

“A high-density molecular genetic map around the weaver locus” by J.H. Millonig, K.J. Millen, M.E. Hatten.

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At the time our manuscript was prepared, we were unaware that the *Girk2* gene had already been mapped in *wv* mice relative to the cerebellar and ataxia phenotypes (Mjaatvedt et al., 1995). In that study, the candidate C → T mutation in *Girk2* was shown to be non-recombinant with the *wv* phenotype on 104 backcross and 124 intercross animals (352 meioses) and the gene was localized on a physical map that resolves the positions of several non-recombinant markers used in our study. Our work confirms and extends the demonstration of tight linkage between *wv* and the *Girk2* gene by mapping a *wv*-specific RFLP, detected with a *Girk2* probe, relative to the cerebellar phenotype. Our study analyzes 264 N2 mice, bringing to 626 the total number of meioses showing no recombination. We regret our oversight with regard to the study of Mjaatvedt et al.

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Mjaatvedt, A.E.,* D.E. Cabin,* S.E. Cole, L.J. Long, G. Breitwieser and R.H. Reeves. 1995. Assessment of a mutation in the H5 domain of *Girk2* as a candidate for the weaver mutation. *Genome Research* 5:453–463.

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