On the origin of the molecular mechanism for protein halophilic adaptation

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To survive in high ionic strength environments, nature has shaped halophilic proteins with a characteristic surface aminoacid composition; acidic residues are found in high proportion whereas lysines are often reduced in number [1,2]. These extremophiles become highly acidic proteins but the molecular mechanism for halophilicity, defined as the dependence of protein stability or enzyme activity with salt concentration, is poorly understood. In the present study we have employed circular dichroism and NMR spectroscopy to explore the influence of surface composition in halophilic adaptation. To that end, the involved aminoacids (lysine, aspartic and glutamic acid) have been exchanged by mutagenesis in the IGg binding domain of the protein L (ProtL). Such replacements have altered the halophilic character of the protein from zero dependence (wild type) to reach the strict halophile regime (all lysine replaced). This acquired salt dependence of ProtL stability is unrelated to the protein charge and correlates with the hydrophobic effect contribution arising from the protein surface. In a second set of modifications, the aspartic and glutamic acid residue composition of the domain 1A of the halophilic ligase N (1ALigN) have been modified in a similar way, but his time with no overall charge modification. Halophilicity is increased when the surface hydrophobic area is reduced. Our results provide a model to explain the molecular basis of protein halophilic adaptation.

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Support was provided from The Department of Industry, Tourism and Trade of the Government of the Autonomous Community of the Basque Country (Etortek Research Programs 2005 / 2007), from the Innovation Technology Department of the Bizkaia County, from the Ministerio de Ciencia y Tecnología (CTQ2006-09101/BQU) and from the Ramon y Cajal program