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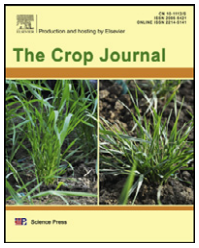

A genetic linkage map of hexaploid naked oat constructed with SSR markers

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ABSTRACT

Naked oat is a unique health food crop in China. Using 202 F_2 individuals derived from a hybrid between the variety 578 and the landrace Sanfensan, we constructed a genetic linkage map consisting of 22 linkage groups covering 2070.50 cM and including 208 simple sequence repeat (SSR) markers. The minimum distance between adjacent markers was 0.01 cM and the average was 9.95 cM. Each linkage group contained 2–22 markers. The largest linkage group covered 174.40 cM and the shortest one covered 36.80 cM, with an average of 94.11 cM. Thirty-six markers (17.3%) showing distorted segregation were distributed across linkage groups LG5 to LG22. This map complements published oat genetic maps and is applicable for quantitative trait locus analysis, gene cloning and molecular marker-assisted selection.

1. Introduction

Naked oat (*Avena nuda* L., AACCDD, $2n = 21$, $x = 7$) is an important health food crop characterized by high protein and β-glucan contents [1,2]. Oats are the basis of various food products including oatmeal, oat milk, and oat chocolate. Oats also serve as feed in some regions. In recent years, molecular marker-based genetic maps have been developed in diploid [3,4], tetraploid [5], and hexaploid [6–14] oats, based primarily on RFLP, AFLP, and DArT markers.

Following the first genetic linkage map of Kanota × Ogle (KO) published in 1995 [6], there have been continued efforts to increase the density of the map with various kinds and numbers of markers. The most comprehensive map of hexaploid hulled oat with 1166 markers covers 1890 cM in the latest reports [7,8,12]. Several other mapping populations were developed from either Kanota or Ogle to enrich the linkage maps, such as the KM (Kanona × Marine), OT (Olge × TAM) and OM (Olge × MAM) maps which cover 736–2049 cM [8–10]. Other mapping populations were developed from Terra × Marion, MN841801-1 × Noble-2 and UFRGS7 × UFRGS910906 [13,15,16]. The first doubled haploid (DH) population used to construct a genetic linkage map in oat was produced in 2008 [14]. The map was improved by increasing the number of markers from 625 to 1058, and eventually covered 1688 cM [17]. More and new kinds of markers, such as SNPs, were used in constructing more recent genetic maps [18,19]. However, the map is still lacking in SSR markers. In this study, our aim was to use a new mapping population of 202 F_2 individuals from a cross of the naked variety 578 and the landrace Sanfensan to

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construct a genetic linkage map based on SSR markers. Our objective was to produce a genetic reference map in a Chinese hexaploid naked oat population.

2. Materials and methods

2.1. Establishing a mapping population

Naked oat variety 578 (large grain) from Bashang, Hebei Province, as male parent was crossed with the landrace Sanfensan (small grain) from Datong, Shanxi, China in 2009. The F_1 was grown in 2010 and an F_2 mapping population containing 202 individuals was generated in 2011. The population showed clear segregation for agronomic traits, particularly grain size.

2.2. Sources of simple sequence repeat (SSR) primers

A total of 4024 pairs of simple sequence repeat (SSR) primers were selected, of which 3600 pairs were developed in the Minor Crop Laboratory, Institute of Crop Science, Chinese Academy of Agricultural Sciences [18], 200 pairs were based on the hexaploid oat transcriptome [19], 124 pairs were from the literature, and 100 primer pairs were from wheat.

