

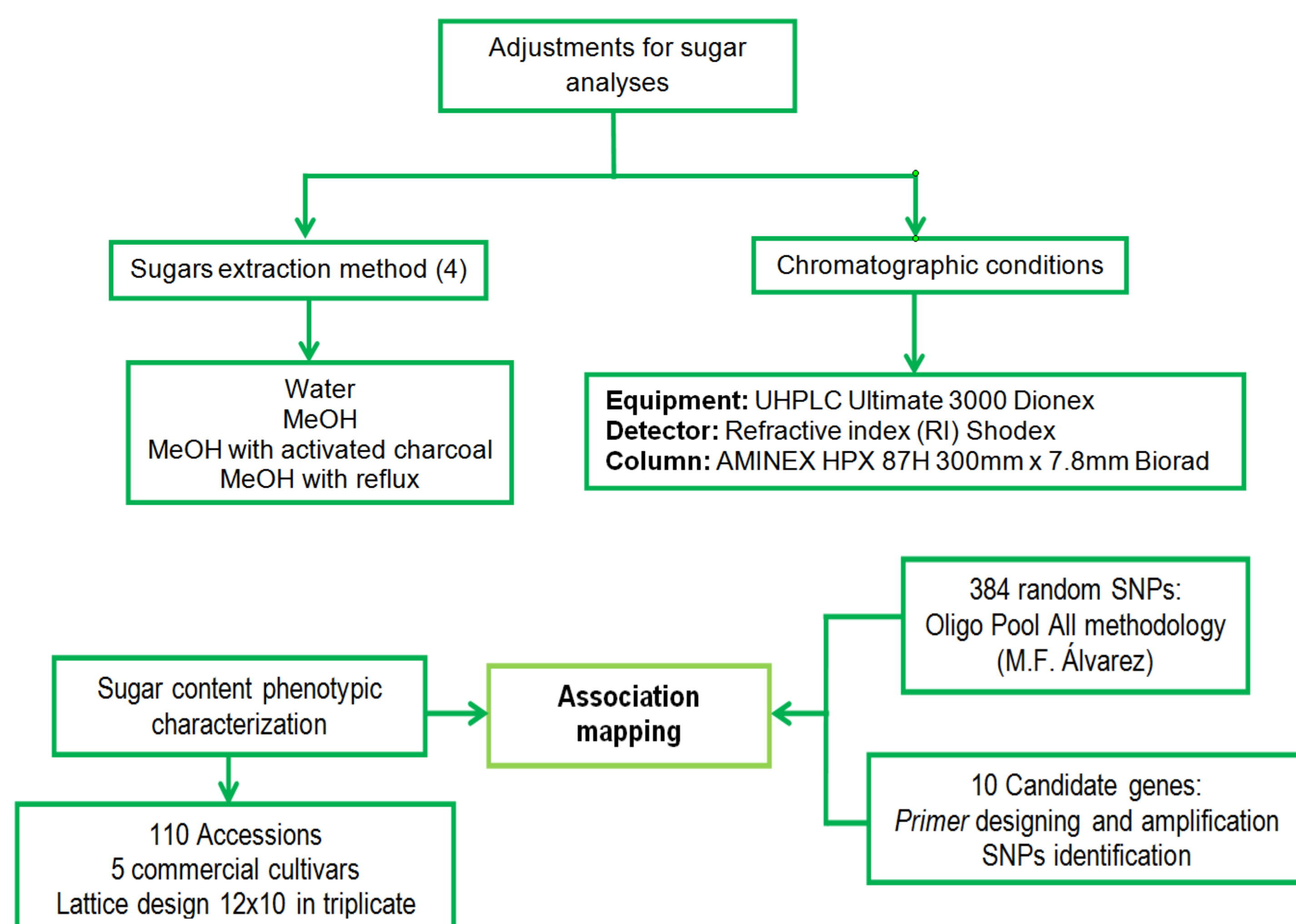
Association genetics of reducing and non-reducing sugar contents with SNP markers in *Solanum tuberosum* group Phureja

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Introduction

Given the changes in worldwide consumption habits, ready to eat products present a high demand which is reflected in the fast growing of potato processing market (Bonilla *et al.*, 2009). Colombia leads the production of the genotypes named "Egg Yolk", which belong to the cultivated group Phureja and present outstanding organoleptic properties. In the present, there are not Phureja cultivars suitable for chip processing because of high levels of reducing sugars (glucose and fructose) in the tubers (Núñez, 2011). During frying process, reducing sugars react at high temperatures with free amino acids causing dark pigments and off-flavours that reduce severely chip quality (van Eck, 2007). Association mapping is a strategy to study the molecular basis of complex traits such as chip color, which is directly related with reducing sugar contents. The identification of genomic regions associated with trait variability is the first step in the development of diagnostic molecular markers that can be used by breeders in processes of marker assisted selection. The main purpose of this research is to establish the genetic association of reducing and non-reducing sugar contents and SNPs markers in a natural population of *Solanum tuberosum* group Phureja

