Radiation Hybrid Mapping: High resolution RH maps of D-genome chromosomes of hexaploid wheat

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Radiation Hybrid (RH) mapping is an efficient physical mapping method as it does not rely on meiotic recombination. It offers a unique opportunity to solve the recombination and map resolution based issues of genetic mapping, for developing high resolution physical maps of wheat chromosomes. To construct RH based high resolution maps of D-genome chromosomes of hexaploid wheat ‘Chinese Spring’ we developed three independent RH panels: seed irradiation based panel (~2000 RHs), pollen plant panel (~600 RHs) and endosperm panel (1000 RHs). Generated RH panels were tested for low marker retention (25%-50%) and breaks in multiple chromosomes using a set of molecular markers. Average marker retention frequencies of the selected seed irradiation, pollen plant and endosperm panel were 3.1%, 28.5% and 45.8%, respectively. Pollen plant panel and endosperm panel showed breaks in multiple chromosomes, whereas seed panel showed breaks in a few chromosomes only. Set of highly informative lines including pollen plant panel (188) and endosperm panels (94) were selected and used for high throughput genotyping. Ninety-four seed panel lines were also included in the study for the sake of comparison among different panels. We developed a high throughput genotyping system based on NimbleGen array and a total of 37,230 markers (6,330 gene markers + 30,900 repeat junction markers) were included in the final genotyping array. Repeat junction markers were designed from Roche-454 genome sequences of the wheat D-genome progenitor, Aegilops tauschii. These markers were tested and validated on nullisomic and tetrasomic lines of all seven D-genome chromosomes of Chinese Spring. Additionally these markers were mapped on deletion stocks of D-genome chromosomes. Genotyping data returned us ~3,500 markers per chromosome. Analysis of data suggested that an average map resolution of ~450 kb can be achieved using this approach. Since in the present study we focused on RH mapping of D-genome chromosomes of ‘Chinese Spring’ it allowed us to compare our results with Aegilops tauschii physical maps. Detailed analysis on construction of radiation induced physical maps, its application in anchoring of BAC contigs and comparative analysis between Chinese Spring and Ae. tauschii D-genome maps will be presented.