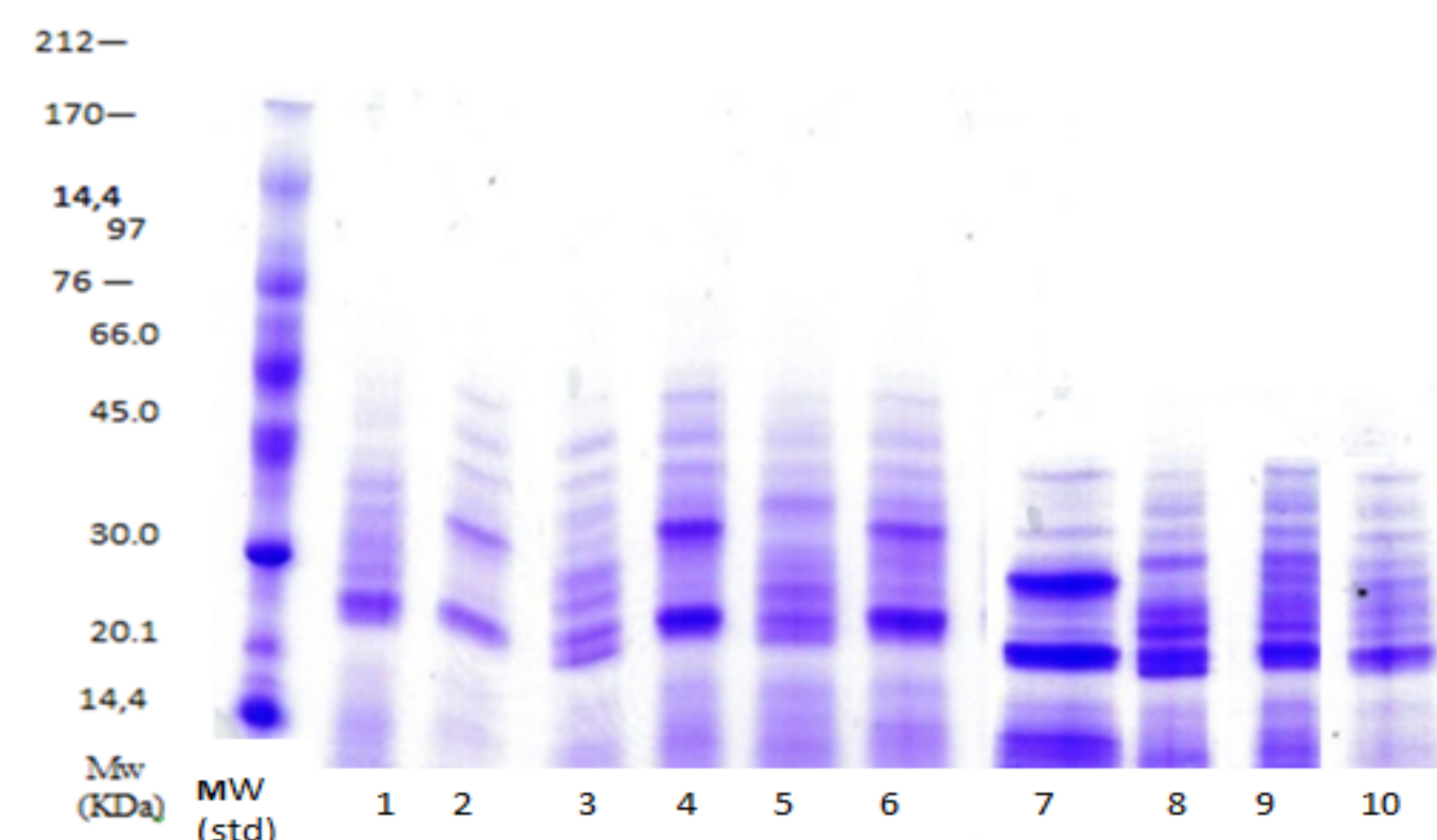


Fig.3. SDS-PAGE of chosen high-protein oat lines. MW indicate molecular weight standards. Lane 1, Belinda; lane 2, CT2826; lane 3, CT2821; lane 4, CT2830; lane 5, CT2831, lane 6, CT2688, lane 7, CT1410; lane 8, CT2804; lane9, CT2832; lane 10, CT1042

