JUSTIFICATION

In recent years, significant progress has been made in the development of genomic resources of two model legumes, *Medicago truncatula* (*e.g.*, Schnabel et al. 2003; Gallardo et al. 2003) and *Lotus japonicus* (*e.g.*, Colebatch et al. 2002; Perry et al. 2003), and the major economic legume, soybean (*Glycine max*) (*e.g.*, Shoemaker et al. 2002; Zhu et al. 2003). International efforts are under way, or will soon be, to sequence the entirety or gene-rich regions of these genomes.

There is an opportunity to bring the achievements in the aforementioned model legumes to bear on other food and feed legumes of major economic importance, including cool-season pulses (pea, lentil, chickpea), warm-season food legumes (peanut, common bean), and alfalfa as a forage legume. Each legume presents unique features that could be addressed with genomic resources developed in the model legumes or soybean as well as additional resources to be developed in the crop itself.

POTENTIAL CROSS-LEGUME THEMES FOR GENOMICS RESEARCH

VERSION 08/06/08

The goal of this conference is to forge a common plan with specific objectives for cross-legume genomics research. In recent years, significant progress has been made in the development of genomic resources of two model legumes, *Medicago truncatula* (*e.g.*, Schnabel et al. 2003; Gallardo et al. 2003) and *Lotus japonicus* (*e.g.*, Colebatch et al. 2002; Perry et al. 2003), and the major economic legume, soybean (*Glycine max*) (*e.g.*, Shoemaker et al. 2002; Zhu et al. 2003). International efforts are under way, or will soon be, to sequence the entirety or gene-rich regions of these genomes.

To facilitate a joint effort and funding strategy towards these goals, one or a few biological theme(s) should be identified and elaborated by the legume genomics community. The main criteria we considered in choosing these themes were: 1) The theme(s) should address a phenomenon that is unique (or quasi-unique) to legumes; legumes should have a competitive advantage; or the theme should solve a major issue in legume production or utilization (e.g., human nutrition); 2) The theme(s) should be as broad and inclusive as possible; and 3) The theme(s) should lead to resources that can be used to solve production or utilization issues at the applied level.

Theme 1: Biotic interactions in legumes

The biotic interaction that comes to mind immediately is the Legume-Rhizobium interaction. Significant progress is being made in unraveling the molecular basis of symbiotic nitrogen fixation in certain legumes, principally the two model legumes (Cullimore and Dénarié 2003; Mergaert et al. 2003; Penmetsa et al. 2003; Mitra et al. 2004; Cook 2004). Furthermore, it is now clear there is significant functional overlap with symbioses between legumes and mycorrhizal fungi. However, this progress needs to be translated to other legume species through genomic approaches (Stougaard 2001). Furthermore, although not unique to the family, disease resistance genes (and gene clusters) have been identified in legumes as well and further understanding of the gene clusters can lead to improved disease resistance (Geffroy et al. 1999, 2000; Young 2000; Jeong et al. 2001; Ashfield et al. 2003, 2004). Indeed one fundamental question the remains poorly understood is the extent to which symbiotic and disease resistance pathways are subject to “cross-talk” in legumes.

In contrast with other botanical families, wind-pollinated species are extremely rare in the legumes (Janzen 1989). Many legume species are pollinated by insects, and, although not unique to the legumes, insect pollination is accompanied by adaptations on the part of the plant host such as specific morphological traits and the production of volatile attractants. Morphological traits include specific inflorescences such as racemes and pseudoracemes and a zygomorphic (bilateral) flower symmetry (Endress 2001; Tucker 2003). Floral volatiles have been studied in several species, including and not limited to, alfalfa and clover (Henning et al. 1992; Jacobsen and Christensen 2002; Tava and Pecetti 1997). Iinformation on factors influencing attractiveness to pollinators can improve hybrid seed production systems in legumes and lead to yield increases based on heterosis.

