# A forward genetic screen identifies modifiers of a voltage- and calcium-activated $\mathrm{K}^{+}$channel in left-right neuronal asymmetry 

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The developing nervous system generates a large diversity of cell types with distinct patterns of gene expression and functions. One way to establish neuronal diversity is to specify neuronal subtypes across the left-right axis. The C. elegans left and right AWC olfactory neurons communicate to specify asymmetric subtypes, AWC ${ }^{\mathrm{OFF}}$ and AWC ${ }^{\mathrm{ON}}$. The default AWC ${ }^{\text {OFF }}$ is specified by a $\mathrm{Ca}^{2+}$-regulated kinase cascade that is activated by influx of $\mathrm{Ca}^{2+}$ through the voltage-gated $\mathrm{Ca}^{2+}$ channel UNC-2/UNC-36. Intercellular communication between the two AWC neurons and other neurons through the NSY5/innexin gap junction network antagonizes unc-2/unc-36 $\mathrm{Ca}^{2+}$ signaling in the induced AWC $^{\mathrm{ON}}$ cell. Our recent data suggest that voltage- and calcium-activated SLO BK potassium channels slo-1 and slo-2 acts redundantly downstream of nsy-5 to inhibit unc$2 / u n c-36 \mathrm{Ca}^{2+}$ signaling in the specification of AWC ${ }^{\mathrm{ON}}$. To identify the genes required for slo-1 function in inhibiting unc-2/unc-36 $\mathrm{Ca}^{2+}$ signaling for promoting AWC ${ }^{\mathrm{ON}}$, we performed a non-biased forward genetic screen to isolate mok (modifier of $\underline{\mathrm{K}}^{+}$channel) mutants that suppress the slo- $1(g f) 2-\mathrm{AWC}^{\mathrm{ON}}$-neuron phenotype. From about 6,000 genomes screened, we identified 16 new mutants that define genes required for slo-1 function in promoting $\mathrm{AWC}^{\mathrm{ON}}$. The molecular lesions of all these mok mutants were identified using one-step whole genome sequencing and SNP mapping. Molecular characterization of these mok genes will begin to address how gap junction-mediated transient signaling coordinates long-term stochastic neuronal subtypes through downstream $\mathrm{Ca}^{2+}$-activated $\mathrm{K}^{+}$channels and MOK molecules. Strategies of forward genetic screens and one-step whole genome sequencing/SNP mapping will be presented in the seminar and workshop.