Material and methods



Results

Mix of sucrose, glucose and fructose standards as well as extracts from two Phureja genotypes, have been used to perform the adjustments of chromatographic conditions. A mix of standards of 400 ppm is shown in Figure 1 where resolution and efficiency of the method are evident. When a sample was analyzed (Figure 2), it was found an extra peak corresponding to citric acid. It is necessary to still perform some other adjustments in the chromatographic conditions as it is evident the presence of a shoulder in the fructose peak, by now is hypothesized that the shoulder corresponds to malic acid as it coelutes with fructose using an initial movil phase of sulfuric acid 8 mM. Further analyses are needed to confirm the identity of this component. Additionally, four sugar extraction methods were tested, it was determined that the method using MeOH allows higher extraction levels and its average concentration owns a significant difference with the others methods, as concluded with the Tukey test (Table 1).

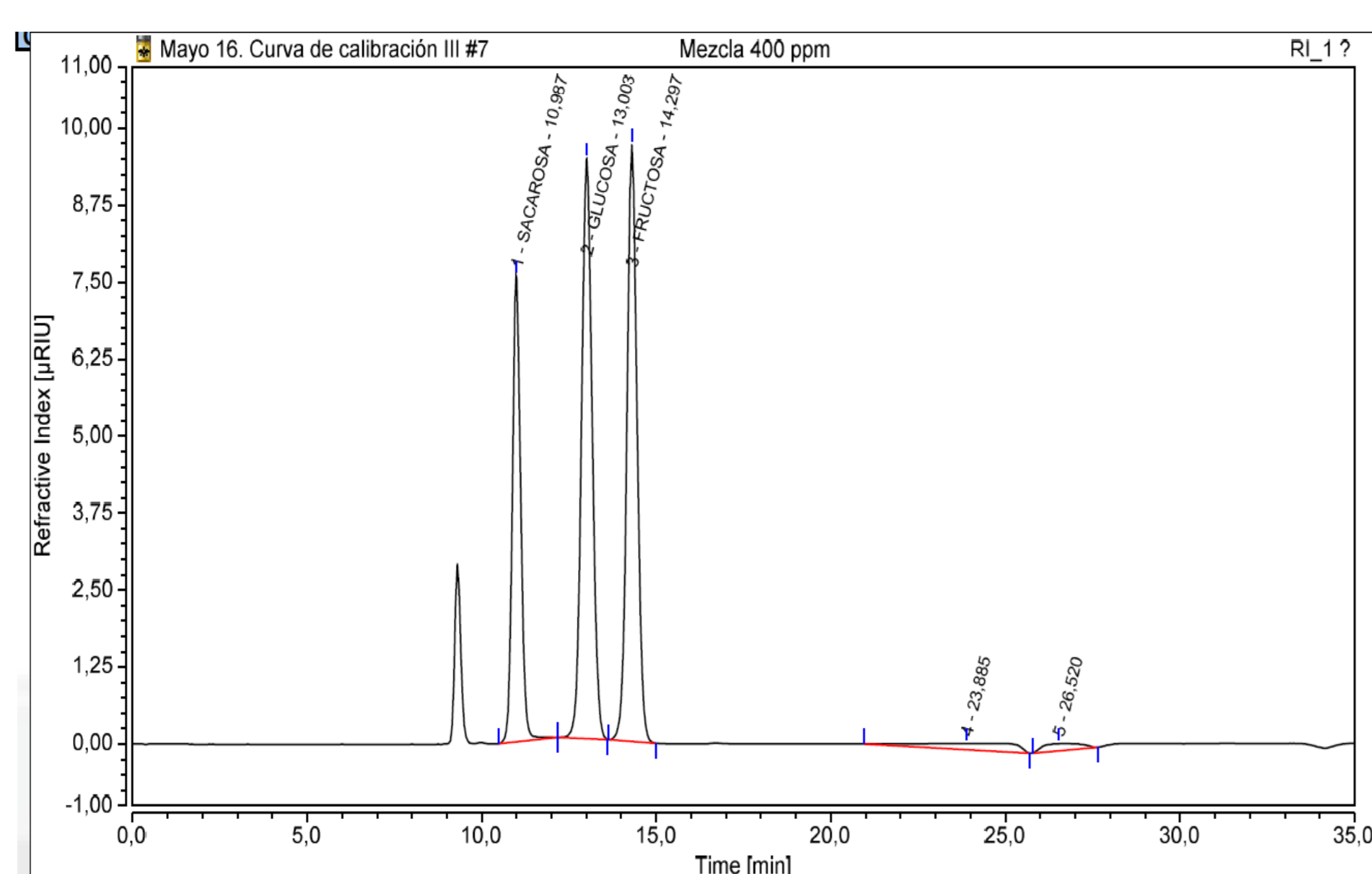


