A major gene for grain cadmium accumulation in oat

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INTRODUCTION

Cadmium is a risk factor in cereal crops due to its high toxicity and accumulation in the body, particularly to liver and kidneys, with associated osteoporosis and cancer. Crop plants uptake Cd from soil as a trace of fertilizers. Oat (*Avena sativa* L.) is widely used in baby foods and also adult consumption is increasing due to reduction of the risk of heart disease caused by β-glucan. The Cd level in plants is directly correlated with that in the soil, but is also affected by genetic factors.

MATERIALS AND METHODS

A population of 150 F_2 plants was derived from a cross between two spring oat individuals, one from cv. Aslak (Boreal Plant Breeding Ltd, Finland) and the other from cv. Salo (Svalöf-Weibull AB, Sweden). The parent Salo was known to have the tendency to accumulate Cd in the field (1). Cadmium accumulation to the grains of the F2 individuals was tested by the developed Cd feeding pot test in the greenhouse (Fig 1.). Cadmium was tested by inductively coupled plasma mass spectrometry (ICP-MS) method. Bulked-segregant analysis (3) was used to find PCR based markers linked to Cd accumulation. MAPMAKER 3.0 software (2) was used for determining linkages between markers. The QTL (quantitative trait locus) affecting Cd accumulation was localized using MAPMAKER/QTL 1.1.

Fig. 1. A preliminary experiment of cadmium accumulation into the oat individuals in the Cd-feeding pot test in the greenhouse

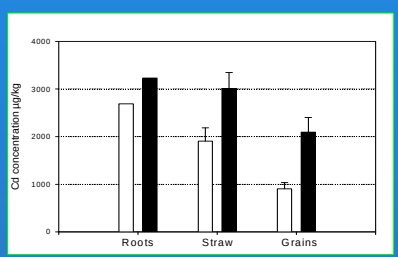

Fig. 2. Cd concentration of roots, straw and grains in Aslak (□) and Salo (■) after Cd feeding pot test. Means with standard error bars, except in roots where no replicates existed.

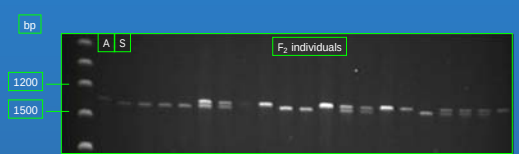

Fig. 4. Codominant SCAR marker AF20. A=Aslak, S=Salo

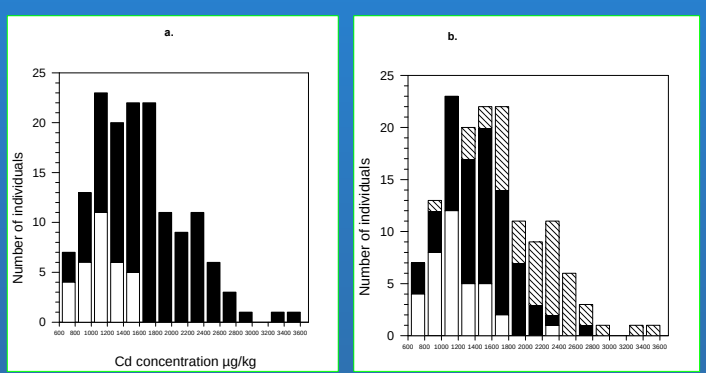

Fig. 3. Grain Cd concentration in the F_2 population based on markers SCAR AF20 (a) and SCAR AF15 (b). Marker genotypes are presented as fills in the columns: □ = homozygotes for Aslak allele, hatched = homozygotes for Salo allele, ■ = heterozygotes (SCAR AF20) or homo- and heterozygotes (SCAR AF15) for Salo allele.

RESULTS AND DISCUSSION

The amount of Cd accumulation is presented in Figs. 2 (parents), and 3 (F2 progeny). The distribution fits the hypothesis of single gene inheritance, the allele for low accumulation being dominant.

The parents, Aslak and Salo, were analyzed with 218 RAPD, 31 SRAP, and 337 REMAP primers or primer combinations, of which 78 (36%), 26 (84%), and 73 (22%) produced polymorphisms, respectively. Four markers (two RAPDs, one REMAP, and one SRAP) were analyzed in the F_2 population, and they were found to be statistically highly significantly associated with grain Cd concentration. The markers were converted into SCAR (sequence characterized amplified region) markers. SCAR AF20 (Fig.4) and SCAR AF15 were the best markers owing to their capability to identify homozygotes for the low (Aslak) allele (Fig.3).

The four markers were assigned to one linkage group which exhibited a QTL for grain Cd accumulation (LOD score > 16, the variance-explained ~50 %).

FURTHER PLANS

In future, we intend to identify candidate genes for Cd accumulation by using bioinformatics, genetics, and genomics tools. Our overall goal to understand the mechanisms and key genes responsible for Cd accumulation in oat. Practical goal is to produce molecular markers tightly linked to the gene to enable the marker assisted selection of low-accumulating cultivars in breeding programmes for healthy oat cultivars.

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