

BIOMASS POTENTIAL OF *POPULUS* IN THE MIDWESTERN UNITED STATES

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The use of *Populus* feedstock for biofuels, bioenergy, and bioproducts is becoming economically feasible as global fossil fuel prices increase. Maximizing biomass production from *Populus* plantations deployed across regional landscapes largely depends on recognizing and evaluating genotype × environment interactions, given broad genetic variation among *Populus* genotypes at strategic (genomic group) and operational (clone) levels. A network of *Populus* regional field tests was established in the Midwest in 1995, 1997, and 2000 to assess productivity of 190 clones grown at Westport, MN (45.7 °N, 95.2 °W), Waseca, MN (only 2000; 44.1 °N, 93.5 °W), Arlington, WI (43.3 °N, 89.4 °W), and Ames, IA (42.0 °N, 93.6 °W). We evaluated biomass production potential of these genotypes throughout plantation development and identified specific clones with yield substantially greater than current commercial controls (Eugenei, NM6). Biomass production of the best six clones in Ames ranged from 1.9 to 2.4 (4 yrs), 5.0 to 9.3 (7 yrs), and 6.4 to 10.9 tons ac⁻¹ yr⁻¹ (9 yrs), while ranges at Arlington were 2.3 to 3.2 (3 yrs), 6.6 to 9.3 (6 yrs), and 7.2 to 9.4 tons ac⁻¹ yr⁻¹ (8 yrs). Biomass of the best six clones at Westport ranged from 1.0 to 1.7 (5 yrs), 3.6 to 4.5 (8 yrs), and 4.0 to 5.0 tons ac⁻¹ yr⁻¹ (10 yrs), while that at Waseca ranged from 4.6 to 6.0 tons ac⁻¹ yr⁻¹ (7 yrs). The three best clones had 1.2 to 2.7 times greater biomass than controls throughout development of the 1995 Westport, 1997 Westport, and 2000 Waseca plantings. Genotype × environment interactions governed biomass production, with clone-mean rank correlations across sites ranging from 0.29 to 0.81. We identified both generalist genotypes (202.37, 5910100, D105, D124, NC14105) with elevated biomass across the region and specialist genotypes (220-5, 7300501, 80X01038, Crandon, NC13563) with exceptional biomass at specific locations.

KEY WORDS: hybrid poplar, tree improvement, productivity, clonal rank, genotype × environment interactions

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