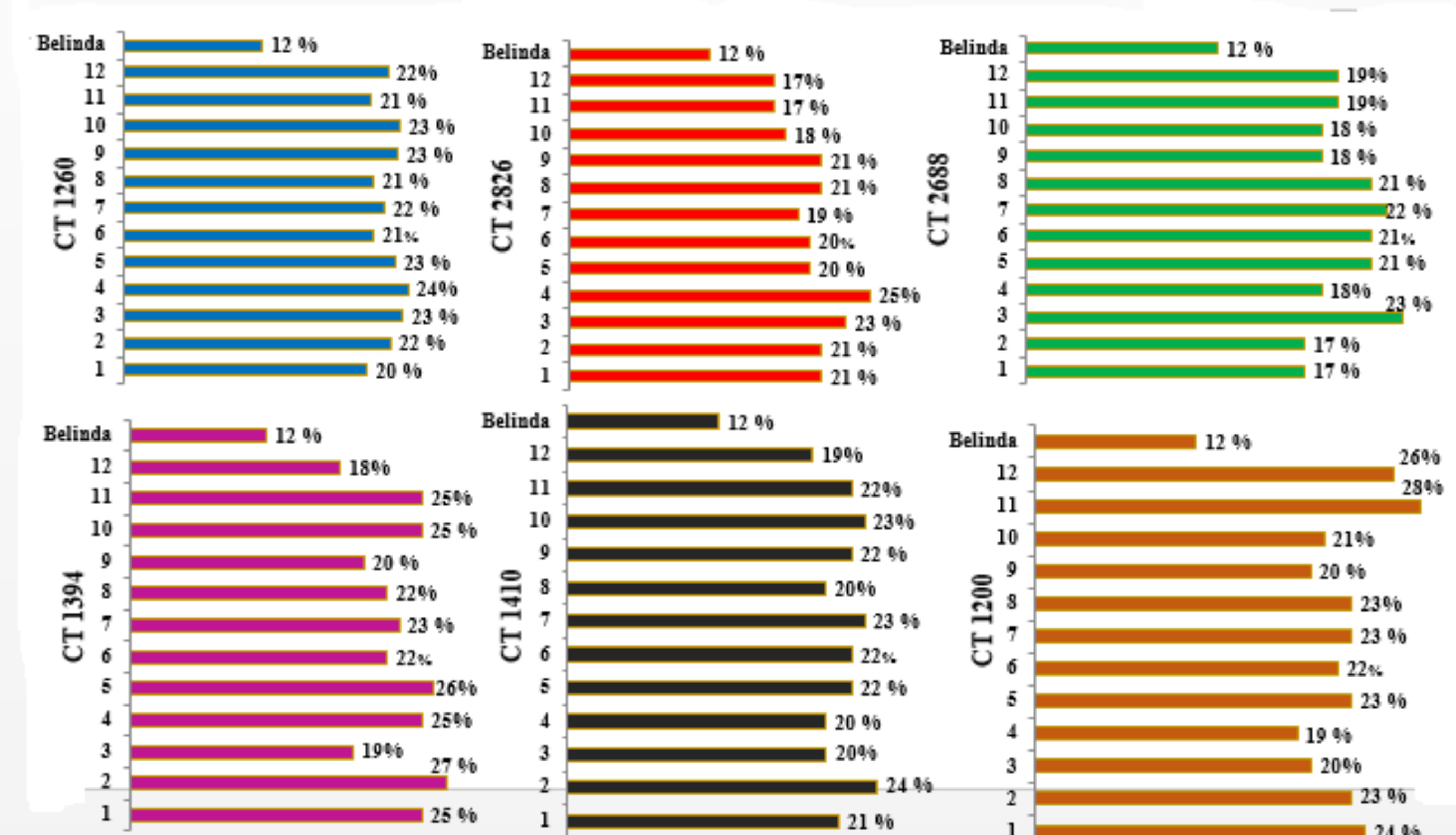


Figure. 4. Protein levels in F2 seeds after crossing with Belinda. After crossing, the F1 seeds were germinated in the greenhouse, plants raised and allowed to self-pollinate. Total protein of individual F2 offspring seeds was determined using an elemental particle analyser

Conclusions

We show here that it will be possible to develop oat varieties with protein levels of 20% or higher. Such lines will be very important in the strive to meet the consumers need for high-protein oat products that still are rich in β -glucan. They will also provide a serious vegetative protein alternative to for example pea, beans and soy bean.