Determining occludin tight junction protein function in fish gill epithelia: *in vivo* and *in vitro* approaches

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In vertebrate epithelia, tight junctions (TJs) form the apical-most component of the cell-cell junctional complex and establish a semi-permeable paracellular barrier that limits the movement of water and solutes between cells. Although physiologists have long known about TJs in the gills of fishes and it is widely accepted that these play a valuable role in regulating water and salt homeostasis, little is known about the dynamics and molecular 'machinery' of the TJ complex in this group. Recent studies identified the transmembrane TJ protein occludin as a component of the TJ complex in fishes, and based on *in vivo* studies (e.g. utilizing ion-poor water exposure to alter hydromineral status), occludin was proposed to play a role in regulating paracellular permeability across gill epithelia. Complementary experimentation utilizing *in vitro* gill models provided additional support for a 'tightening' role for occludin in the gill. However, species-specific differences were noted. Furthermore, preliminary evidence using siRNA 'knockdown' of the occludin gene in a cultured gill model suggests that the extent of the occludin 'tightening' effect may rely upon the abundance of other TJ proteins (e.g. claudins) within the TJ complex of the gill epithelium.