

Origins and Diversity of Rush Skeletonweed (*Chondrilla juncea*) from Three Continents

J. Gaskin¹, C. L. Kinter², M. Schwarzländer³, G. P. Markin⁴,
S. Novak⁵ and J. F. Smith⁵

¹USDA Agricultural Research Service, Northern Plains Agricultural Research Laboratory, 1500 N. Central Ave., Sidney, MT 59270 USA john.gaskin@ars.usda.gov

²Idaho Department of Fish and Game, Idaho Natural Heritage Program, 600 South Walnut, Boise, ID 83707 USA

³University of Idaho, Department of Plant, Soil and Entomological Sciences, Moscow, ID 83844 USA

⁴USDA Forest Service, Rocky Mountain Research Station, 1648 S. 7th Ave., Bozeman, MT 59717 USA

⁵Department of Biological Sciences, Boise State University Boise, ID 83725 USA

Abstract

Rush skeletonweed (*Chondrilla juncea* L.) is an invasive apomictic perennial plant in Australia, South- and North America, accidentally introduced from Eurasia, which shows differential resistance/tolerance to some herbicides and classical biological control agents. Rush skeletonweed biotypes have been locally described using morphology, phenology, isozyme patterns, and resistance to control agents, but studies comparing invasions on different continents and determining exact origins of invasive genotypes do not exist or are lacking in detail. Commonly available molecular tools and bulk analysis capacity now make it possible to determine genetic diversity within invasions and their origins. We investigated over 1000 plants from three invaded continents using highly variable AFLP (Amplified Fragment Length Polymorphism) markers, and found 13 distinct genotypes (three from Australia, three from Argentina, and seven from North America). No genotypes were shared between continents. Certain regions in North America, such as California, contain only one genotype of the weed. We then investigated over 1000 plants from the native Eurasian range to determine, as accurately as possible, origins of the invasive genotypes, including those that are currently resistant to strains of rust (*Puccinia chondrillina* Bubak & Syd.) used in biological control programs. This information can be used to screen for pathogens and other agents that will not be resisted or tolerated by certain rush skeletonweed genotypes. Understanding global intraspecific diversity and exact origins can improve management of differentially-resistant/tolerant weed biotypes, enhance efficacy of future agent selection, and increase cooperation between invaded regions.