The overall goal of this project is to test the biopsychosocial model of childhood disruptive behavior by examining longitudinal trajectories of conduct problems (CP) and symptoms of Attention Deficit Hyperactivity Disorder (ADHD) in school-age children and adolescents. Biopsychosocial models have been proposed to explain development of childhood disruptive disorders associated with ADHD symptoms and CP (Dodge & Petit, 2003), and research has identified both shared environmental and genetic risk factors for these disruptive behavior symptoms (Waschbusch, 2002). However, while ADHD and CP are commonly comorbid, they are not universally comorbid, and often follow a sequential, overlapping pattern whereby early ADHD symptoms precede emergence of later comorbid CP (Lahey & Loeber, 1997). Distinctions among unique and joint developmental trajectories of these symptom clusters may relate to previously identified correlates, including age and puberty, environment (e.g. family stress, peer influences), and genetic risk.

The biopsychosocial model assumes that both biological predisposition (i.e. genetic risk) and environmental factors contribute to disruptive behavior outcomes through additive, interactive, and transactional associations, and that the predictive effects of these associations may vary across development. However, despite the appeal and general acceptance of the biopsychosocial model to explain the emergence of ADHD and CP, to date this theory has not been rigorously tested at multiple time points, across both sexes, and with the inclusion of a priori identified genotypes as moderators. Specific candidate genes associated with dopaminergic and serotonergic neural pathways have been repeatedly identified in studies of disruptive behaviors. In particular, interactions between childhood adversity and the low-activity Monoamine oxidase A (MAOA) and promoter region tandem-repeat on dopamine D4 receptor (DRD4) genotypes have been associated with higher levels of disruptive behaviors (e.g., Kim-Cohen et al., 2006; Martel et al., 2011). Similarly, the valene/valene polymorphism at codon 158 on the catechol O-methyltransferase (COMT) gene has been associated with higher levels of CP in children with ADHD (Casi et al., 2008). However, no single gene has emerged as necessary or sufficient to cause disruptive behavior disorders, and molecular genetic studies examining single genes are often limited by low power and Type 1 error. Thus, in order to test these important developmental and moderating processes across time, it is necessary that 1) this be examined in a representative, community sample of youth covering developmentally salient ages; 2) HI, CP and environmental stress be repeatedly tested in a multi-method, multi-wave design; and 3) the research should aim to replicate previously identified, specific g x e findings for disruptive behavioral outcomes.

The proposed study intends to fill several significant gaps in the literature by conducting secondary analyses of an ongoing, 8-wave, prospective study following 3rd, 6th and 9th grade youths (N=682) and a parent over 21 months (Hankin, Jenness, Abela, & Smolen, 2011). The parent study was originally designed to test development of depression in youth, but contains ample data to address my aims.

**Aim 1.** Test whether the severity of ADHD in school age youth potentiates the emergence of CP more strongly than CP potentiates the emergence of ADHD. **Hypothesis 1a:** Higher initial levels of ADHD will be associated with higher intercept and slope of CP. **Hypothesis 1b:** ADHD severity will predict subsequent changes in CP, such that ADHD at Time X will predict severity of CP at Time X+1. **Hypothesis 1c:** Development will moderate the predictive effect of ADHD on CP, with the magnitude of association between these two behavioral problems declining with increased age.

**Aim 2.** Test the effects of environmental risk on patterns of disruptive behavior development. **Hypothesis 2a:** Lower socioeconomic status and inconsistent parenting will be associated with higher intercepts and slopes of CP and ADHD. **Hypothesis 2b:** Stressful life events in the family, peer and school domains will predict subsequent scores of CP and ADHD, such that stress at Time X will predict severities of both ADHD and CP at Time X+1, over and above the effects specified in Hypothesis 2a. **Hypothesis 2c:** The predictive strengths of the stressors in Hypothesis 2b will demonstrate a domain by age interaction, such that the effect of family stressors will decline over age and the effects of peer and school stressors will increase.

**Aim 3.** Test the main and moderating effects of a priori theoretically specified candidate genes on CP and ADHD. **Hypothesis 3a:** Genetic risk will demonstrate main effects on the intercept and slope for development of both ADHD and CP. **Hypothesis 3b:** Genetic risk will increase the strength of behavioral and environmental predictors on disruptive behavior outcomes. **Hypothesis 3c:** Gene x environment interactions will demonstrate developmental and environmental specificity, with MAOA and DRD4 showing interactions with family stress in elementary school, and COMT showing the strongest interactions with peer and school stress during middle and high school ages.