2.3. Screening SSR primers and detecting genotypes by PCR

Genomic DNA was extracted from young leaves of field-grown plants by the CTAB method [20]. The PCR equipment was manufactured by Bio-Rad. In a 20 μL system for PCR amplification, the reaction solution contained 50 ng of DNA,

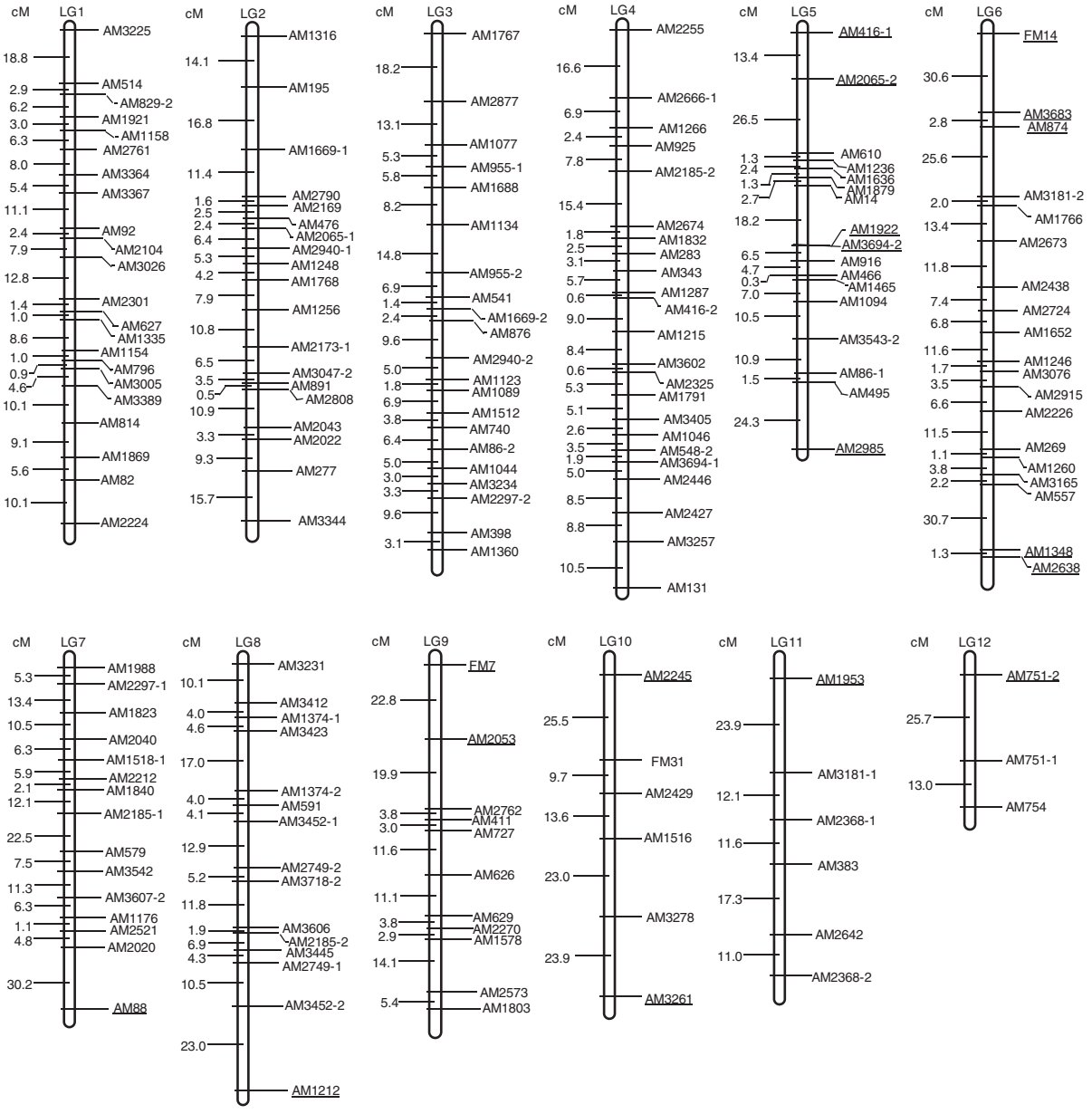

Fig. 1 – Genetic linkage map of naked oat constructed with SSR markers. Markers with distorted segregation are underlined.