Sodium and Chloride Concentration in Leaf, Woody, and Root Tissue of *Populus* Irrigated with Landfill Leachate

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There are few reports in the literature about the response of different genomic groups and clones of *Populus* to elevated levels of sodium (Na^+) and chloride (Cl^-). In addition, there is an increasing need to understand the variation in salt tolerance and tissue composition of such genotypes over multiple growing seasons in field settings. Therefore, field trials of a mixture of genotypes representing numerous genomic groups offers an opportunity to identify and select clones that exhibit broad variation in tolerance to salt environments. Such information is important for making recommendations to resource managers that will help to increase the successful utilization of landfill leachate as a fertilization and irrigation source for species and interspecific hybrids of the genus *Populus*. We irrigated eight *Populus* clones (NC13460, NC14018, NC14104, NC14106, DM115, DN5, NM2, NM6) with fertilized well water (control) (N, P, K) or municipal solid waste landfill leachate weekly during 2005 and 2006 in Rhinelander, Wisconsin, USA (45.6 °N, 89.4 °W). During Aug. 2006, we tested for differences in total Na^+ and Cl^- concentration in preplanting and harvest soils, and in leaf, woody (stems + branches), and root tissue. The leachate-irrigated soils at harvest had the greatest Na^+ ($P < 0.0001$) and Cl^- ($P = 0.0013$) levels. The irrigation × clone × tissue interaction influenced the distribution of Na^+ ($P = 0.0240$) and Cl^- ($P = 0.0073$). Clones exhibited elevated total tree Cl^- concentration and increased biomass (NC14104, NM2, NM6), elevated Cl^- and decreased biomass (NC14018, NC14106, DM115), or mid levels of Cl^- and biomass (NC13460, DN5). Tissue concentrations with leachate were 17 (Na^+) and four (Cl^-) times greater than water. Sodium and Cl^- levels were greatest in roots and leaves, respectively. The broad variation among genotypes for tissue Na^+ and Cl^- concentrations substantiated the need for extensive genotypic screening before deployment.

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