

### Comparative Proteome Analysis of *Hansenula polymorpha* DL1 and A16

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Proteomic responses of methylotrophic yeasts (*Hansenula polymorpha* DL1 and A16) to growth medium tuning by carbon source shift were monitored and analyzed through two-dimensional gel electrophoresis. Through comparative proteome analyses, the intracellular proteins showing complex expression patterns were systematically sorted into: 1) proteins that are commonly expressed with comparable high abundance in both strains; 2) strain-specific proteins that are expressed at high level only in a particular strain; 3) strain-specific and methanol-induced proteins that are expressed only in the presence of methanol; and 4) strain-specific and constitutively-expressed proteins that are expressed consistently irrespective of carbon source shift without extreme change in expression level. As a result, DL1 has such distinct metabolic characteristics as enhanced metabolic activities both in glycerol uptake and glyoxylate by-pass cycle, as compared to A16. Our systematic approach to the detailed analysis of proteomic responses will be greatly useful in more completely understanding global physiologies of *H. polymorpha*, as sufficient proteome databases for various methylotrophic yeasts are established further.