Figure 1. Chromatogram of a standard mix in a concentration of 400 ppm

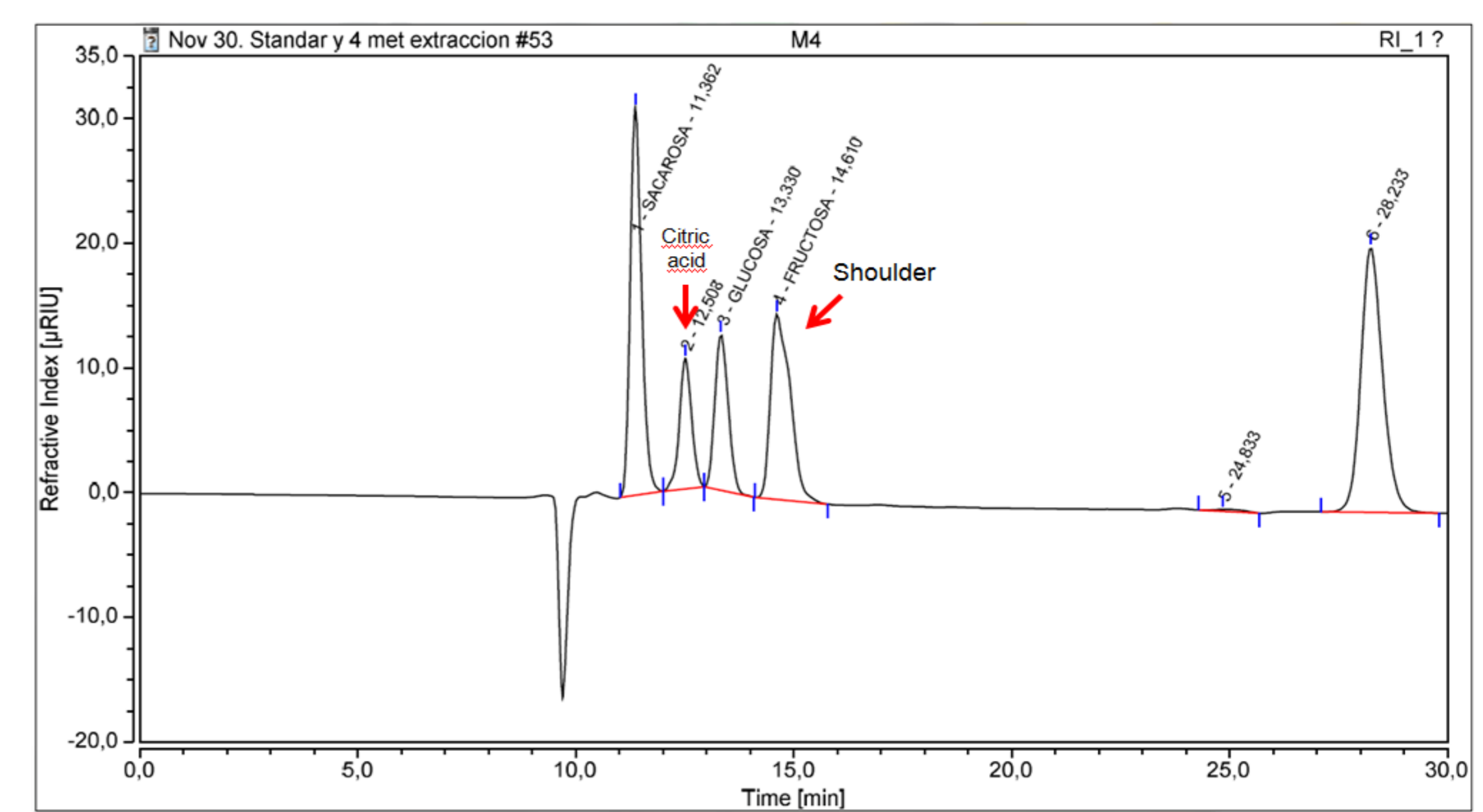


Figure 2. Chromatogram of sugar extract from Galeras cultivar

Table 1. Average concentration of sucrose for each extraction method. Averages with different letters indicates significant differences according to Tukey test ($p < 0.05$).

Method	Average sucrose concentration (ppm)
Water	2566,22 a
MeOH	4925,64 c
MeOH with activated charcoal	3479,68 ab
MeOH with reflux	4322,76 b

With the purpose of performing the association analysis using the candidate gene approach, by now seven candidates genes have been selected for primed designing (Table 2).

Table 2. Candidate genes selected for primer designing, previously reported with association to chip quality and/or sugar contents in potato

Candidate gene	Function	Chromosome
<i>InvGE</i>	Apoplatic invertase	IX
<i>Pain-1</i>	Vacuolar acid invertase	III
<i>Stp23</i>	Plastidic starch phosphorylase	III
<i>StpL</i>	Plastidic starch phosphorylase	V
<i>AGPaseS-a</i>	ADP-glucose pyrophosphorylase	I
<i>Sssl</i>	Soluble starch synthase	III
<i>GWD</i>	Glucan-water dikinase	V

References