Interestingly, leaf volatiles also play an important in communications with insects, particularly as a defense mechanism by attracting predators of herbivores (Pichersky and Gershenzon 2002), including in lima bean (Arimura et al. 2000) and *Lotus japonicus* (Ozawa et al. 2002). Consideration of the molecular signaling taking place between legumes and Rhizobium, pathogens, pollinators, and herbivores and carnivores, suggest legumes as a model for the study of molecular signaling in general among organisms.

Theme 2: Legume contributions to human nutrition and well-being

Legumes provide the largest source of vegetable protein in human and livestock diets and produce health-promoting secondary compounds that can protect against human cancers, cardiovascular disease and diabetes (Peterson and Dwyer 1998; Kris-Etherton et al. 2002; Bathena and Velasquez 2002; Jenkins et al. 2003; Madar and Stark 2003). Notably, some of these same compounds have important native function in the plant, especially to provide protection against the pathogens and pests and allow molecular communications between the legume hosts and symbionts (See Theme 1; Dixon et al. 2002; Ndakidemi and Dakora 2003). Legume seeds are also rich in dietary, soluble fibers that reduce the blood cholesterol level (Andersen et al. 1984; Gdala 1998; Guillon & Champ 2002). In addition to their antioxidant effects, phenolics also have an antimutagenic effect (González de Mejía et al. 1999; Cardado-Martínez et al. 2002). Legumes also produce phytoestrogens, a weaker version of estrogen. Phytoestrogens (isoflavones), alone or in combination with soybean seed proteins, have been proposed with varying success to alleviate post-menopausal symptoms. They also play a role as antioxidants and have been implicated in the reduction of cancer and cardiovascular disease incidence (Kris-Etherton et al. 2002).

Conversely, certain legumes produce anti-nutritional factors, such as trypsin inhibitors and phytohaemagglutinins (Berger 2003; Gupta 1987). Peanut allergenicity is a widespread and severe problem (Spergel and Fiedler 2001). Genomic approaches, including metabolomics and proteomics, are particularly useful to gain a better understanding of the metabolical pathways involved but also to potentially eliminate some of these anti-nutritional factors. Altogether, some of these secondary compounds are largely restricted to legumes. They are fascinating both because of its importance to human and animal health as well as the insights it can provide into the biochemistry of plants.

Theme 3: Yield potential and heterosis

Potential cereal yields are 2-3 fold higher than those of legumes (Evans 1993). Part of this discrepancy is probably due to trade-offs with legume-specific processes. These include biotic activities such as nitrogen fixation (an energy-intensive process) and mycorrhizal relationships. In addition, high protein (all legumes) and oil levels (some legumes such as soybean and peanut) in seeds also require more metabolic energy than seeds made up mainly of carbohydrates as is the case for cereals. It has also been argued – on theoretical grounds - that the basic plant type of cereals is more effective at building yield than that of legumes because the former has less overlap between the vegetative and reproductive phases (Cohen 1966). The question that is raised is to what extent these trade-offs can be at least partially circumvented and what the molecular and biochemical basis is for such a goal.

One of the possible ways pathways to increased grain yield is the utilization of heterosis (Gepts 1998; Lewers et al. 1998; Pandini et al. 2002). The main obstacle to such strategy is the economic production of hybrid seeds given that many major grain legume species, such as soybean, bean, pea, and peanut, are primarily selfing. Many of these species have close relatives that have higher levels of cross-pollination (e.g., bean: Webster et al. 1977, 1980). This observation suggests that these close relatives could be used as a source of genetic diversity and/or information to increase the level of outcrossing and, thus, the production of hybrid seeds. Because the pollen vectors will likely be insects (bees, bumblebees), increasing the attractiveness of flowers to these insects will play a large role. In this respect, this theme links up with the previous theme as the characterization of signal (volatiles: e.g., Henning et al. 1992, in alfalfa) and reward (nectar) molecules will need to be characterized. Recent research shows that the composition of nectar is more complex than what was previously realized, providing new avenues for research (Carter and Thornburg 2004).